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Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 270181610 residues

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Listing first 1000 summaries

Database :

Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 300	11.6	44.6	20	15	US-10-348-431-68	Sequence 68, Appl	C 373	11.6	44.6	50	17	US-10-131-827-7195	Sequence 7195, Ap
C 301	11.6	44.6	20	15	US-10-289-762-2900	Sequence 2900, Appl	C 374	11.6	44.6	50	17	US-10-335-181-9	Sequence 9, Appl
C 302	11.6	44.6	20	17	US-10-317-253-21	Sequence 21, Appl	C 375	11.4	43.8	20	16	US-10-289-762-3342	Sequence 3342, Ap
303	11.6	44.6	20	17	US-10-317-253-56	Sequence 56, Appl	376	11.4	43.8	21	14	US-10-190-279-26	Sequence 26, Appl
304	11.6	44.6	21	15	US-10-165-099-278	Sequence 278, Appl	C 377	11.4	43.8	21	15	US-10-340-123-9	Sequence 9, Appl

C 378	11.4	43.8	23	9	US-09-216-393-334	Sequence 334, App	C 451	11.4	43.8	50	16	US-10-131-827-477	Sequence 477, App
C 379	11.4	43.8	23	10	US-09-993-312-32	Sequence 32, Appl	C 452	11.4	43.8	50	16	US-10-131-827-2211	Sequence 2211, App
C 380	11.4	43.8	23	15	US-10-321-856-334	Sequence 334, App	C 453	11.4	43.8	50	16	US-10-131-827-3050	Sequence 3050, App
C 381	11.4	43.8	25	14	US-10-098-263B-10173	Sequence 13064, A	C 454	11.4	43.8	50	16	US-10-131-827-3377	Sequence 3377, App
C 382	11.4	43.8	25	15	US-10-098-263B-12237	Sequence 12237, A	C 455	11.4	43.8	50	16	US-10-131-827-3854	Sequence 3854, App
C 383	11.4	43.8	25	15	US-10-098-263B-12237	Sequence 12237, A	C 456	11.4	43.8	50	16	US-10-131-827-6732	Sequence 6732, App
C 384	11.4	43.8	25	15	US-10-098-263B-26218	Sequence 26218, A	C 457	11.4	43.8	50	16	US-10-131-827-7122	Sequence 7122, App
C 385	11.4	43.8	25	15	US-10-098-263B-27374	Sequence 27374, A	C 458	11.4	43.8	50	16	US-10-131-827-7416	Sequence 7416, App
C 386	11.4	43.8	25	15	US-10-098-263B-30370	Sequence 30370, A	C 459	11.4	43.8	50	16	US-10-131-827-7495	Sequence 7495, App
C 387	11.4	43.8	25	15	US-10-098-263B-35358	Sequence 35358, A	C 460	11.4	43.8	50	16	US-10-131-827-8099	Sequence 8099, App
C 388	11.4	43.8	25	15	US-10-098-263B-38915	Sequence 38915, A	C 461	11.2	43.1	18	9	US-09-067-638B-32	Sequence 32, Appl
C 389	11.4	43.8	25	15	US-10-098-263B-39614	Sequence 39614, A	C 462	11.2	43.1	18	15	US-10-116-325-32	Sequence 32, Appl
C 390	11.4	43.8	25	15	US-10-098-263B-49152	Sequence 49152, A	C 463	11.2	43.1	18	15	US-10-388-263-32	Sequence 32, Appl
C 391	11.4	43.8	25	15	US-10-098-263B-49908	Sequence 49908, A	C 464	11.2	43.1	18	17	US-10-698-689-32	Sequence 196, Appl
C 392	11.4	43.8	25	15	US-10-098-263B-50273	Sequence 50273, A	C 465	11.2	43.1	18	17	US-10-698-689-196	Sequence 32, Appl
C 393	11.4	43.8	25	15	US-10-098-263B-50557	Sequence 50557, A	C 466	11.2	43.1	18	18	US-10-830-475-32	Sequence 17, Appl
C 394	11.4	43.8	25	15	US-10-098-263B-52926	Sequence 52926, A	C 467	11.2	43.1	20	15	US-10-286-927-17	Sequence 2584, App
C 395	11.4	43.8	25	15	US-10-098-263B-60773	Sequence 60773, A	C 468	11.2	43.1	20	16	US-10-289-762-2584	Sequence 6523, App
C 396	11.4	43.8	25	15	US-10-098-263B-66167	Sequence 66167, A	C 469	11.2	43.1	20	16	US-10-289-762-6523	Sequence 34, Appl
C 397	11.4	43.8	25	15	US-10-098-263B-72519	Sequence 72519, A	C 470	11.2	43.1	20	18	US-10-738-986-34	Sequence 450, App
C 398	11.4	43.8	25	15	US-10-098-263B-77424	Sequence 77424, A	C 471	11.2	43.1	20	18	US-10-712-795-450	Sequence 771, App
C 399	11.4	43.8	25	15	US-10-098-263B-85888	Sequence 85888, A	C 472	11.2	43.1	20	18	US-10-712-795-771	Sequence 9, Appl
C 400	11.4	43.8	25	15	US-10-098-263B-86849	Sequence 86849, A	C 473	11.2	43.1	21	15	US-10-286-927-9	Sequence 19102, A
C 401	11.4	43.8	25	15	US-10-098-263B-90726	Sequence 90726, A	C 474	11.2	43.1	21	18	US-10-786-720-19102	Sequence 19103, A
C 402	11.4	43.8	25	15	US-10-098-263B-93617	Sequence 93617, A	C 475	11.2	43.1	21	18	US-10-786-720-19103	Sequence 19104, A
C 403	11.4	43.8	25	15	US-10-098-263B-97194	Sequence 97194, A	C 476	11.2	43.1	21	18	US-10-786-720-19105	Sequence 19105, A
C 404	11.4	43.8	25	15	US-10-098-263B-98079	Sequence 98079, A	C 477	11.2	43.1	21	18	US-10-786-720-19106	Sequence 19106, A
C 405	11.4	43.8	25	15	US-10-098-263B-98080	Sequence 98080, A	C 478	11.2	43.1	21	18	US-10-786-720-19107	Sequence 19107, A
C 406	11.4	43.8	25	15	US-10-098-263B-107420	Sequence 107420, A	C 479	11.2	43.1	21	18	US-10-786-720-19107	Sequence 19564, A
C 407	11.4	43.8	25	15	US-10-098-263B-113394	Sequence 113394, A	C 480	11.2	43.1	21	18	US-10-786-720-19564	Sequence 19565, A
C 408	11.4	43.8	25	15	US-10-098-263B-115034	Sequence 115034, A	C 481	11.2	43.1	21	18	US-10-786-720-19565	Sequence 19566, A
C 409	11.4	43.8	25	15	US-10-098-263B-119065	Sequence 119065, A	C 482	11.2	43.1	22	16	US-10-300-369-13	Sequence 3290, App
C 410	11.4	43.8	25	15	US-10-098-263B-123299	Sequence 123299, A	C 483	11.2	43.1	22	10	US-09-940-185-3290	Sequence 13, Appl
C 411	11.4	43.8	25	15	US-10-098-263B-128519	Sequence 128519, A	C 484	11.2	43.1	25	10	US-09-982-665-264	Sequence 264, App
C 412	11.4	43.8	25	15	US-10-098-263B-128838	Sequence 128838, A	C 485	11.2	43.1	25	14	US-10-215-112-419	Sequence 419, App
C 413	11.4	43.8	25	17	US-10-717-597-2020	Sequence 2020, App	C 486	11.2	43.1	25	14	US-10-215-112-724	Sequence 724, App
C 414	11.4	43.8	25	17	US-10-717-597-2020	Sequence 2020, App	C 487	11.2	43.1	25	14	US-10-215-112-5099	Sequence 5099, App
C 415	11.4	43.8	25	17	US-10-775-169-3954	Sequence 2954, App	C 488	11.2	43.1	25	14	US-10-215-112-5363	Sequence 5363, App
C 416	11.4	43.8	25	17	US-10-775-169-3954	Sequence 7025, App	C 489	11.2	43.1	25	14	US-10-215-112-5565	Sequence 5565, App
C 417	11.4	43.8	26	9	US-09-738-625-7025	Sequence 80, Appl	C 490	11.2	43.1	25	14	US-10-215-112-8628	Sequence 8628, App
C 418	11.4	43.8	26	14	US-10-234-432-80	Sequence 80, Appl	C 491	11.2	43.1	25	14	US-10-215-112-11067	Sequence 11067, App
C 419	11.4	43.8	29	15	US-10-182-616-18	Sequence 18, Appl	C 492	11.2	43.1	25	14	US-10-215-112-12429	Sequence 12429, App
C 420	11.4	43.8	30	15	US-10-091-841-22	Sequence 22, Appl	C 493	11.2	43.1	25	14	US-10-215-112-14406	Sequence 14406, App
C 421	11.4	43.8	30	15	US-10-091-841-47	Sequence 47, Appl	C 494	11.2	43.1	25	14	US-10-215-112-14701	Sequence 14701, App
C 422	11.4	43.8	30	17	US-10-148-989A-7	Sequence 7, Appl	C 495	11.2	43.1	25	15	US-10-098-263B-4326	Sequence 4326, App
C 423	11.4	43.8	30	17	US-10-629-313-87	Sequence 87, Appl	C 496	11.2	43.1	25	15	US-10-098-263B-7253	Sequence 7253, App
C 424	11.4	43.8	31	13	US-10-004-832-4	Sequence 4, Appl	C 497	11.2	43.1	25	15	US-10-098-263B-7837	Sequence 7837, App
C 425	11.4	43.8	31	16	US-10-063-040-24	Sequence 24, Appl	C 498	11.2	43.1	25	15	US-10-098-263B-7837	Sequence 13371, App
C 426	11.4	43.8	32	8	US-08-970-266-2	Sequence 2, Appl	C 499	11.2	43.1	25	15	US-10-098-263B-13371	Sequence 9, Appl
C 427	11.4	43.8	32	8	US-08-744-685-2	Sequence 2, Appl	C 500	11.2	43.1	25	15	US-10-098-263B-39910	Sequence 39910, App
C 428	11.4	43.8	32	14	US-10-068-851-14	Sequence 14, Appl	C 501	11.2	43.1	25	15	US-10-098-263B-42795	Sequence 42795, App
C 429	11.4	43.8	32	16	US-10-613-779-96	Sequence 96, Appl	C 502	11.2	43.1	25	15	US-10-098-263B-44070	Sequence 44070, App
C 430	11.4	43.8	33	14	US-10-179-046-33	Sequence 33, Appl	C 503	11.2	43.1	25	15	US-10-098-263B-49726	Sequence 49726, App
C 431	11.4	43.8	33	14	US-10-179-046-35	Sequence 35, Appl	C 504	11.2	43.1	25	15	US-10-098-263B-53621	Sequence 53621, App
C 432	11.4	43.8	34	9	US-09-862-847-4	Sequence 4, Appl	C 505	11.2	43.1	25	15	US-10-098-263B-55566	Sequence 55566, App
C 433	11.4	43.8	34	10	US-09-906-179A-171	Sequence 171, App	C 506	11.2	43.1	25	15	US-10-098-263B-55988	Sequence 55988, App
C 434	11.4	43.8	35	10	US-09-906-179A-168	Sequence 168, App	C 507	11.2	43.1	25	15	US-10-098-263B-61870	Sequence 61870, App
C 435	11.4	43.8	35	15	US-10-021-425-10	Sequence 10, Appl	C 508	11.2	43.1	25	15	US-10-098-263B-63454	Sequence 63454, App
C 436	11.4	43.8	35	16	US-10-422-366-55	Sequence 55, Appl	C 509	11.2	43.1	25	15	US-10-098-263B-68477	Sequence 68477, App
C 437	11.4	43.8	37	9	US-09-117-447-4	Sequence 4, Appl	C 510	11.2	43.1	25	15	US-10-098-263B-70566	Sequence 70566, App
C 438	11.4	43.8	38	10	US-09-776-474-1678	Sequence 1678, App	C 511	11.2	43.1	25	15	US-10-098-263B-73666	Sequence 73666, App
C 439	11.4	43.8	38	18	US-10-741-789A-41	Sequence 41, Appl	C 512	11.2	43.1	25	15	US-10-098-263B-85095	Sequence 85095, App
C 440	11.4	43.8	39	10	US-09-994-064-28	Sequence 28, Appl	C 513	11.2	43.1	25	15	US-10-098-263B-85144	Sequence 85144, App
C 441	11.4	43.8	39	11	US-09-993-777-28	Sequence 28, Appl	C 514	11.2	43.1	25	15	US-10-098-263B-92804	Sequence 92804, App
C 442	11.4	43.8	40	14	US-10-067-956-5	Sequence 5, Appl	C 515	11.2	43.1	25	15	US-10-098-263B-94323	Sequence 94323, App
C 443	11.4	43.8	40	16	US-10-447-839A-88	Sequence 88, Appl	C 516	11.2	43.1	25	15	US-10-098-263B-94334	Sequence 94334, App
C 444	11.4	43.8	41	16	US-10-035-833A-982	Sequence 982, App	C 517	11.2	43.1	25	15	US-10-098-263B-95247	Sequence 95247, App
C 445	11.4	43.8	41	16	US-10-035-833A-6992	Sequence 6992, App	C 518	11.2	43.1	25	15	US-10-098-263B-99385	Sequence 99385, App
C 446	11.4	43.8	42	15	US-10-200-381A-69	Sequence 69, Appl	C 519	11.2	43.1	25	15	US-10-098-263B-101327	Sequence 101327, App
C 447	11.4	43.8	42	10	US-09-832-899-6	Sequence 6, Appl	C 520	11.2	43.1	25	15	US-10-098-263B-102581	Sequence 102581, App
C 448	11.4	43.8	47	15	US-10-170-097-1086	Sequence 1086, App	C 521	11.2	43.1	25	15	US-10-098-263B-103784	Sequence 103784, App
C 449	11.4	43.8	47	16	US-10-349-143-1052	Sequence 1052, App	C 522	11.2	43.1	25	15	US-10-098-263B-103784	Sequence 103784, App
C 450	11.4	43.8	50	16	US-10-131-827-457	Sequence 457, App	C 523	11.2	43.1	25	15	US-10-098-263B-108251	Sequence 108251, App

524	11.2	43.1	25	15	US-10-098-263B-108252	Sequence 108252,	c 597	11.2	43.1	45	9	US-09-999-832A-50	Sequence 50, Appl
525	11.2	43.1	25	15	US-10-098-263B-108598	Sequence 108598,	c 598	11.2	43.1	45	10	US-09-978-189-50	Sequence 50, Appl
526	11.2	43.1	25	15	US-10-098-263B-114646	Sequence 114646,	c 599	11.2	43.1	45	10	US-09-978-608A-50	Sequence 50, Appl
527	11.2	43.1	25	15	US-10-098-263B-116700	Sequence 116700,	c 600	11.2	43.1	45	10	US-09-978-585A-50	Sequence 50, Appl
528	11.2	43.1	25	15	US-10-098-263B-120734	Sequence 120734,	c 601	11.2	43.1	45	10	US-09-978-191A-50	Sequence 50, Appl
529	11.2	43.1	25	15	US-10-098-263B-121916	Sequence 121916,	c 602	11.2	43.1	45	10	US-09-978-403A-50	Sequence 50, Appl
530	11.2	43.1	25	15	US-10-032-585-4307	Sequence 4307, Ap	c 603	11.2	43.1	45	10	US-09-978-564A-50	Sequence 50, Appl
531	11.2	43.1	25	17	US-10-775-169-2041	Sequence 2041, Ap	c 604	11.2	43.1	45	10	US-09-999-833A-50	Sequence 50, Appl
532	11.2	43.1	25	17	US-10-775-169-2042	Sequence 2042, Ap	c 605	11.2	43.1	45	10	US-09-981-915A-50	Sequence 50, Appl
533	11.2	43.1	25	17	US-10-775-169-4567	Sequence 4567, Ap	c 606	11.2	43.1	45	10	US-09-978-824-50	Sequence 50, Appl
534	11.2	43.1	25	17	US-10-775-169-4568	Sequence 4568, Ap	c 607	11.2	43.1	45	10	US-09-918-585A-50	Sequence 50, Appl
535	11.2	43.1	25	15	US-10-436-826-67	Sequence 67, Appl	c 608	11.2	43.1	45	10	US-09-999-834A-50	Sequence 50, Appl
536	11.2	43.1	27	16	US-10-312-503A-36	Sequence 36, Appl	c 609	11.2	43.1	45	10	US-09-978-423A-50	Sequence 50, Appl
537	11.2	43.1	27	16	US-10-312-503A-40	Sequence 40, Appl	c 610	11.2	43.1	45	10	US-09-978-192A-50	Sequence 50, Appl
538	11.2	43.1	28	9	US-09-944-411-19	Sequence 19, Appl	c 611	11.2	43.1	45	10	US-09-999-830A-50	Sequence 50, Appl
539	11.2	43.1	28	9	US-09-759-352-17	Sequence 17, Appl	c 612	11.2	43.1	45	10	US-09-978-757A-50	Sequence 50, Appl
540	11.2	43.1	28	9	US-09-887-880-24	Sequence 24, Appl	c 613	11.2	43.1	45	10	US-09-978-187B-50	Sequence 50, Appl
541	11.2	43.1	28	15	US-10-260-516-19	Sequence 19, Appl	c 614	11.2	43.1	45	10	US-09-978-643A-50	Sequence 50, Appl
542	11.2	43.1	28	15	US-10-360-123A-26	Sequence 26, Appl	c 615	11.2	43.1	45	10	US-09-978-375A-50	Sequence 50, Appl
543	11.2	43.1	28	15	US-10-360-123A-32	Sequence 32, Appl	c 616	11.2	43.1	45	10	US-09-978-298A-50	Sequence 50, Appl
544	11.2	43.1	28	15	US-10-360-123A-33	Sequence 33, Appl	c 617	11.2	43.1	45	10	US-09-978-188A-50	Sequence 50, Appl
545	11.2	43.1	28	17	US-10-220-481-341	Sequence 341, App	c 618	11.2	43.1	45	10	US-09-978-681A-50	Sequence 50, Appl
546	11.2	43.1	29	9	US-09-863-040-43	Sequence 43, Appl	c 619	11.2	43.1	45	10	US-09-978-194A-50	Sequence 50, Appl
547	11.2	43.1	29	10	US-09-069-228-5	Sequence 5, Appl	c 620	11.2	43.1	45	10	US-09-999-829A-50	Sequence 50, Appl
548	11.2	43.1	29	15	US-10-454-210-43	Sequence 43, Appl	c 621	11.2	43.1	45	10	US-09-978-299A-50	Sequence 50, Appl
549	11.2	43.1	29	18	US-10-849-518-5	Sequence 5, Appl	c 622	11.2	43.1	45	10	US-09-978-544A-50	Sequence 50, Appl
550	11.2	43.1	30	16	US-10-632-117-3	Sequence 33, Appl	c 623	11.2	43.1	45	10	US-09-978-665A-50	Sequence 50, Appl
551	11.2	43.1	31	9	US-09-738-599-13	Sequence 13, Appl	c 624	11.2	43.1	45	10	US-09-978-802A-50	Sequence 50, Appl
552	11.2	43.1	31	10	US-09-961-077-284	Sequence 284, App	c 625	11.2	43.1	45	11	US-09-999-831A-50	Sequence 50, Appl
553	11.2	43.1	32	9	US-09-887-880-25	Sequence 25, Appl	c 626	11.2	43.1	45	14	US-10-017-081A-50	Sequence 50, Appl
554	11.2	43.1	32	15	US-10-314-861-20	Sequence 20, Appl	c 627	11.2	43.1	45	14	US-10-167-749-50	Sequence 50, Appl
555	11.2	43.1	33	17	US-10-479-787-24	Sequence 24, Appl	c 628	11.2	43.1	45	14	US-10-013-921A-50	Sequence 50, Appl
556	11.2	43.1	34	14	US-10-071-485-95	Sequence 95, Appl	c 629	11.2	43.1	45	14	US-10-013-922A-50	Sequence 50, Appl
557	11.2	43.1	34	16	US-10-607-631-27	Sequence 27, Appl	c 630	11.2	43.1	45	14	US-10-016-177A-50	Sequence 50, Appl
558	11.2	43.1	34	16	US-10-607-631-28	Sequence 28, Appl	c 631	11.2	43.1	45	15	US-10-166-709A-50	Sequence 50, Appl
559	11.2	43.1	35	15	US-10-456-097-4	Sequence 4, Appl	c 632	11.2	43.1	45	15	US-10-143-031A-50	Sequence 50, Appl
560	11.2	43.1	36	9	US-09-887-880-18	Sequence 18, Appl	c 633	11.2	43.1	45	15	US-10-143-030A-50	Sequence 50, Appl
561	11.2	43.1	36	9	US-09-887-880-19	Sequence 19, Appl	c 634	11.2	43.1	45	15	US-10-002-967A-50	Sequence 50, Appl
562	11.2	43.1	36	9	US-09-887-880-20	Sequence 20, Appl	c 635	11.2	43.1	45	15	US-10-017-083A-50	Sequence 50, Appl
563	11.2	43.1	36	9	US-09-887-880-21	Sequence 21, Appl	c 636	11.2	43.1	45	15	US-10-145-128A-50	Sequence 50, Appl
564	11.2	43.1	36	9	US-09-887-880-26	Sequence 26, Appl	c 637	11.2	43.1	45	15	US-10-017-191A-50	Sequence 50, Appl
565	11.2	43.1	36	9	US-09-887-880-30	Sequence 29, Appl	c 638	11.2	43.1	45	15	US-10-143-028A-50	Sequence 50, Appl
566	11.2	43.1	36	9	US-09-887-880-30	Sequence 30, Appl	c 639	11.2	43.1	45	15	US-10-143-029A-50	Sequence 50, Appl
567	11.2	43.1	37	15	US-10-267-217-21	Sequence 21, Appl	c 640	11.2	43.1	45	15	US-10-145-089A-50	Sequence 50, Appl
568	11.2	43.1	38	9	US-09-874-389-14	Sequence 14, Appl	c 641	11.2	43.1	45	15	US-10-165-067A-50	Sequence 50, Appl
569	11.2	43.1	38	9	US-09-874-389-15	Sequence 15, Appl	c 642	11.2	43.1	45	15	US-10-145-017A-50	Sequence 50, Appl
570	11.2	43.1	38	10	US-09-921-650-14	Sequence 14, Appl	c 643	11.2	43.1	45	15	US-10-164-728A-50	Sequence 50, Appl
571	11.2	43.1	38	11	US-09-921-650-15	Sequence 15, Appl	c 644	11.2	43.1	45	15	US-10-013-926A-50	Sequence 50, Appl
572	11.2	43.1	38	11	US-09-241-347-14	Sequence 14, Appl	c 645	11.2	43.1	45	15	US-10-165-247A-50	Sequence 50, Appl
573	11.2	43.1	38	11	US-09-241-347-15	Sequence 15, Appl	c 646	11.2	43.1	45	15	US-10-145-124A-50	Sequence 50, Appl
574	11.2	43.1	38	14	US-10-032-393-66	Sequence 66, Appl	c 647	11.2	43.1	45	15	US-10-160-502A-50	Sequence 50, Appl
575	11.2	43.1	38	15	US-10-301-516-11	Sequence 11, Appl	c 648	11.2	43.1	45	15	US-10-145-087A-50	Sequence 50, Appl
576	11.2	43.1	38	15	US-10-301-516-12	Sequence 12, Appl	c 649	11.2	43.1	45	15	US-10-017-086A-50	Sequence 50, Appl
577	11.2	43.1	38	15	US-10-326-671-55	Sequence 55, Appl	c 650	11.2	43.1	45	15	US-10-164-829A-50	Sequence 50, Appl
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580	11.2	43.1	40	9	US-09-887-880-23	Sequence 23, Appl	c 653	11.2	43.1	45	15	US-10-020-445A-50	Sequence 50, Appl
581	11.2	43.1	40	9	US-09-887-880-27	Sequence 27, Appl	c 654	11.2	43.1	45	15	US-10-013-924A-50	Sequence 50, Appl
582	11.2	43.1	41	16	US-10-035-833A-3207	Sequence 3207, Ap	c 655	11.2	43.1	45	15	US-10-017-084A-50	Sequence 50, Appl
583	11.2	43.1	41	16	US-10-035-833A-5718	Sequence 5718, Ap	c 656	11.2	43.1	45	15	US-10-145-016A-50	Sequence 50, Appl
584	11.2	43.1	42	9	US-09-929-962-2	Sequence 2, Appl	c 657	11.2	43.1	45	15	US-10-145-088A-50	Sequence 50, Appl
585	11.2	43.1	42	14	US-10-210-747-2	Sequence 2, Appl	c 658	11.2	43.1	45	15	US-10-145-092A-50	Sequence 50, Appl
586	11.2	43.1	42	15	US-10-171-452A-6	Sequence 6, Appl	c 659	11.2	43.1	45	15	US-10-145-129A-50	Sequence 50, Appl
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588	11.2	43.1	42	15	US-10-353-708-6	Sequence 6, Appl	c 661	11.2	43.1	45	15	US-10-165-353A-50	Sequence 50, Appl
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590	11.2	43.1	43	15	US-10-032-585-1841	Sequence 1841, Ap	c 663	11.2	43.1	45	15	US-10-170-481A-50	Sequence 50, Appl
591	11.2	43.1	44	9	US-09-887-880-28	Sequence 28, Appl	c 664	11.2	43.1	45	15	US-10-172-039A-50	Sequence 50, Appl
592	11.2	43.1	44	16	US-10-300-369-18	Sequence 18, Appl	c 665	11.2	43.1	45	15	US-10-210-028-50	Sequence 50, Appl
593	11.2	43.1	44	16	US-10-300-369-20	Sequence 20, Appl	c 666	11.2	43.1	45	15	US-10-017-085A-50	Sequence 50, Appl
594	11.2	43.1	45	9	US-09-978-295A-50	Sequence 50, Appl	c 667	11.2	43.1	45	15	US-10-013-916A-50	Sequence 50, Appl
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c 816	11	42.3	37	15	US-10-156-306-2508	Sequence 2508, Ap	c 889	10.8	41.5	24	15	US-10-214-419-171	Sequence 171, App
c 817	11	42.3	37	15	US-10-201-365-24	Sequence 24, Appl	890	10.8	41.5	25	10	US-09-940-185-4721	Sequence 4721, Ap
c 818	11	42.3	37	15	US-10-160-539-27	Sequence 27, Appl	891	10.8	41.5	25	14	US-10-215-112-5973	Sequence 5973, Ap
c 819	11	42.3	37	16	US-10-138-674-20350	Sequence 20350, A	892	10.8	41.5	25	14	US-10-215-112-6099	Sequence 6099, Ap
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c 823	11	42.3	38	10	US-09-930-423-2971	Sequence 2971, Ap	896	10.8	41.5	25	15	US-10-098-263B-2855	Sequence 2855, Ap
c 824	11	42.3	38	10	US-09-745-337A-2971	Sequence 2971, Ap	897	10.8	41.5	25	15	US-10-098-263B-5766	Sequence 5766, Ap
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c 826	11	42.3	38	15	US-10-186-442-28	Sequence 28, Appl	899	10.8	41.5	25	15	US-10-098-263B-7470	Sequence 7470, Ap
c 827	11	42.3	38	16	US-10-644-187-28	Sequence 28, Appl	900	10.8	41.5	25	15	US-10-098-263B-8699	Sequence 8699, Ap
c 828	11	42.3	39	17	US-10-477-469-12	Sequence 12, Appl	901	10.8	41.5	25	15	US-10-098-263B-8700	Sequence 8700, Ap
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c 831	11	42.3	41	15	US-10-219-195-3	Sequence 3, Appli	904	10.8	41.5	25	15	US-10-098-263B-17197	Sequence 17197, A
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c 835	11	42.3	41	16	US-10-411-066-97	Sequence 97, Appl	908	10.8	41.5	25	15	US-10-098-263B-33171	Sequence 33171, A
c 836	11	42.3	41	16	US-10-035-833A-4836	Sequence 4836, Ap	909	10.8	41.5	25	15	US-10-098-263B-37359	Sequence 37359, A
c 837	11	42.3	41	17	US-10-451-923-11	Sequence 11, Appl	910	10.8	41.5	25	15	US-10-098-263B-37359	Sequence 37359, A
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c 839	11	42.3	47	15	US-10-037-986-307	Sequence 307, App	912	10.8	41.5	25	15	US-10-098-263B-51297	Sequence 51297, A
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c 846	11	42.3	48	17	US-10-833-439-25	Sequence 25, Appl	919	10.8	41.5	25	15	US-10-098-263B-88587	Sequence 88587, A
c 847	11	42.3	48	18	US-10-833-745-25	Sequence 25, Appl	920	10.8	41.5	25	15	US-10-098-263B-90796	Sequence 90796, A
c 848	11	42.3	48	18	US-10-833-744-25	Sequence 25, Appl	921	10.8	41.5	25	15	US-10-098-263B-94238	Sequence 94238, A
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c 850	11	42.3	49	15	US-10-298-796-56	Sequence 56, Appl	923	10.8	41.5	25	15	US-10-098-263B-94658	Sequence 94658, A
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c 854	11	42.3	50	16	US-10-131-827-732	Sequence 732, App	927	10.8	41.5	25	15	US-10-098-263B-95406	Sequence 95406, A
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c 859	11	42.3	50	16	US-10-131-827-7476	Sequence 7476, Ap	932	10.8	41.5	25	15	US-10-098-263B-101588	Sequence 101588, A
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c 861	10.8	41.5	17	10	US-09-780-533A-1510	Sequence 1510, Ap	934	10.8	41.5	25	15	US-10-098-263B-106794	Sequence 106794, A
c 862	10.8	41.5	17	10	US-09-780-533A-2318	Sequence 2318, Ap	935	10.8	41.5	25	15	US-10-098-263B-107486	Sequence 107486, A
c 863	10.8	41.5	17	10	US-09-780-533A-2687	Sequence 2687, Ap	936	10.8	41.5	25	15	US-10-098-263B-109160	Sequence 109160, A
c 864	10.8	41.5	17	10	US-09-877-478-673	Sequence 673, App	937	10.8	41.5	25	15	US-10-098-263B-111657	Sequence 111657, A
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c 873	10.8	41.5	20	17	US-10-619-739-1857	Sequence 1857, Ap	946	10.8	41.5	25	15	US-10-098-263B-120233	Sequence 120233, A
c 874	10.8	41.5	20	18	US-10-407-136-6	Sequence 6, Appli	947	10.8	41.5	25	15	US-10-098-263B-120257	Sequence 120257, A
c 875	10.8	41.5	20	18	US-10-770-824-15	Sequence 15, Appl	948	10.8	41.5	25	15	US-10-098-263B-120827	Sequence 120827, A
c 876	10.8	41.5	21	15	US-10-168-517-13	Sequence 13, Appl	949	10.8	41.5	25	15	US-10-098-263B-120893	Sequence 120893, A
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c 879	10.8	41.5	22	17	US-10-236-417-269	Sequence 269, App	952	10.8	41.5	25	15	US-10-098-263B-129212	Sequence 129212, A
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c 884	10.8	41.5	24	9	US-09-819-964-19	Sequence 19, Appl	957	10.8	41.5	27	18	US-10-401-0499-10	Sequence 10, Appl
c 885	10.8	41.5	24	9	US-09-875-228-21	Sequence 21, Appl	958	10.8	41.5	28	14	US-10-080-505-57	Sequence 57, Appl
c 886	10.8	41.5	24	10	US-09-940-185-1171	Sequence 1171, Ap	959	10.8	41.5	28	17	US-10-687-046-57	Sequence 57, Appl
c 887	10.8	41.5	24	10	US-09-940-185-2178	Sequence 2178, Ap	960	10.8	41.5	29	15	US-10-054-536-27	Sequence 27, Appl
c 888	10.8	41.5	24	15	US-10-340-123-11	Sequence 11, Appl	961	10.8	41.5	29	15	US-10-444-575-47	Sequence 47, Appl


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; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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US-10-215-112-6258

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RESULT 5
US-10-098-263B-53769/c
; Sequence 53769, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53769
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-53769

Query Match      59.2%; Score 15.4; DB 15; Length 25;
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Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 6
US-10-215-112-3516/c
; Sequence 3516, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3516
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3516

Query Match      58.5%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 7
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; Sequence 6804, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
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; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6804

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Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
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RESULT 8
US-10-215-112-6930/c
; Sequence 6930, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
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; SEQ ID NO 6930
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; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6930

Query Match      58.5%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
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Db 21 TCACAGACTCGGTACCTCAAT 2

RESULT 9
US-10-098-263B-27628/c
; Sequence 27628, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
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; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-27628

Query Match 56.2%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTTTTCGCAGATCGGTACTCTC 23
DB 23 TCTTTTCGCAGATCGGTACTCTC 3

RESULT 10
US-10-215-112-6384/c
; Sequence 6384, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6384
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6384.

Query Match 55.4%; Score 14.4; DB 14; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCTTTTCGCAGATCGGTACTCTCA 25
DB 24 GTCTTTTCGCAGATCGGTACTCTCA 1

RESULT 11
US-10-098-263B-61172
; Sequence 61172, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-61172

Query Match 55.4%; Score 14.4; DB 15; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACTCT 22
DB 1 TCGTAGATCGGTACTCT 16

RESULT 12
US-09-884-465A-37/c
; Sequence 37, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-37

Query Match 55.4%; Score 14.4; DB 10; Length 40;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTTCGCAGATCGGTACTCTCAAT 26
DB 37 TTTTCCAGATAGGTACTTCCAT 14

RESULT 13
US-10-215-112-5215/c
; Sequence 5215, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5215
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-5215

Query Match 54.6%; Score 14.2; DB 14; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACTCTCAA 25
DB 19 TCACACAGACAGGTACTCTCAA 1

```

; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42442
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42442

Query Match      53.8%; Score 14; DB 15; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTCTTTCGAGATCGGTACTCT 23
Db 22 GTCGTTTCACAGGTCGGGAATCT 1

RESULT 17
US-10-098-263B-126762/c
; Sequence 126762, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 126762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-126762

Query Match      53.8%; Score 14; DB 15; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGTCTTTCGAGATCGGTACTCT 22
Db 23 CGTCTTTCGAGATCGGTACTCT 2

RESULT 18
US-10-170-097-998/c
; Sequence 998, Application US/10170097
; Publication No. US20030228582A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Iliya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267

US-10-098-263B-129509/c
; Sequence 129509, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129509
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129509

Query Match      54.6%; Score 14.2; DB 15; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCA 25
Db 19 TCACAGACGGTACTCTCA 1

RESULT 15
US-10-297-277-10/c
; Sequence 10, Application US/10297277
; Publication No. US20030215828A1
; GENERAL INFORMATION:
; APPLICANT: Mitsuhashi, Masato
; APPLICANT: Kambara, Hideki
; APPLICANT: Matsunaga, Hiroko
; APPLICANT: Kawamura, Masafumi
; TITLE OF INVENTION: GENE MARKERS FOR LUNG CANCER
; FILE REFERENCE: HITACHI.046VPC
; CURRENT APPLICATION NUMBER: US/10/297,277
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/215,727
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/243,976
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 7013 Primer P10.
US-10-297-277-10

Query Match      54.6%; Score 14.2; DB 15; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCAGATCGGTACTCTCAAT 26
Db 30 CGCAGATCGGAACCTTAAT 12

RESULT 16
US-10-098-263B-42442/c
; Sequence 42442, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
```


; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 998
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-482-145 : polymorphic base A or G
US-10-170-097-998

Query Match 53.8%; Score 14; DB 15; Length 47;
Best Local Similarity 70.8%; Pred. No. 7.3e+03;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACCTCAA 25
Db 43 GTCCTTCGAGATCGGTACCTCAA 20

RESULT 19

US-09-940-185-1626/c
; Sequence 1626, Application US/09940185
; Publication No. US2003009639A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1626
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1626

Query Match 53.1%; Score 13.8; DB 10; Length 24;
Best Local Similarity 88.2%; Pred. No. 9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGATCGGTACCTCAAT 26
Db 22 CAGATCGGTACCTCAAT 6

RESULT 20

US-10-403-232-67/c
; Sequence 67, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patentin version 3.2

; SEQ ID NO 67
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-403-232-67

Query Match 53.1%; Score 13.8; DB 15; Length 32;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTCGACATCGGTACCT 22
Db 26 TTCGACGCTTGTACCT 10

RESULT 21

US-10-403-232-71/c
; Sequence 71, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Quideng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 71
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-403-232-71

Query Match 53.1%; Score 13.8; DB 15; Length 32;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTCGACATCGGTACCT 22
Db 26 TTCGACGCTTGTACCT 10

RESULT 22

US-10-131-827-1645
; Sequence 1645, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1645
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-131-827-1645

Query Match 53.1%; Score 13.8; DB 16; Length 50;
Best Local Similarity 72.0%; Pred. No. 9.2e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GTCTTCGAGATCGGTACCTCAAT 26
Db 4 GTCTCAAGGGTATCGGTACCTCAAT 28

RESULT 23

US-10-215-112-3642/c
; Sequence 3642, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3642

Query Match 52.3%; Score 13.6; DB 14; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
Db 22 TCACAGACACGTACCTCAAT 3

RESULT 24

US-09-965-101-41
; Sequence 41, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-41

Query Match 52.3%; Score 13.6; DB 11; Length 34;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
Db 10 TCGCAGATCGATACCAGGAT 29

RESULT 25

US-10-160-670A-5/c
; Sequence 5, Application US/10160670A
; Publication No. US20030224066A1
; GENERAL INFORMATION:
; APPLICANT: National Yang-Ming University
; APPLICANT: Wu, Rong-Tsun
; TITLE OF INVENTION: Polysaccharide Extract of Dioscorea Sp. and an Orally Active
; TITLE OF INVENTION: Pharmaceutical Composition Comprising the Same
; FILE REFERENCE: 1111-4070
; CURRENT APPLICATION NUMBER: US/10/160,670A
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-670A-5

Query Match 51.5%; Score 13.4; DB 15; Length 24;
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTCGAGATCGGTACCTCA 24
Db 24 GTCTTCGAGAGAGAACTTCA 2

RESULT 26

US-09-180-394-3/c
; Sequence 3, Application US/09180394
; Patent No. US20020115206A1
; GENERAL INFORMATION:
; APPLICANT: M. Sawada
; TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter F. Corless
; STREET: Dike, Bronstein, Roberts & Cushman, LLP 130 Water St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-4280
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,394
; FILING DATE: 1998-11-05
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP98/00949
; FILING DATE: 1998-03-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Peter F. Corless
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 1526-48781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-523-3400
; TELEFAX: (617)-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
US-09-180-394-3

Query Match
Best Local Similarity 51.5%; Score 13.4; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACCTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 27
US-09-848-986-3/c
; Sequence 3, Application US/09048986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE REFERENCE: Methods of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/848,986
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-6 primer sense sequence
US-09-848-986-3

Query Match
Best Local Similarity 51.5%; Score 13.4; DB 10; Length 25;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACCTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 28
US-10-098-263B-80455/c
; Sequence 80455, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; CURRENT APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-80455

Query Match
51.5%; Score 13.4; DB 15; Length 25;

; LENGTH: 25
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
US-09-180-394-3

Query Match
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTCGAGATCGGTACCTC 23
Db 23 CGTCTTCAGAGATCGGGTCTC 1

RESULT 29
US-10-233-121A-3/c
; Sequence 3, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer oligonucleotide
US-10-233-121A-3

Query Match
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGAGATCGGTACCTCA 24
Db 24 GTCCTTCGAGAGAGGAAGTCTCA 2

RESULT 30
US-10-602-234-3/c
; Sequence 3, Application US/10602234
; Publication No. US20040072346A1
; GENERAL INFORMATION:
; APPLICANT: M. Sawada
; TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter F. Corless
; STREET: Dike, Bronstein, Roberts & Cushman, LLP 130 Water St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-4280
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/602,234
; FILING DATE: 23-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/180,394
; FILING DATE: 1998-11-05
```

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; APPLICATION NUMBER: PCT/JP98/00949
; FILING DATE: 1998-03-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Peter F. Corless
; REGISTRATION NUMBER: 33 860
; REFERENCE/DOCKET NUMBER: 1526-48781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-523-3400
; TELEFAX: (617)-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-602-234-3

Query Match          51.5%; Score 13.4; DB 16; Length 25;
Best Local Similarity 73.9%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCCTTCGACATCGGTACCTCA 24
Db 24 GTCCTTCGACAGAGAACTTCA 2

RESULT 31
US-9-875-228-31
; Sequence 31, Application US/09875228
; Patent No. US20020136707A1
; GENERAL INFORMATION:
; APPLICANT: Yu, D.
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
; FILE REFERENCE: 34802200900
; CURRENT APPLICATION NUMBER: US/09/875,228
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/127,834
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/076,545
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/054,523
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence is
; OTHER INFORMATION: produced synthetically.
US-9-875-228-31

Query Match          51.5%; Score 13.4; DB 9; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
Db 1 GATCGGTACCTCACT 15

RESULT 32
US-9-989-339-15
; Sequence 15, Application US/09989339
; Publication No. US2003008886A1
; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl
; APPLICANT: Famodu, Layo
; APPLICANT: Rafalski, Jan A.
; APPLICANT: Ramaker, Michael
; APPLICANT: Tarczynski, Mitchell C.
; APPLICANT: Thorpe, Catherine
; TITLE OF INVENTION: PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
; FILE REFERENCE: BB-1067-B
; CURRENT APPLICATION NUMBER: US/09/989,339
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 08/703,829
; PRIOR FILING DATE: 1996-08-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-9-989-339-15

Query Match          51.5%; Score 13.4; DB 10; Length 31;
Best Local Similarity 93.3%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
Db 1 GATCGGTACCTCACT 15

RESULT 33
US-10-295-798-20
; Sequence 20, Application US/10295798
; Publication No. US20030162225A1
; GENERAL INFORMATION:
; APPLICANT: Isis Innovation Ltd
; APPLICANT: James, William Siward
; APPLICANT: Hope, James
; APPLICANT: Tahiri-Alaoui, Abdesamad
; TITLE OF INVENTION: Ligands Specific for an isoform of the prion protein
; FILE REFERENCE: KILBURN1130
; CURRENT APPLICATION NUMBER: US/10/295,798
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PCT/GB01/02228
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: GB 0012054.3
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Aptamer
US-10-295-798-20

Query Match          51.5%; Score 13.4; DB 15; Length 48;
Best Local Similarity 52.2%; Pred. No. 1.4e+04;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 CTTTCGCGATCGGTACCTCAAT 26
Db 6 CUAGCGCACAGCGUACCUU 28

RESULT 34
US-10-215-112-5216/c
; Sequence 5216, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
```

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; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5216
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-5216

Query Match      50.8%; Score 13.2; DB 14; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      7 TCGCAGATCGGTACCTCA 24
        ||||| ||||| ||||| |||||
DB      18 TCACAGACAGGTACCTCA 1

RESULT 35
US-10-098-263B-86304/c
; Sequence 86304, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86304
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86304

Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      7 TCGCAGATCGGTACCTCA 24
        ||||| ||||| ||||| |||||
DB      22 TCGCAGATCGTTCTCTAA 5

RESULT 36
US-10-098-263B-121702/c
; Sequence 121702, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121702
```

```
Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      4 CTTTCGCGATCGGTACC 21
        ||||| ||||| ||||| |||||
DB      23 CTTTCGTAGATGGGTCCC 6

RESULT 37
US-10-098-263B-128873/c
; Sequence 128873, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 128873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-128873

Query Match      50.8%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      7 TCGCAGATCGGTACCTCA 24
        ||||| ||||| ||||| |||||
DB      18 TCACAGACAGGTACCTCA 1

RESULT 38
US-09-729-821-13
; Sequence 13, Application US/09729821
; Publication No. US20020069430A1
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-13

Query Match      50.8%; Score 13.2; DB 9; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      9 GCAGATCGGTACCTCAAT 26
        ||||| ||||| ||||| |||||
DB      3 GCAGATGGCTTCTCAAT 20

RESULT 39
```

US-09-729-821-19
; Sequence 19, Application US/09729821
; Publication No. US20020069430A1
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-19

Query Match 50.8%; Score 13.2; DB 9; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCAGATCGGTACCTCAAT 26
||||| | | | |
Db 3 GCAGATGGCTTCCTCAAT 20

RESULT 40
US-09-729-821-13
; Sequence 13, Application US/09729821
; Publication No. US20040093647A9
; GENERAL INFORMATION:
; APPLICANT: KISAKA, HIROAKI
; APPLICANT: KIDA, TAKAO
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC PLANTS HAVING IMPROVED AMINO ACID
; TITLE OF INVENTION: COMPOSITION
; FILE REFERENCE: 200496USO
; CURRENT APPLICATION NUMBER: US/09/729,821
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11-376719
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-729-821-13

Query Match 50.8%; Score 13.2; DB 11; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCAGATCGGTACCTCAAT 26
||||| | | | |
Db 3 GCAGATGGCTTCCTCAAT 20

Search completed: November 24, 2004, 03:43:00
Job time : 131.018 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1246.54 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	55.4	35	8	A2959628
2	13.8	53.1	44	8	B2289495
3	13.8	53.1	49	9	TA58C07Q
4	13.8	53.1	50	7	CN921174
5	13.6	52.3	50	1	AU105805
6	13.6	52.3	50	1	AU107934
7	13.4	51.5	37	9	TA344B09Q
8	13.2	50.8	49	8	BH642496
9	13	50.0	39	9	TA60E09Q
10	12.8	49.2	27	8	A2838579
11	12.8	49.2	43	9	BX891607
12	12.8	49.2	44	8	A2486826
13	12.8	49.2	45	8	BH628960
14	12.8	49.2	49	8	BH846331
15	12.4	47.7	34	1	AA972865
16	12.4	47.7	39	9	CR360589
17	12.4	47.7	49	6	CA935542
18	12.4	47.7	50	1	AU105437
19	12.2	46.9	22	9	AJ590848
20	12.2	46.9	43	1	AV847149
21	12.2	46.9	45	9	AL766296
22	12	46.2	26	8	A2985231
23	12	46.2	28	7	CN973502
24	12	46.2	37	9	TA383E12Q

42	8	BH796117	46.2	12	c	25
43	8	AZ778700	46.2	12	c	26
44	8	BZ664508	46.2	27	c	27
45	9	CL521995	46.2	28	c	28
46	9	CL521997	46.2	29	c	29
47	8	AZ462540	46.2	30	c	30
48	8	AJ594944	46.2	31	c	31
49	8	AZ805662	46.2	32	c	32
50	8	AZ803827	46.2	33	c	33
51	8	AZ797143	46.2	34	c	34
52	8	AZ942892	46.2	35	c	35
53	8	CL655958	46.2	36	c	36
54	8	AZ810604	46.2	37	c	37
55	8	AZ803114	46.2	38	c	38
56	8	AZ805718	46.2	39	c	39
57	8	AZ810670	46.2	40	c	40
58	8	AZ799177	46.2	41	c	41
59	8	BX660365	46.2	42	c	42
60	8	BH853770	46.2	43	c	43
61	9	AL756145	46.2	44	c	44
62	7	CF640952	46.2	45	c	45
63	8	BZ357881	46.2	46	c	46
64	8	BZ357881	46.2	47	c	47
65	8	BZ357881	46.2	48	c	48
66	8	BZ357881	46.2	49	c	49
67	8	BZ357881	46.2	50	c	50
68	8	BZ357881	46.2	51	c	51
69	8	BZ357881	46.2	52	c	52
70	8	BZ357881	46.2	53	c	53
71	8	BZ357881	46.2	54	c	54
72	8	BZ357881	46.2	55	c	55
73	8	BZ357881	46.2	56	c	56
74	8	BZ357881	46.2	57	c	57
75	8	BZ357881	46.2	58	c	58
76	8	BZ357881	46.2	59	c	59
77	8	BZ357881	46.2	60	c	60
78	8	BZ357881	46.2	61	c	61
79	8	BZ357881	46.2	62	c	62
80	8	BZ357881	46.2	63	c	63
81	8	BZ357881	46.2	64	c	64
82	8	BZ357881	46.2	65	c	65
83	8	BZ357881	46.2	66	c	66
84	8	BZ357881	46.2	67	c	67
85	8	BZ357881	46.2	68	c	68
86	8	BZ357881	46.2	69	c	69
87	8	BZ357881	46.2	70	c	70
88	8	BZ357881	46.2	71	c	71
89	8	BZ357881	46.2	72	c	72
90	8	BZ357881	46.2	73	c	73
91	8	BZ357881	46.2	74	c	74
92	8	BZ357881	46.2	75	c	75
93	8	BZ357881	46.2	76	c	76
94	8	BZ357881	46.2	77	c	77
95	8	BZ357881	46.2	78	c	78
96	8	BZ357881	46.2	79	c	79
97	8	BZ357881	46.2	80	c	80
98	8	BZ357881	46.2	81	c	81
99	8	BZ357881	46.2	82	c	82
100	8	BZ357881	46.2	83	c	83
101	8	BZ357881	46.2	84	c	84
102	8	BZ357881	46.2	85	c	85
103	8	BZ357881	46.2	86	c	86
104	8	BZ357881	46.2	87	c	87
105	8	BZ357881	46.2	88	c	88
106	8	BZ357881	46.2	89	c	89
107	8	BZ357881	46.2	90	c	90
108	8	BZ357881	46.2	91	c	91
109	8	BZ357881	46.2	92	c	92
110	8	BZ357881	46.2	93	c	93
111	8	BZ357881	46.2	94	c	94
112	8	BZ357881	46.2	95	c	95
113	8	BZ357881	46.2	96	c	96
114	8	BZ357881	46.2	97	c	97
115	8	BZ357881	46.2	98	c	98
116	8	BZ357881	46.2	99	c	99
117	8	BZ357881	46.2	100	c	100

c 98	11.2	43.1	22	9	AJ591018	Arabidops	c 171	10.8	41.5	36	1	AU257681	AU257681
c 99	11.2	43.1	26	8	CC459557	SALK_1304	c 172	10.8	41.5	37	1	AI876199	uj59b06.y
c 100	11.2	43.1	32	8	CC454447	02S2028-0	c 173	10.8	41.5	37	8	BZ354507	SALK_1252
c 101	11.2	43.1	34	1	AA706263	ag91404.x	c 174	10.8	41.5	37	8	BZ382343	SALK_1181
c 102	11.2	43.1	35	1	AV954369	AV954369	c 175	10.8	41.5	37	8	BZ382741	SALK_1187
c 103	11.2	43.1	35	8	BH863096	BH863096	c 176	10.8	41.5	38	8	BZ382108	SALK_1178
c 104	11.2	43.1	36	9	AL944446	Arabidops	c 177	10.8	41.5	38	8	BZ382870	SALK_1190
c 105	11.2	43.1	37	2	AW245295	2820036.3	c 178	10.8	41.5	38	9	CC795484	SALK_0809
c 106	11.2	43.1	38	6	CB884322	EST00153	c 179	10.8	41.5	39	2	BE512831	601171854
c 107	11.2	43.1	38	9	CG706098	01S0651-0	c 180	10.8	41.5	39	6	CF331123	NACL--07-
c 108	11.2	43.1	41	9	DME547050	Arabidops	c 181	10.8	41.5	39	9	AL942107	Arabidops
c 109	11.2	43.1	42	5	BQ589344	BQ589344	c 182	10.8	41.5	39	7	W78594	me8e07.r1
c 110	11.2	43.1	43	1	AA966127	uc82a05.x	c 183	10.8	41.5	40	8	BH608730	5f22.L1L8
c 111	11.2	43.1	45	1	AA449195	uc39310.x	c 184	10.8	41.5	40	8	BZ769399	SALK_1421
c 112	11.2	43.1	45	8	AL755968	Arabidops	c 185	10.8	41.5	40	4	BG284664	602408844
c 113	11.2	43.1	45	9	AL757297	Arabidops	c 186	10.8	41.5	41	4	BJ031143	BJ031143
c 114	11.2	43.1	49	9	AL757297	Arabidops	c 187	10.8	41.5	43	1	AA734820	YP38402.r
c 115	11.2	43.1	50	1	AA210000	mu39c03.x	c 188	10.8	41.5	43	1	AI364988	6T21g10.x
c 116	11.2	43.1	50	1	AU105834	AU105834	c 189	10.8	41.5	43	8	BZ591170	3590.1.82
c 117	11.2	43.1	50	1	AU107495	AU107495	c 190	10.8	41.5	43	2	BE267956	601125354
c 118	11.2	43.1	50	1	AU107497	AU107497	c 191	10.8	41.5	45	2	BE513871	601316443
c 119	11.2	43.1	50	1	AU107497	AU107497	c 192	10.8	41.5	45	2	BE560611	601345809
c 120	11.2	43.1	50	1	AU107502	AU107502	c 193	10.8	41.5	46	2	BE267872	601125422
c 121	11.2	43.1	50	8	BH789191	SALK_0009	c 194	10.8	41.5	47	2	BE270087	601185780
c 122	11.2	43.1	50	8	BH905738	SALK_1076	c 195	10.8	41.5	47	2	BE267896	601125461
c 123	11.2	43.1	26	8	CC606035	YMO609.3	c 196	10.8	41.5	47	2	BE267896	601125461
c 124	11.2	43.1	30	8	AZ782713	2M0023M2.1	c 197	10.8	41.5	47	2	BE267896	601125461
c 125	11.2	43.1	32	9	TA66010	AZ7660120	c 200	10.8	41.5	48	5	BE561502	601346576
c 126	11.2	43.1	34	9	TA66010	AZ7660120	c 201	10.8	41.5	48	8	BE561502	601346576
c 127	11.2	43.1	35	8	AQ254734	EP(3)3554	c 202	10.8	41.5	49	2	BE561502	601346576
c 128	11.2	43.1	36	9	CR405252	Arabidops	c 203	10.8	41.5	49	2	BE561502	601346576
c 129	11.2	43.1	37	5	BQ595099	BQ595099	c 204	10.8	41.5	49	6	CF099786	rd77Q06.y
c 130	11.2	43.1	37	6	CB724584	EST0401.R	c 205	10.8	41.5	49	7	T47207	YB53g11.r1
c 131	11.2	43.1	37	8	AZ640839	CC458595	c 206	10.8	41.5	49	8	AZ619548	1M0451A19
c 132	11.2	43.1	39	8	CC458595	SALK_1201	c 207	10.8	41.5	50	1	AU103380	AU103380
c 133	11.2	43.1	39	8	BX656234	Arabidops	c 208	10.8	41.5	50	1	AU104588	AU104588
c 134	11.2	43.1	40	8	BH905777	BH905777	c 209	10.8	41.5	50	1	AU105397	AU105397
c 135	11.2	43.1	40	8	BH905777	BH905777	c 210	10.8	41.5	50	1	AU105399	AU105399
c 136	11.2	43.1	40	8	AZ798444	2M0055G15	c 211	10.8	41.5	50	1	AU105400	AU105400
c 137	11.2	43.1	41	8	AZ798444	2M0055G15	c 212	10.8	41.5	50	1	AU105402	AU105402
c 138	11.2	43.1	43	1	AA502093	AL756491	c 213	10.8	41.5	50	1	AU105402	AU105402
c 139	11.2	43.1	44	9	AL756491	Arabidops	c 214	10.8	41.5	50	9	CG710737	SALK_1033
c 140	11.2	43.1	44	9	AL756491	Arabidops	c 215	10.8	41.5	50	9	CG722042	1119070B0
c 141	11.2	43.1	45	2	BE251857	BE251857	c 216	10.6	40.8	30	1	AJ799595	AJ799595
c 142	11.2	43.1	46	1	AV851679	AV851679	c 217	10.6	40.8	30	7	T61480	Yc06a06.r1
c 143	11.2	43.1	46	8	BH798621	BH798621	c 218	10.6	40.8	30	9	AJ622413	Drosophi1
c 144	11.2	43.1	48	8	AZ308119	IM0010L13	c 219	10.6	40.8	31	9	AL938308	Arabidops
c 145	11.2	43.1	49	8	AZ596631	IM0410F06	c 220	10.6	40.8	34	1	AL932495	ow97a06.s
c 146	11.2	43.1	49	8	CC886568	SALK_1487	c 221	10.6	40.8	34	1	AL472306	tj87a09.x
c 147	11.2	43.1	50	1	AU105215	AU105215	c 222	10.6	40.8	35	8	BH865745	SALK_0997
c 148	11.2	43.1	50	4	BI416961	hasp002XP	c 223	10.6	40.8	35	9	CL675637	FR10115b
c 149	11.2	43.1	50	5	BQ479330	ku33a12.y	c 224	10.6	40.8	37	2	BF794126	602255692
c 150	11.2	43.1	50	9	BX208307	Danio rer	c 225	10.6	40.8	37	8	BH792052	SALK_0625
c 151	11.2	43.1	50	9	AJ671616	AJ671616	c 226	10.6	40.8	38	9	AL753738	Arabidops
c 152	10.8	41.5	24	1	AJ671616	2M0105P14	c 227	10.6	40.8	38	9	AL753738	Arabidops
c 153	10.8	41.5	25	7	L32038	HUMXP278A.H	c 228	10.6	40.8	39	9	CR359706	T. brucei
c 154	10.8	41.5	25	8	BZ595389	SALK_0869	c 229	10.6	40.8	40	1	AA864982	ch01b06.s
c 155	10.8	41.5	25	8	AL97886	T. brucei	c 230	10.6	40.8	40	1	AA864982	ch01b06.s
c 156	10.8	41.5	29	8	CC057376	CC057376	c 231	10.6	40.8	41	9	TA26A10P	AG0312.Sa
c 157	10.8	41.5	30	4	BM398771	BM398771	c 232	10.6	40.8	41	9	TA26A10P	AG0312.Sa
c 158	10.8	41.5	30	8	BH846479	BH846479	c 233	10.6	40.8	41	9	TA26A10P	AG0312.Sa
c 159	10.8	41.5	30	6	C01612	C01612	c 234	10.6	40.8	42	8	AZ344983	1M0079M14
c 160	10.8	41.5	31	7	T48676	T48676	c 235	10.6	40.8	42	8	AZ344983	1M0079M14
c 161	10.8	41.5	31	8	AZ773758	2M0001N22	c 236	10.6	40.8	44	8	BH902418	SALK_0371
c 162	10.8	41.5	31	8	BH847453	SALK_0544	c 237	10.6	40.8	44	8	BH902418	SALK_0371
c 163	10.8	41.5	31	8	BH847728	SALK_0559	c 238	10.6	40.8	45	9	BX534920	Arabidops
c 164	10.8	41.5	31	8	BH847760	BH847760	c 239	10.6	40.8	45	9	BX534920	Arabidops
c 165	10.8	41.5	31	8	BH847765	BH847765	c 240	10.6	40.8	46	1	AA059894	am19e11.s
c 166	10.8	41.5	32	8	BH846623	SALK_0093	c 241	10.6	40.8	47	1	AA059894	am19e11.s
c 167	10.8	41.5	34	1	AI654467	tg91c04.x	c 242	10.6	40.8	47	1	AA059894	am19e11.s
c 168	10.8	41.5	34	1	BZ291138	SALK_1124	c 243	10.6	40.8	48	9	AG204311	pan trogl
c 169	10.8	41.5	34	8	AZ839096	2M0135N03	c 244	10.6	40.8	48	9	AG204311	pan trogl
c 170	10.8	41.5	35	8	AZ839096	2M0135N03	c 245	10.6	40.8	49	1	AV848976	Arabidops

C 244	10.6	40.8	49	2	AW071297	AW071297 xa63f07.x	C 317	10.4	40.0	50	8	BZ287226	BZ287226	BZ287226	SALK_0205
C 245	10.6	40.8	50	1	AU103850	AU103850 AU103850	C 318	10.4	40.0	50	9	BX890678	BX890678	BX890678	Arabidops
C 246	10.6	40.8	50	1	AU104951	AU104951 AU104951	C 319	10.2	39.2	19	8	AZ810607	AZ810607	AZ810607	2M0076D14
C 247	10.6	40.8	50	1	AU106027	AU106027 AU106027	C 320	10.2	39.2	19	8	AZ810643	AZ810643	AZ810643	2M0076L16
C 248	10.6	40.8	50	1	AU106644	AU106644 AU106644	C 321	10.2	39.2	20	8	AZ816645	AZ816645	AZ816645	1M0115N07
C 249	10.6	40.8	50	1	AU106645	AU106645 AU106645	C 322	10.2	39.2	20	8	AZ807939	AZ807939	AZ807939	2M0071F07
C 250	10.6	40.8	50	1	AU107510	AU107510 AU107510	C 323	10.2	39.2	20	8	AZ817227	AZ817227	AZ817227	2M0086P21
C 251	10.6	40.8	50	1	AU107510	AU107510 AU107510	C 324	10.2	39.2	20	8	AZ822119	AZ822119	AZ822119	2M0095M03
C 252	10.6	40.8	50	8	AQ073822	EP(3)3211	C 325	10.2	39.2	21	8	AZ303723	AZ303723	AZ303723	1M0028K01
C 253	10.6	40.8	50	9	AZ944956	2M020611	C 326	10.2	39.2	21	8	AZ303723	AZ303723	AZ303723	1M0028K01
C 254	10.6	40.8	50	9	CC882869	02F6160-1	C 327	10.2	39.2	21	8	AZ471445	AZ471445	AZ471445	2M0286K01
C 255	10.4	40.0	21	8	AZ360212	1M0103K04	C 328	10.2	39.2	21	8	AZ828796	AZ828796	AZ828796	2M0106G04
C 256	10.4	40.0	28	6	CF321235	HD--12-G1	C 329	10.2	39.2	21	8	AZ828796	AZ828796	AZ828796	2M0106G04
C 257	10.4	40.0	30	8	BZ765015	SALK_1278	C 330	10.2	39.2	22	8	AZ799125	AZ799125	AZ799125	2M0056N19
C 258	10.4	40.0	31	8	BZ357533	SALK_1308	C 331	10.2	39.2	22	8	AZ807377	AZ807377	AZ807377	2M0070L11
C 259	10.4	40.0	31	8	BZ357535	SALK_1308	C 332	10.2	39.2	22	8	AZ808061	AZ808061	AZ808061	2M0071D23
C 260	10.4	40.0	32	9	CL519910	SAI7E10 F	C 333	10.2	39.2	22	8	AZ808062	AZ808062	AZ808062	2M0071D24
C 261	10.4	40.0	32	9	AG188480	Pan trogl	C 334	10.2	39.2	22	8	AZ813858	AZ813858	AZ813858	2M0081P21
C 262	10.4	40.0	33	7	D25860	HUMGS04237	C 335	10.2	39.2	22	8	AZ830066	AZ830066	AZ830066	2M0109M06
C 263	10.4	40.0	33	9	AG202038	Pan trogl	C 336	10.2	39.2	22	8	AZ832004	AZ832004	AZ832004	2M0112M04
C 264	10.4	40.0	34	1	AA967101	ua40c08.r	C 337	10.2	39.2	22	8	AZ832575	AZ832575	AZ832575	2M0113M01
C 265	10.4	40.0	34	1	AV845568	AV845568	C 338	10.2	39.2	22	8	AZ833754	AZ833754	AZ833754	2M0116L02
C 266	10.4	40.0	34	8	BH857135	BH857135 SALK_0766	C 339	10.2	39.2	22	8	AZ833754	AZ833754	AZ833754	2M0116L02
C 267	10.4	40.0	37	1	AI647510	uk40e11.x	C 340	10.2	39.2	23	8	AZ806754	AZ806754	AZ806754	2M0069G05
C 268	10.4	40.0	37	5	B0587309	E012339-0	C 341	10.2	39.2	23	8	AZ808048	AZ808048	AZ808048	2M0071D13
C 269	10.4	40.0	38	8	BH905215	SALK_1057	C 342	10.2	39.2	23	8	AZ808766	AZ808766	AZ808766	2M0072D21
C 270	10.4	40.0	39	8	CC053623	SALK_0458	C 343	10.2	39.2	23	8	AZ810539	AZ810539	AZ810539	2M0076D12
C 271	10.4	40.0	40	1	AA631276	rq92c01.s	C 344	10.2	39.2	23	8	AZ822128	AZ822128	AZ822128	2M0095O02
C 272	10.4	40.0	40	8	AZ311244	1M0026N06	C 345	10.2	39.2	23	8	AZ822132	AZ822132	AZ822132	2M0095P01
C 273	10.4	40.0	40	9	AB082694	Drosophi1	C 346	10.2	39.2	23	8	AZ829501	AZ829501	AZ829501	2M0107O12
C 274	10.4	40.0	41	4	BJ034814	BJ034814	C 347	10.2	39.2	23	8	AZ832568	AZ832568	AZ832568	2M0113K05
C 275	10.4	40.0	42	1	AL754611	Arabidops	C 348	10.2	39.2	24	8	AZ303525	AZ303525	AZ303525	1M0003E20
C 276	10.4	40.0	42	8	AA627436	nq47h01.s	C 349	10.2	39.2	24	8	AZ303599	AZ303599	AZ303599	1M0003O17
C 277	10.4	40.0	42	8	BH865278	SALK_0980	C 350	10.2	39.2	24	8	AZ825913	AZ825913	AZ825913	2M0101B22
C 278	10.4	40.0	43	6	CF308230	ABF--01-P	C 351	10.2	39.2	24	8	AZ825913	AZ825913	AZ825913	2M0101B22
C 279	10.4	40.0	43	8	CL183341	XE744 Bay	C 352	10.2	39.2	24	8	AZ946318	AZ946318	AZ946318	2M0208N02
C 280	10.4	40.0	44	9	AL756121	Arabidops	C 353	10.2	39.2	24	8	AZ946318	AZ946318	AZ946318	2M0208N02
C 281	10.4	40.0	45	9	CL439197	PST8831-N	C 354	10.2	39.2	25	8	AZ341661	AZ341661	AZ341661	2M0280K02
C 282	10.4	40.0	46	7	W92934	me39c11.r1	C 355	10.2	39.2	25	8	AZ807384	AZ807384	AZ807384	2M0070N09
C 283	10.4	40.0	47	4	BH835227	603089126	C 356	10.2	39.2	25	8	AZ807988	AZ807988	AZ807988	2M0071B15
C 284	10.4	40.0	48	8	BH757340	SALK_0560	C 357	10.2	39.2	25	8	AZ817162	AZ817162	AZ817162	2M0086N14
C 285	10.4	40.0	48	8	BH813146	SALK_0637	C 358	10.2	39.2	25	8	AZ832533	AZ832533	AZ832533	2M0113E02
C 286	10.4	40.0	49	4	BH281964	ki23e08.y	C 359	10.2	39.2	25	8	AZ988387	AZ988387	AZ988387	2M0271P13
C 287	10.4	40.0	49	8	AZ438829	IM0229B10	C 360	10.2	39.2	25	8	AZ998374	AZ998374	AZ998374	2M0285117
C 288	10.4	40.0	49	8	BH626011	1007110F0	C 361	10.2	39.2	26	8	AZ308315	AZ308315	AZ308315	1M0011L08
C 289	10.4	40.0	49	9	CL528213	EY10202-3	C 362	10.2	39.2	26	8	AZ807322	AZ807322	AZ807322	2M0039B07
C 290	10.4	40.0	49	9	CL705938	EY08057-3	C 363	10.2	39.2	26	8	AZ8093250	AZ8093250	AZ8093250	2M0073J08
C 291	10.4	40.0	50	1	AU102580	AU102580	C 364	10.2	39.2	26	8	AZ810543	AZ810543	AZ810543	2M0076F07
C 292	10.4	40.0	50	1	AU102861	AU102861	C 365	10.2	39.2	26	8	AZ830220	AZ830220	AZ830220	2M0109N18
C 293	10.4	40.0	50	1	AU104159	AU104159	C 366	10.2	39.2	26	8	AZ832614	AZ832614	AZ832614	2M0113K18
C 294	10.4	40.0	50	1	AU104160	AU104160	C 367	10.2	39.2	26	8	AZ832633	AZ832633	AZ832633	2M0113O14
C 295	10.4	40.0	50	1	AU105806	AU105806	C 368	10.2	39.2	26	8	AZ866540	AZ866540	AZ866540	2M0177M03
C 296	10.4	40.0	50	1	AU105807	AU105807	C 369	10.2	39.2	26	8	AZ957509	AZ957509	AZ957509	2M0224119
C 297	10.4	40.0	50	1	AU105808	AU105808	C 370	10.2	39.2	26	8	AZ972389	AZ972389	AZ972389	2M0246B15
C 298	10.4	40.0	50	1	AU105809	AU105809	C 371	10.2	39.2	26	9	CL656519	PR10126D	CL656519	1M0029P09
C 299	10.4	40.0	50	1	AU105810	AU105810	C 372	10.2	39.2	27	8	AZ313034	AZ313034	AZ313034	1M0029P09
C 300	10.4	40.0	50	1	AU105811	AU105811	C 373	10.2	39.2	27	8	AZ313131	AZ313131	AZ313131	1M0029B21
C 301	10.4	40.0	50	1	AU105812	AU105812	C 374	10.2	39.2	27	8	AZ791292	AZ791292	AZ791292	2M0041I07
C 302	10.4	40.0	50	1	AU105813	AU105813	C 375	10.2	39.2	27	8	AZ794515	AZ794515	AZ794515	2M0048O14
C 303	10.4	40.0	50	1	AU105814	AU105814	C 376	10.2	39.2	27	8	AZ795786	AZ795786	AZ795786	2M0051M10
C 304	10.4	40.0	50	1	AU105816	AU105816	C 377	10.2	39.2	27	8	AZ796535	AZ796535	AZ796535	2M0052M14
C 305	10.4	40.0	50	1	AU105817	AU105817	C 378	10.2	39.2	27	8	AZ799212	AZ799212	AZ799212	2M0056M17
C 306	10.4	40.0	50	1	AU105818	AU105818	C 379	10.2	39.2	27	8	AZ799549	AZ799549	AZ799549	2M0057F04
C 307	10.4	40.0	50	1	AU105819	AU105819	C 380	10.2	39.2	27	8	AZ799604	AZ799604	AZ799604	2M0057J07
C 308	10.4	40.0	50	1	AU105820	AU105820	C 381	10.2	39.2	27	8	AZ800386	AZ800386	AZ800386	2M0058C19
C 309	10.4	40.0	50	1	AU105821	AU105821	C 382	10.2	39.2	27	8	AZ801592	AZ801592	AZ801592	2M0060C08
C 310	10.4	40.0	50	1	AU105822	AU105822	C 383	10.2	39.2	27	8	AZ806789	AZ806789	AZ806789	2M0069N05
C 311	10.4	40.0	50	1	AU105824	AU105824	C 384	10.2	39.2	27	8	AZ808042	AZ808042	AZ808042	2M0071M17
C 312	10.4	40.0	50	1	AU105825	AU105825	C 385	10.2	39.2	27	8	AZ808073	AZ808073	AZ808073	2M0071H19
C 313	10.4	40.0	50	1	AU105826	AU105826	C 386	10.2	39.2	27	8	AZ810590	AZ810590	AZ810590	2M0076P07
C 314	10.4	40.0	50	1	AU107943	AU107943	C 387	10.2	39.2	27	8	AZ819504	AZ819504	AZ819504	2M0091K08
C 315	10.4	40.0	50	4	BM565712	rt01d07.y	C 388	10.2	39.2	27	8	AZ820845	AZ820845	AZ820845	2M0093N17
C 316	10.4	40.0	50	6	CF292903	30DG5--01	C 389	10.2	39.2	27	8	AZ821277	AZ821277	AZ821277	2M0094A06

390	10.2	39.2	27	8	AZ826443	AZ826443	2M0102M09	463	10.2	39.2	29	8	AZ807973	AZ807973	2M0071M10
391	10.2	39.2	27	8	AZ832524	AZ832524	2M0113B03	464	10.2	39.2	29	8	AZ808472	AZ808472	2M0072H05
392	10.2	39.2	27	8	AZ833744	AZ833744	2M0116I05	465	10.2	39.2	29	8	AZ808587	AZ808587	2M0072M11
393	10.2	39.2	27	8	AZ837747	AZ837747	2M0133I11	466	10.2	39.2	29	8	AZ808606	AZ808606	2M0072P12
394	10.2	39.2	27	8	AZ839333	AZ839333	2M0135I22	467	10.2	39.2	29	8	AZ808768	AZ808768	2M0072O23
395	10.2	39.2	27	8	AZ847608	AZ847608	2M0148P13	468	10.2	39.2	29	8	AZ809230	AZ809230	2M0073F11
396	10.2	39.2	27	8	AZ868099	AZ868099	2M0179N07	469	10.2	39.2	29	8	AZ815939	AZ815939	2M0084O06
397	10.2	39.2	27	8	AZ869082	AZ869082	2M0181K06	470	10.2	39.2	29	8	AZ822251	AZ822251	2M0095K17
398	10.2	39.2	27	8	AZ869858	AZ869858	2M0197L09	471	10.2	39.2	29	8	AZ826392	AZ826392	2M0102O06
399	10.2	39.2	27	8	AZ893858	AZ893858	2M0208L15	472	10.2	39.2	29	8	AZ828971	AZ828971	2M0106O15
400	10.2	39.2	27	8	AZ946486	AZ946486	2M0208L15	473	10.2	39.2	29	8	AZ829352	AZ829352	2M0107A04
401	10.2	39.2	27	8	AZ948876	AZ948876	2M0212P05	474	10.2	39.2	29	8	AZ830289	AZ830289	2M0109O20
402	10.2	39.2	27	8	AZ960932	AZ960932	2M0229K08	475	10.2	39.2	29	8	AZ836266	AZ836266	2M0131J05
403	10.2	39.2	27	8	AZ965764	AZ965764	2M0236D02	476	10.2	39.2	29	8	AZ836960	AZ836960	2M0132E10
404	10.2	39.2	27	8	AZ966578	AZ966578	2M0237D11	477	10.2	39.2	29	8	AZ837020	AZ837020	2M0133D19
405	10.2	39.2	27	8	AZ991875	AZ991875	2M0276L14	478	10.2	39.2	29	8	AZ837893	AZ837893	2M0133L24
406	10.2	39.2	27	8	AZ994786	AZ994786	2M0280E20	479	10.2	39.2	29	8	AZ837943	AZ837943	2M0134J03
407	10.2	39.2	27	8	AZ998457	AZ998457	2M0285J23	480	10.2	39.2	29	8	AZ838373	AZ838373	2M0134J03
408	10.2	39.2	27	8	AZ998457	AZ998457	2M0285J23	481	10.2	39.2	29	8	AZ838437	AZ838437	2M0134L24
409	10.2	39.2	27	8	AZ784399	AZ784399	2M0027O03	482	10.2	39.2	29	8	AZ838658	AZ838658	2M0135B22
410	10.2	39.2	27	8	AZ791425	AZ791425	2M0041P15	483	10.2	39.2	29	8	AZ839306	AZ839306	2M0135B22
411	10.2	39.2	27	8	AZ798860	AZ798860	2M0056A08	484	10.2	39.2	29	8	AZ839342	AZ839342	2M0135K19
412	10.2	39.2	27	8	AZ798896	AZ798896	2M0056D09	485	10.2	39.2	29	8	AZ839382	AZ839382	2M0136L04
413	10.2	39.2	27	8	AZ799537	AZ799537	2M0057N04	486	10.2	39.2	29	8	AZ839920	AZ839920	2M0136D13
414	10.2	39.2	27	8	AZ806783	AZ806783	2M0069M05	487	10.2	39.2	29	8	AZ840691	AZ840691	2M0138B19
415	10.2	39.2	27	8	AZ806940	AZ806940	2M0069O15	488	10.2	39.2	29	8	AZ841372	AZ841372	2M0138M17
416	10.2	39.2	27	8	AZ806940	AZ806940	2M0069O15	489	10.2	39.2	29	8	AZ844769	AZ844769	2M0144G17
417	10.2	39.2	27	8	AZ807481	AZ807481	2M0070C24	490	10.2	39.2	29	8	AZ845446	AZ845446	2M0145E15
418	10.2	39.2	27	8	AZ808673	AZ808673	2M0073N15	491	10.2	39.2	29	8	AZ846108	AZ846108	2M0146J09
419	10.2	39.2	27	8	AZ809358	AZ809358	2M0074J23	492	10.2	39.2	29	8	AZ846128	AZ846128	2M0146M12
420	10.2	39.2	27	8	AZ810078	AZ810078	2M0079L15	493	10.2	39.2	29	8	AZ847552	AZ847552	2M0148L08
421	10.2	39.2	27	8	AZ812559	AZ812559	2M0079L15	494	10.2	39.2	29	8	AZ849587	AZ849587	2M0151N06
422	10.2	39.2	27	8	AZ828902	AZ828902	2M0107B03	495	10.2	39.2	29	8	AZ852552	AZ852552	2M0155L19
423	10.2	39.2	27	8	AZ829336	AZ829336	2M0107B03	496	10.2	39.2	29	8	AZ853928	AZ853928	2M0157O16
424	10.2	39.2	27	8	AZ832120	AZ832120	2M0112K18	497	10.2	39.2	29	8	AZ856704	AZ856704	2M0161A14
425	10.2	39.2	27	8	AZ832580	AZ832580	2M0113N03	498	10.2	39.2	29	8	AZ857502	AZ857502	2M0162N16
426	10.2	39.2	27	8	AZ835018	AZ835018	2M0129G04	499	10.2	39.2	29	8	AZ864014	AZ864014	2M0173F19
427	10.2	39.2	27	8	AZ835127	AZ835127	2M0132O10	500	10.2	39.2	29	8	AZ866656	AZ866656	2M0177P11
428	10.2	39.2	27	8	AZ837079	AZ837079	2M0132O10	501	10.2	39.2	29	8	AZ867550	AZ867550	2M0178F20
429	10.2	39.2	27	8	AZ839120	AZ839120	2M0135B10	502	10.2	39.2	29	8	AZ867573	AZ867573	2M0178F20
430	10.2	39.2	27	8	AZ839216	AZ839216	2M0135D14	503	10.2	39.2	29	8	AZ868052	AZ868052	2M0179F07
431	10.2	39.2	27	8	AZ839362	AZ839362	2M0135N23	504	10.2	39.2	29	8	AZ873428	AZ873428	2M0187L10
432	10.2	39.2	27	8	AZ842062	AZ842062	2M0140E22	505	10.2	39.2	29	8	AZ875048	AZ875048	2M0189G23
433	10.2	39.2	27	8	AZ846096	AZ846096	2M0146H09	506	10.2	39.2	29	8	AZ876254	AZ876254	2M0191K12
434	10.2	39.2	27	8	AZ847733	AZ847733	2M0148L19	507	10.2	39.2	29	8	AZ87923	AZ87923	2M0196J13
435	10.2	39.2	27	8	AZ850325	AZ850325	2M0152F11	508	10.2	39.2	29	8	AZ8941569	AZ8941569	2M0201D19
436	10.2	39.2	27	8	AZ856565	AZ856565	2M0161I01	509	10.2	39.2	29	8	AZ942033	AZ942033	2M0202O50
437	10.2	39.2	27	8	AZ864495	AZ864495	2M0174C08	510	10.2	39.2	29	8	AZ944219	AZ944219	2M0205K09
438	10.2	39.2	27	8	AZ868530	AZ868530	2M0180I17	511	10.2	39.2	29	8	AZ944228	AZ944228	2M0205M07
439	10.2	39.2	27	8	AZ874994	AZ874994	2M0189N14	512	10.2	39.2	29	8	AZ944399	AZ944399	2M0205J19
440	10.2	39.2	27	8	AZ938515	AZ938515	2M0197D09	513	10.2	39.2	29	8	AZ944852	AZ944852	2M0206G06
441	10.2	39.2	27	8	AZ947154	AZ947154	2M0209F16	514	10.2	39.2	29	8	AZ947000	AZ947000	2M0209J05
442	10.2	39.2	27	8	AZ950140	AZ950140	2M0214A08	515	10.2	39.2	29	8	AZ947090	AZ947090	2M0209K08
443	10.2	39.2	27	8	AZ950293	AZ950293	2M0214L17	516	10.2	39.2	29	8	AZ948862	AZ948862	2M0212N03
444	10.2	39.2	27	8	AZ955343	AZ955343	2M0222H21	517	10.2	39.2	29	8	AZ950397	AZ950397	2M0214O22
445	10.2	39.2	27	8	AZ955862	AZ955862	2M0223C07	518	10.2	39.2	29	8	AZ952485	AZ952485	2M0217P13
446	10.2	39.2	27	8	AZ956564	AZ956564	2M0224E11	519	10.2	39.2	29	8	AZ955096	AZ955096	2M0221M01
447	10.2	39.2	27	8	AZ957301	AZ957301	2M0224E11	520	10.2	39.2	29	8	AZ955972	AZ955972	2M0222H16
448	10.2	39.2	27	8	AZ957480	AZ957480	2M0224D17	521	10.2	39.2	29	8	AZ957539	AZ957539	2M0224O16
449	10.2	39.2	27	8	AZ958126	AZ958126	2M0225H17	522	10.2	39.2	29	8	AZ957539	AZ957539	2M0224N19
450	10.2	39.2	27	8	AZ960208	AZ960208	2M0228K08	523	10.2	39.2	29	8	AZ957539	AZ957539	2M0225A15
451	10.2	39.2	27	8	AZ965963	AZ965963	2M0236G13	524	10.2	39.2	29	8	AZ958089	AZ958089	2M0225E22
452	10.2	39.2	27	8	AZ970840	AZ970840	2M0244D08	525	10.2	39.2	29	8	AZ958190	AZ958190	2M0230H12
453	10.2	39.2	27	8	AZ972403	AZ972403	2M0246D17	526	10.2	39.2	29	8	AZ961641	AZ961641	2M0230H12
454	10.2	39.2	27	8	AZ981711	AZ981711	2M0262C15	527	10.2	39.2	29	8	AZ963957	AZ963957	2M0233M23
455	10.2	39.2	27	8	AZ988873	AZ988873	2M0272I03	528	10.2	39.2	29	8	AZ966026	AZ966026	2M0236B20
456	10.2	39.2	27	8	AZ991007	AZ991007	2M0275C01	529	10.2	39.2	29	8	AZ966609	AZ966609	2M0237L12
457	10.2	39.2	27	8	AZ991213	AZ991213	2M0275I15	530	10.2	39.2	29	8	AZ972797	AZ972797	2M0247H06
458	10.2	39.2	27	8	AZ991736	AZ991736	2M0276D07	531	10.2	39.2	29	8	AZ972933	AZ972933	2M0246C13
459	10.2	39.2	27	8	AZ991886	AZ991886	2M0276N13	532	10.2	39.2	29	8	AZ972972	AZ972972	2M0247H06
460	10.2	39.2	27	8	AZ999615	AZ999615	2M0287I01	533	10.2	39.2	29	8	AZ975143	AZ975143	2M0250C07
461	10.2	39.2	27	8	AZ990698	AZ990698	2M0039M18	534	10.2	39.2	29	8	AZ975947	AZ975947	2M0251O08
462	10.2	39.2	27	8	AZ803584	AZ803584	2M0064M03	535	10.2	39.2	29	8	AZ976696	AZ976696	2M0252E16

536	10.2	39.2	29	8	AZ978859	2M0255B22	AZ978859	2M0255B22	609	10.2	39.2	30	8	AZ857530	2M0162C23
537	10.2	39.2	29	8	AZ979444	2M0256F09	AZ979444	2M0256F09	610	10.2	39.2	30	8	AZ861962	2M0169E05
538	10.2	39.2	29	8	AZ979467	2M0256J09	AZ979467	2M0256J09	611	10.2	39.2	30	8	AZ862555	2M0170J17
539	10.2	39.2	29	8	AZ979505	2M0256P12	AZ979505	2M0256P12	612	10.2	39.2	30	8	AZ863351	2M0171M18
540	10.2	39.2	29	8	AZ980127	2M0257L02	AZ980127	2M0257L02	613	10.2	39.2	30	8	AZ865376	2M0175O22
541	10.2	39.2	29	8	AZ980803	2M0258A04	AZ980803	2M0258A04	614	10.2	39.2	30	8	AZ867225	2M0178B06
542	10.2	39.2	29	8	AZ982334	2M0263B08	AZ982334	2M0263B08	615	10.2	39.2	30	8	AZ868611	2M0180S24
543	10.2	39.2	29	8	AZ982439	2M0263D13	AZ982439	2M0263D13	616	10.2	39.2	30	8	AZ869107	2M0181F03
544	10.2	39.2	29	8	AZ984536	2M0267K20	AZ984536	2M0267K20	617	10.2	39.2	30	8	AZ869999	2M0182N17
545	10.2	39.2	29	8	AZ988276	2M0271K09	AZ988276	2M0271K09	618	10.2	39.2	30	8	AZ871865	2M0185A04
546	10.2	39.2	29	8	AZ989655	2M0273C02	AZ989655	2M0273C02	619	10.2	39.2	30	8	AZ873389	2M0187E10
547	10.2	39.2	29	8	AZ989655	2M0273C03	AZ989655	2M0273C03	620	10.2	39.2	30	8	AZ874186	2M0188A16
548	10.2	39.2	29	8	AZ990421	2M0274E11	AZ990421	2M0274E11	621	10.2	39.2	30	8	AZ936961	2M0195A06
549	10.2	39.2	29	8	AZ990528	2M0274I15	AZ990528	2M0274I15	622	10.2	39.2	30	8	AZ937764	2M0196M06
550	10.2	39.2	29	8	AZ990565	2M0274O18	AZ990565	2M0274O18	623	10.2	39.2	30	8	AZ938710	2M0197E22
551	10.2	39.2	29	8	AZ990639	2M0274O24	AZ990639	2M0274O24	624	10.2	39.2	30	8	AZ943674	2M0204L20
552	10.2	39.2	29	8	AZ991039	2M0275I02	AZ991039	2M0275I02	625	10.2	39.2	30	8	AZ945910	2M0207P22
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554	10.2	39.2	29	8	AZ991194	2M0275B17	AZ991194	2M0275B17	627	10.2	39.2	30	8	AZ947065	2M0209F12
555	10.2	39.2	29	8	AZ991204	2M0275G17	AZ991204	2M0275G17	628	10.2	39.2	30	8	AZ947527	2M0210G14
556	10.2	39.2	29	8	AZ991324	2M0275M19	AZ991324	2M0275M19	629	10.2	39.2	30	8	AZ948181	2M0211H07
557	10.2	39.2	29	8	AZ991333	2M0275O20	AZ991333	2M0275O20	630	10.2	39.2	30	8	AZ948361	2M0211F23
558	10.2	39.2	29	8	AZ991778	2M0276K11	AZ991778	2M0276K11	631	10.2	39.2	30	8	AZ948369	2M0211H19
559	10.2	39.2	29	8	AZ991800	2M0276G09	AZ991800	2M0276G09	632	10.2	39.2	30	8	AZ948819	2M0212F06
560	10.2	39.2	29	8	AZ991835	2M0276E15	AZ991835	2M0276E15	633	10.2	39.2	30	8	AZ949638	2M0213K01
561	10.2	39.2	29	8	AZ991844	2M0276F18	AZ991844	2M0276F18	634	10.2	39.2	30	8	AZ950186	2M0214I08
562	10.2	39.2	29	8	AZ991898	2M0276P14	AZ991898	2M0276P14	635	10.2	39.2	30	8	AZ950989	2M0215H14
563	10.2	39.2	29	8	AZ991927	2M0276P19	AZ991927	2M0276P19	636	10.2	39.2	30	8	AZ953191	2M0218L16
564	10.2	39.2	29	8	AZ991953	2M0276J23	AZ991953	2M0276J23	637	10.2	39.2	30	8	AZ953639	2M0219B01
565	10.2	39.2	29	8	AZ991972	2M0276N19	AZ991972	2M0276N19	638	10.2	39.2	30	8	AZ955241	2M0221P15
566	10.2	39.2	29	8	AZ991979	2M0276O21	AZ991979	2M0276O21	639	10.2	39.2	30	8	AZ955367	2M0221L23
567	10.2	39.2	29	8	AZ992645	2M0277E20	AZ992645	2M0277E20	640	10.2	39.2	30	8	AZ958813	2M0226F14
568	10.2	39.2	29	8	AZ992674	2M0277J19	AZ992674	2M0277J19	641	10.2	39.2	30	8	AZ964444	2M0234F07
569	10.2	39.2	29	8	AZ995222	2M0281A03	AZ995222	2M0281A03	642	10.2	39.2	30	8	AZ969397	2M0242H09
570	10.2	39.2	30	8	AZ119002	1M0038H19	AZ119002	1M0038H19	643	10.2	39.2	30	8	AZ970104	2M0243B08
571	10.2	39.2	30	8	AZ790771	2M0039K20	AZ790771	2M0039K20	644	10.2	39.2	30	8	AZ973179	2M0247L14
572	10.2	39.2	30	8	AZ803600	2M0064F03	AZ803600	2M0064F03	645	10.2	39.2	30	8	AZ974462	2M0249K05
573	10.2	39.2	30	8	AZ804386	2M0065O16	AZ804386	2M0065O16	646	10.2	39.2	30	8	AZ975128	2M0250O05
574	10.2	39.2	30	8	AZ805635	2M0067E10	AZ805635	2M0067E10	647	10.2	39.2	30	8	AZ975394	2M0250N20
575	10.2	39.2	30	8	AZ808562	2M0072I08	AZ808562	2M0072I08	648	10.2	39.2	30	8	AZ977930	2M0254F04
576	10.2	39.2	30	8	AZ808589	2M0072N07	AZ808589	2M0072N07	649	10.2	39.2	30	8	AZ978604	2M0255F06
577	10.2	39.2	30	8	AZ817222	2M0086M24	AZ817222	2M0086M24	650	10.2	39.2	30	8	AZ982577	2M0263L19
578	10.2	39.2	30	8	AZ829526	2M0107E17	AZ829526	2M0107E17	651	10.2	39.2	30	8	AZ985411	2M0267E18
579	10.2	39.2	30	8	AZ829704	2M0107F20	AZ829704	2M0107F20	652	10.2	39.2	30	8	AZ987758	2M0270L23
580	10.2	39.2	30	8	AZ832660	2M0113E19	AZ832660	2M0113E19	653	10.2	39.2	30	8	AZ990317	2M0274C01
581	10.2	39.2	30	8	AZ837070	2M0132N07	AZ837070	2M0132N07	654	10.2	39.2	30	8	AZ990618	2M0274K19
582	10.2	39.2	30	8	AZ837657	2M0133J01	AZ837657	2M0133J01	655	10.2	39.2	30	8	AZ990637	2M0274O20
583	10.2	39.2	30	8	AZ838321	2M0134A03	AZ838321	2M0134A03	656	10.2	39.2	30	8	AZ991051	2M0275K02
584	10.2	39.2	30	8	AZ838416	2M0134A11	AZ838416	2M0134A11	657	10.2	39.2	30	8	AZ991195	2M0275E18
585	10.2	39.2	30	8	AZ838494	2M0134O11	AZ838494	2M0134O11	658	10.2	39.2	30	8	AZ991235	2M0275M15
586	10.2	39.2	30	8	AZ839722	2M0136B04	AZ839722	2M0136B04	659	10.2	39.2	30	8	AZ991250	2M0275O18
587	10.2	39.2	30	8	AZ839735	2M0136D05	AZ839735	2M0136D05	660	10.2	39.2	30	8	AZ991316	2M0275K23
588	10.2	39.2	30	8	AZ839758	2M0136H04	AZ839758	2M0136H04	661	10.2	39.2	30	8	AZ991336	2M0275O23
589	10.2	39.2	30	8	AZ839786	2M0136M02	AZ839786	2M0136M02	662	10.2	39.2	30	8	AZ991788	2M0276M09
590	10.2	39.2	30	8	AZ839788	2M0136M04	AZ839788	2M0136M04	663	10.2	39.2	30	8	AZ992456	2M0277D09
591	10.2	39.2	30	8	AZ839900	2M0136P10	AZ839900	2M0136P10	664	10.2	39.2	30	8	AZ992609	2M0277O13
592	10.2	39.2	30	8	AZ840014	2M0136C24	AZ840014	2M0136C24	665	10.2	39.2	30	8	AZ992640	2M0277D20
593	10.2	39.2	30	8	AZ840026	2M0136B24	AZ840026	2M0136B24	666	10.2	39.2	30	8	AZ992708	2M0277O23
594	10.2	39.2	30	8	AZ843426	2M0142J15	AZ843426	2M0142J15	667	10.2	39.2	30	8	AZ993143	2M0278L04
595	10.2	39.2	30	8	AZ846173	2M0146E15	AZ846173	2M0146E15	668	10.2	39.2	30	8	AZ993180	2M0278D07
596	10.2	39.2	30	8	AZ846310	2M0146M24	AZ846310	2M0146M24	669	10.2	39.2	30	8	AZ994847	2M0280O24
597	10.2	39.2	30	8	AZ847602	2M0148D17	AZ847602	2M0148D17	670	10.2	39.2	30	8	AZ996296	2M0282L22
598	10.2	39.2	30	8	AZ847620	2M0148H13	AZ847620	2M0148H13	671	10.2	39.2	30	8	BH906106	SALK 1092
599	10.2	39.2	30	8	AZ848426	2M0149I22	AZ848426	2M0149I22	672	10.2	39.2	30	9	CL610227	EY08868-5
600	10.2	39.2	30	8	AZ848931	2M0150H09	AZ848931	2M0150H09	673	10.2	39.2	31	8	AZ806127	2M0068C03
601	10.2	39.2	30	8	AZ851249	2M0153I23	AZ851249	2M0153I23	674	10.2	39.2	31	8	AZ806944	2M0069P16
602	10.2	39.2	30	8	AZ852447	2M0155K12	AZ852447	2M0155K12	675	10.2	39.2	31	8	AZ807391	2M0070F07
603	10.2	39.2	30	8	AZ852472	2M0155M19	AZ852472	2M0155M19	676	10.2	39.2	31	8	AZ807531	2M0070M19
604	10.2	39.2	30	8	AZ852582	2M0155A23	AZ852582	2M0155A23	677	10.2	39.2	31	8	AZ807948	2M0071H10
605	10.2	39.2	30	8	AZ852622	2M0155M23	AZ852622	2M0155M23	678	10.2	39.2	31	8	AZ808111	2M0071P23
606	10.2	39.2	30	8	AZ853915	2M0157M15	AZ853915	2M0157M15	679	10.2	39.2	31	8	AZ809197	2M0073P05
607	10.2	39.2	30	8	AZ854509	2M0158E10	AZ854509	2M0158E10	680	10.2	39.2	31	8	AZ820919	2M0093O20
608	10.2	39.2	30	8	AZ855251	2M0159A13	AZ855251	2M0159A13	681	10.2	39.2	31	8	AZ831604	2M0111L20

682	10.2	39.2	31	8	AZ832155	2M0112D24	755	10.2	39.2	31	8	AZ991782	2M0276H24	1
683	10.2	39.2	31	8	AZ832809	2M0113B20	756	10.2	39.2	31	8	AZ991943	2M0276H24	2
684	10.2	39.2	31	8	AZ836914	2M0132B06	757	10.2	39.2	31	8	AZ991951	2M0276K21	3
685	10.2	39.2	31	8	AZ837069	2M0132M12	758	10.2	39.2	31	8	AZ991957	2M0279A06	4
686	10.2	39.2	31	8	AZ837184	2M0132A22	759	10.2	39.2	31	8	AZ993789	2M0280A03	5
687	10.2	39.2	31	8	AZ838326	2M0134B02	760	10.2	39.2	31	8	AZ994488	2M0281O22	6
688	10.2	39.2	31	8	AZ838401	2M0134O01	761	10.2	39.2	31	8	AZ996181	2M0282I14	7
689	10.2	39.2	31	8	AZ838570	2M0134M13	762	10.2	39.2	31	8	AZ996181	2M0282I14	8
690	10.2	39.2	31	8	AZ838577	2M0134N16	763	10.2	39.2	32	5	BQ584220	S013209W-	9
691	10.2	39.2	31	8	AZ838581	2M0134O14	764	10.2	39.2	32	8	AZ360143	1M0103H18	10
692	10.2	39.2	31	8	AZ838677	2M0134P20	765	10.2	39.2	32	8	AZ803522	2M0064B01	11
693	10.2	39.2	31	8	AZ839355	2M0135M20	766	10.2	39.2	32	8	AZ805623	2M0067B08	12
694	10.2	39.2	31	8	AZ839737	2M0136E01	767	10.2	39.2	32	8	AZ810455	2M0076B05	13
695	10.2	39.2	31	8	AZ839817	2M0136B09	768	10.2	39.2	32	8	AZ819491	2M0091I07	14
696	10.2	39.2	31	8	AZ839874	2M0136L08	769	10.2	39.2	32	8	AZ832716	2M0113L07	15
697	10.2	39.2	31	8	AZ839879	2M0136N13	770	10.2	39.2	32	8	AZ832817	2M0113P23	16
698	10.2	39.2	31	8	AZ839979	2M0136A21	771	10.2	39.2	32	8	AZ836418	2M0131E14	17
699	10.2	39.2	31	8	AZ840068	2M0136N19	772	10.2	39.2	32	8	AZ837059	2M0132L08	18
700	10.2	39.2	31	8	AZ840618	2M0138D16	773	10.2	39.2	32	8	AZ837065	2M0132M08	19
701	10.2	39.2	31	8	AZ840757	2M0138M21	774	10.2	39.2	32	8	AZ837128	2M0132G18	20
702	10.2	39.2	31	8	AZ844613	2M0144L03	775	10.2	39.2	32	8	AZ837159	2M0132M15	21
703	10.2	39.2	31	8	AZ846161	2M0146C15	776	10.2	39.2	32	8	AZ837251	2M0132M19	22
704	10.2	39.2	31	8	AZ846193	2M0146I13	777	10.2	39.2	32	8	AZ838330	2M0134B06	23
705	10.2	39.2	31	8	AZ847512	2M0148J08	778	10.2	39.2	32	8	AZ838389	2M0134M01	24
706	10.2	39.2	31	8	AZ847662	2M0148O15	779	10.2	39.2	32	8	AZ838575	2M0134N14	25
707	10.2	39.2	31	8	AZ848397	2M0149D19	780	10.2	39.2	32	8	AZ838669	2M0134N24	26
708	10.2	39.2	31	8	AZ848907	2M0150A21	781	10.2	39.2	32	8	AZ839051	2M0135E06	27
709	10.2	39.2	31	8	AZ849534	2M0151E01	782	10.2	39.2	32	8	AZ839197	2M0135F10	28
710	10.2	39.2	31	8	AZ849626	2M0151E11	783	10.2	39.2	32	8	AZ839931	2M0136E18	29
711	10.2	39.2	31	8	AZ851886	2M0155G09	784	10.2	39.2	32	8	AZ840447	2M0138E06	30
712	10.2	39.2	31	8	AZ852376	2M0155G09	785	10.2	39.2	32	8	AZ843370	2M0143P08	31
713	10.2	39.2	31	8	AZ853312	2M0156L24	786	10.2	39.2	32	8	AZ848851	2M0150J02	32
714	10.2	39.2	31	8	AZ853949	2M0157C20	787	10.2	39.2	32	8	AZ852354	2M0155I17	33
715	10.2	39.2	31	8	AZ855674	2M0161G18	788	10.2	39.2	32	8	AZ862527	2M0170F13	34
716	10.2	39.2	31	8	AZ862384	2M0170L02	789	10.2	39.2	32	8	AZ863862	2M0173J07	35
717	10.2	39.2	31	8	AZ863759	2M0173G04	790	10.2	39.2	32	8	AZ864470	2M0174N05	36
718	10.2	39.2	31	8	AZ866666	2M0177B16	791	10.2	39.2	32	8	AZ867383	2M0178O07	37
719	10.2	39.2	31	8	AZ867945	2M0179C05	792	10.2	39.2	32	8	AZ867496	2M0178B22	38
720	10.2	39.2	31	8	AZ868583	2M0180B24	793	10.2	39.2	32	8	AZ868610	2M0180G21	39
721	10.2	39.2	31	8	AZ869784	2M0182I03	794	10.2	39.2	32	8	AZ875696	2M0190C19	40
722	10.2	39.2	31	8	AZ877191	2M0192O17	795	10.2	39.2	32	8	AZ877060	2M0192D01	41
723	10.2	39.2	31	8	AZ937090	2M0195H07	796	10.2	39.2	32	8	AZ937706	2M0196D01	42
724	10.2	39.2	31	8	AZ937090	2M0208H05	797	10.2	39.2	32	8	AZ937854	2M0196M09	43
725	10.2	39.2	31	8	AZ948419	2M0211P23	798	10.2	39.2	32	8	AZ941503	2M0201H13	44
726	10.2	39.2	31	8	AZ948419	2M0212K15	799	10.2	39.2	32	8	AZ945843	2M0207B19	45
727	10.2	39.2	31	8	AZ950178	2M0214G12	800	10.2	39.2	32	8	AZ947024	2M0209O02	46
728	10.2	39.2	31	8	AZ950345	2M0214F20	801	10.2	39.2	32	8	AZ949070	2M0212C22	47
729	10.2	39.2	31	8	AZ952436	2M0217G17	802	10.2	39.2	32	8	AZ950941	2M0215O12	48
730	10.2	39.2	31	8	AZ956025	2M0222A23	803	10.2	39.2	32	8	AZ951847	2M0216M21	49
731	10.2	39.2	31	8	AZ956788	2M0223L19	804	10.2	39.2	32	8	AZ952214	2M0217A02	50
732	10.2	39.2	31	8	AZ956788	2M0225A17	805	10.2	39.2	32	8	AZ952293	2M0217N05	51
733	10.2	39.2	31	8	AZ961858	2M0225O19	806	10.2	39.2	32	8	AZ954415	2M0220P02	52
734	10.2	39.2	31	8	AZ964331	2M0234B05	807	10.2	39.2	32	8	AZ954415	2M0224E23	53
735	10.2	39.2	31	8	AZ964536	2M0234F16	808	10.2	39.2	32	8	AZ957489	2M0225N20	54
736	10.2	39.2	31	8	AZ965330	2M0235D22	809	10.2	39.2	32	8	AZ958237	2M0232S06	55
737	10.2	39.2	31	8	AZ967454	2M0238H23	810	10.2	39.2	32	8	AZ960127	2M0232L06	56
738	10.2	39.2	31	8	AZ969428	2M0242M12	811	10.2	39.2	32	8	AZ966696	2M0237N16	57
739	10.2	39.2	31	8	AZ970731	2M0244A03	812	10.2	39.2	32	8	AZ968749	2M0241C18	58
740	10.2	39.2	31	8	AZ972460	2M0246N16	813	10.2	39.2	32	8	AZ975177	2M0250H12	59
741	10.2	39.2	31	8	AZ973678	2M0248C06	814	10.2	39.2	32	8	AZ975961	2M0251A17	60
742	10.2	39.2	31	8	AZ979252	2M0263C19	815	10.2	39.2	32	8	AZ980331	2M0257N15	61
743	10.2	39.2	31	8	AZ981340	2M0264N09	816	10.2	39.2	32	8	AZ982302	2M0263L06	62
744	10.2	39.2	31	8	AZ983140	2M0268O01	817	10.2	39.2	32	8	AZ983254	2M0264A24	63
745	10.2	39.2	31	8	AZ986024	2M0268O01	818	10.2	39.2	32	8	AZ983254	2M0264A24	64
746	10.2	39.2	31	8	AZ990320	2M0274C04	819	10.2	39.2	32	8	AZ986769	2M0270M17	65
747	10.2	39.2	31	8	AZ990552	2M0274M17	820	10.2	39.2	32	8	AZ990558	2M0274K24	66
748	10.2	39.2	31	8	AZ990607	2M0274I20	821	10.2	39.2	32	8	AZ990638	2M0274O22	67
749	10.2	39.2	31	8	AZ991193	2M0275E16	822	10.2	39.2	32	8	AZ991181	2M0275C14	68
750	10.2	39.2	31	8	AZ991234	2M0275M14	823	10.2	39.2	32	8	AZ991280	2M0275G21	69
751	10.2	39.2	31	8	AZ991242	2M0275N16	824	10.2	39.2	32	8	AZ991280	2M0277P09	70
752	10.2	39.2	31	8	AZ991318	2M0275L19	825	10.2	39.2	32	8	AZ992523	2M0275C14	71
753	10.2	39.2	31	8	AZ991325	2M0275M20	826	10.2	39.2	32	8	AZ996949	2M0283L14	72
754	10.2	39.2	31	8	AZ991326	2M0275M22	827	10.2	39.2	33	8	AZ997790	2M0284O22	73
755	10.2	39.2	31	8	AZ991642	2M0276D01	827	10.2	39.2	33	8	AQ073302	1(2)R0791	74
												AZ391565	1M0153F16	75

828	10.2	39.2	33	8	A2826390	AZ826390	2M0102003	901	10.2	39.2	35	8	A2938626	AZ938626	2M0197H13
829	10.2	39.2	33	8	A2838402	AZ838402	2M0134002	902	10.2	39.2	35	8	A2946432	AZ946432	2M0208B18
830	10.2	39.2	33	8	A2838431	AZ838431	2M0134D10	903	10.2	39.2	35	8	A2947164	AZ947164	2M0209H14
831	10.2	39.2	33	8	A2839073	AZ839073	2M0135105	904	10.2	39.2	35	8	A2952355	AZ952355	2M0217I12
832	10.2	39.2	33	8	A2839159	AZ839159	2M0135110	905	10.2	39.2	35	8	A2953900	AZ953900	2M0219A21
833	10.2	39.2	33	8	A2845297	AZ845297	2M0145101	906	10.2	39.2	35	8	A2956772	AZ956772	2M0223I20
834	10.2	39.2	33	8	A2854110	AZ854110	2M0157R20	907	10.2	39.2	35	8	A2958131	AZ958131	2M0225I16
835	10.2	39.2	33	8	A2862423	AZ862423	2M0170C08	908	10.2	39.2	35	8	A2961764	AZ961764	2M0230N18
836	10.2	39.2	33	8	A2863745	AZ863745	2M0173E02	909	10.2	39.2	35	8	A2970172	AZ970172	2M0234A14
837	10.2	39.2	33	8	A2940735	AZ940735	2M0200A15	910	10.2	39.2	35	8	A2979538	AZ979538	2M0256F15
838	10.2	39.2	33	8	A2942324	AZ942324	2M0203N18	911	10.2	39.2	35	8	A2980857	AZ980857	2M0258L05
839	10.2	39.2	33	8	A2952522	AZ952522	2M0217F22	912	10.2	39.2	35	8	A2983984	AZ983984	2M0265O15
840	10.2	39.2	33	8	A2952958	AZ952958	2M0218B06	913	10.2	39.2	35	8	A2984070	AZ984070	2M0265K24
841	10.2	39.2	33	8	A2955142	AZ955142	2M0221E08	914	10.2	39.2	35	8	A2986047	AZ986047	2M0268C07
842	10.2	39.2	33	8	A2957332	AZ957332	2M0224J12	915	10.2	39.2	35	8	BZ596652	BZ596652	SALK 0929
843	10.2	39.2	33	8	A2957440	AZ957440	2M0224M11	916	10.2	39.2	36	8	A2791443	AZ791443	2M0041C23
844	10.2	39.2	33	8	A2958047	AZ958047	2M0225H15	917	10.2	39.2	36	8	A2810526	AZ810526	2M0076A09
845	10.2	39.2	33	8	A2958229	AZ958229	2M0225L24	918	10.2	39.2	36	8	A2837047	AZ837047	2M0132J07
846	10.2	39.2	33	8	A2960194	AZ960194	2M0228H12	919	10.2	39.2	36	8	A2839996	AZ839996	2M0136P18
847	10.2	39.2	33	8	A2967483	AZ967483	2M0238N19	920	10.2	39.2	36	8	A2874214	AZ874214	2M0188F15
848	10.2	39.2	33	8	A2967973	AZ967973	2M0240F10	921	10.2	39.2	36	8	A2947026	AZ947026	2M0209O04
849	10.2	39.2	33	8	A2968802	AZ968802	2M0241M16	922	10.2	39.2	36	8	A2949119	AZ949119	2M0212L23
850	10.2	39.2	33	8	A2970166	AZ970166	2M0243P07	923	10.2	39.2	36	8	A2950188	AZ950188	2M0214I10
851	10.2	39.2	33	8	A2983785	AZ983785	2M0265L06	924	10.2	39.2	36	8	A2958098	AZ958098	2M0225C13
852	10.2	39.2	33	8	A2986967	AZ986967	2M0269E22	925	10.2	39.2	36	8	A2974514	AZ974514	2M0249E10
853	10.2	39.2	33	8	A2990307	AZ990307	2M0274A03	926	10.2	39.2	36	8	A2974570	AZ974570	2M0249P08
854	10.2	39.2	33	8	A2990553	AZ990553	2M0274M18	927	10.2	39.2	36	8	A2983835	AZ983835	2M0265E10
855	10.2	39.2	33	8	A2991008	AZ991008	2M0275C04	928	10.2	39.2	36	8	A2984658	AZ984658	2M0266B16
856	10.2	39.2	33	8	A2993876	AZ993876	2M0279A07	929	10.2	39.2	36	8	A2991248	AZ991248	2M0275O16
857	10.2	39.2	33	8	A2994505	AZ994505	2M0280D02	930	10.2	39.2	36	8	A2994842	AZ994842	2M0280O19
858	10.2	39.2	33	8	A2996961	AZ996961	2M0283N14	931	10.2	39.2	36	9	AL757413	AL757413	ArabiDops
859	10.2	39.2	33	8	BH758934	BH758934	P(5'why)11	932	10.2	39.2	36	9	BX893025	BX893025	ArabiDops
860	10.2	39.2	33	1	AU255089	AU255089	SALK 1451	933	10.2	39.2	37	4	BG340929	BG340929	602462648
861	10.2	39.2	34	8	A2784465	AZ784465	2M0027012	934	10.2	39.2	37	8	A2810690	AZ810690	2M0076121
862	10.2	39.2	34	8	A2800395	AZ800395	2M0058D23	935	10.2	39.2	37	8	A2835881	AZ835881	2M0130P17
863	10.2	39.2	34	8	A280395	AZ80395	2M0058D23	936	10.2	39.2	37	8	A2838465	AZ838465	2M0134J09
864	10.2	39.2	34	8	A2820901	AZ820901	2M0093K24	937	10.2	39.2	37	8	A2839334	AZ839334	2M0135I23
865	10.2	39.2	34	8	A2832199	AZ832199	2M0112P22	938	10.2	39.2	37	8	A2839725	AZ839725	2M0136C01
866	10.2	39.2	34	8	A2836559	AZ836559	2M0131M19	939	10.2	39.2	37	8	A2840073	AZ840073	2M0136N24
867	10.2	39.2	34	8	A2838543	AZ838543	2M0134H14	940	10.2	39.2	37	8	A2846075	AZ846075	2M0146D12
868	10.2	39.2	34	8	A2838578	AZ838578	2M0134N17	941	10.2	39.2	37	8	A2846252	AZ846252	2M0146C22
869	10.2	39.2	34	8	A2839356	AZ839356	2M0135M21	942	10.2	39.2	37	8	A2877196	AZ877196	2M0192O22
870	10.2	39.2	34	8	A2839978	AZ839978	2M0136M18	943	10.2	39.2	37	8	A2958064	AZ958064	2M0225L08
871	10.2	39.2	34	8	A2840431	AZ840431	2M0138C02	944	10.2	39.2	37	8	A2960363	AZ960363	2M0228F22
872	10.2	39.2	34	8	A2845481	AZ845480	2M0145K15	945	10.2	39.2	37	8	A2966579	AZ966579	2M0237D12
873	10.2	39.2	34	8	A2846247	AZ846247	2M0146B23	946	10.2	39.2	37	8	A2966608	AZ966608	2M0237L11
874	10.2	39.2	34	8	A2846782	AZ846782	2M0147D09	947	10.2	39.2	37	8	A2978697	AZ978697	2M0255F12
875	10.2	39.2	34	8	A2847627	AZ847627	2M0148I14	948	10.2	39.2	37	8	A2989928	AZ989928	2M0273N24
876	10.2	39.2	34	8	A2852328	AZ852328	2M0155J17	949	10.2	39.2	37	8	A2991963	AZ991963	2M0276G21
877	10.2	39.2	34	8	A2853746	AZ853746	2M0157F04	950	10.2	39.2	37	8	A2995580	AZ995580	2M0281F19
878	10.2	39.2	34	8	A2855078	AZ855078	2M0159A03	951	10.2	39.2	37	8	BH789722	BH789722	SALK 0445
879	10.2	39.2	34	8	A2860323	AZ860323	2M0166G14	952	10.2	39.2	37	9	AL770434	AL770434	ArabiDops
880	10.2	39.2	34	8	A2875088	AZ875088	2M0189N23	953	10.2	39.2	38	2	BE739510	BE739510	601556438
881	10.2	39.2	34	8	A2875578	AZ875578	2M0190H01	954	10.2	39.2	38	8	A2839728	AZ839728	2M0136C04
882	10.2	39.2	34	8	A2942009	AZ942009	2M0202C04	955	10.2	39.2	38	8	A2839728	AZ839728	2M0136C04
883	10.2	39.2	34	8	A2947569	AZ947569	2M0210N15	956	10.2	39.2	38	8	A2945774	AZ945774	2M0207M17
884	10.2	39.2	34	8	A2950380	AZ950380	2M0214K11	957	10.2	39.2	38	8	A2947169	AZ947169	2M0209J15
885	10.2	39.2	34	8	A2950520	AZ950520	2M0214L22	958	10.2	39.2	38	8	A2947546	AZ947546	2M0210J15
886	10.2	39.2	34	8	A2955329	AZ955329	2M0221F19	959	10.2	39.2	38	8	A2952470	AZ952470	2M0217M16
887	10.2	39.2	34	8	A2960338	AZ960338	2M0229L08	960	10.2	39.2	38	8	A2958109	AZ958109	2M0225E16
888	10.2	39.2	34	8	A2966536	AZ966536	2M0237L01	961	10.2	39.2	38	8	A2991799	AZ991799	2M0276O08
889	10.2	39.2	34	8	A2973866	AZ973866	2M0248D13	962	10.2	39.2	38	8	A2996969	AZ996969	2M0283O16
890	10.2	39.2	34	8	A2979561	AZ979561	2M0256J15	963	10.2	39.2	38	8	BH853122	BH853122	SALK 0760
891	10.2	39.2	34	8	A2984814	AZ984814	2M0266P19	964	10.2	39.2	38	8	BZ766550	BZ766550	SALK 1375
892	10.2	39.2	34	8	A2985987	AZ985987	2M0268H03	965	10.2	39.2	38	9	BX536344	BX536344	ArabiDops
893	10.2	39.2	34	8	A2990626	AZ990626	2M0274M19	966	10.2	39.2	39	1	AU266424	AU266424	ArabiDops
894	10.2	39.2	34	8	A2991298	AZ991298	2M0275F20	967	10.2	39.2	39	7	D74282	D74282	CELKO79A5F
895	10.2	39.2	34	8	A2999092	AZ999092	2M0286K17	968	10.2	39.2	39	8	A2337982	AZ337982	1M0068E19
896	10.2	39.2	35	8	A2999098	AZ999098	2M0286K17	969	10.2	39.2	39	8	A2807468	AZ807468	2M0070A21
897	10.2	39.2	35	8	A2822134	AZ822134	2M0070D04	970	10.2	39.2	39	8	A2810534	AZ810534	2M0076C07
898	10.2	39.2	35	8	A2835004	AZ835004	2M0129D04	971	10.2	39.2	39	8	A2838400	AZ838400	2M0134N06
899	10.2	39.2	35	8	A2839805	AZ839805	2M0136P03	972	10.2	39.2	39	8	A2838622	AZ838622	2M0134F22
900	10.2	39.2	35	8	A2846212	AZ846212	2M0146L14	973	10.2	39.2	39	8	A2862284	AZ862284	2M0169J19


```
974 10.2 39.2 39 8 AZ862314 2M0169P23
975 10.2 39.2 39 8 AZ942083 2M0202P04
976 10.2 39.2 39 8 AZ942716 2M0203A03
977 10.2 39.2 39 8 AZ947232 2M0209D20
978 10.2 39.2 39 8 AZ958896 2M0226D20
979 10.2 39.2 39 8 AZ970039 2M0243J03
980 10.2 39.2 39 8 AZ989699 2M0273G07
981 10.2 39.2 39 8 AZ990508 2M0274R15
982 10.2 39.2 39 8 AZ990997 2M0275A03
983 10.2 39.2 40 8 AZ805795 2M0067F20
984 10.2 39.2 40 8 AZ829666 2M0107O16
985 10.2 39.2 40 8 AZ834909 2M0117B21
986 10.2 39.2 40 8 AZ838469 2M0134K07
987 10.2 39.2 40 8 AZ838520 2M0134D15
988 10.2 39.2 40 8 AZ847468 2M0148M01
989 10.2 39.2 40 8 AZ855417 2M0159M20
990 10.2 39.2 40 8 AZ942732 2M0203B02
991 10.2 39.2 40 8 AZ951777 2M0216P17
992 10.2 39.2 40 8 AZ952424 2M0217B17
993 10.2 39.2 40 8 AZ953244 2M0218G22
994 10.2 39.2 40 8 AZ955197 2M0221N10
995 10.2 39.2 40 8 AZ971816 2M0245N23
996 10.2 39.2 40 8 AZ975993 2M0251G13
997 10.2 39.2 40 8 AZ990597 2M0274G19
998 10.2 39.2 40 9 BX660365 Arabidops
999 10.2 39.2 41 7 D19129 MUSGS01345
1000 10.2 39.2 41 8 AZ839173 2M0135L07
```

ALIGNMENTS

```
RESULT 1
AZ959628 35 bp DNA linear GSS 27-APR-2001
LOCUS 2M0227D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0227D23 F, genomic survey sequence.
ACCESSION AZ959628.1 GI:13830855
VERSION AZ959628
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, W., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weises, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: D column: 23
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227D23"
/sex="Female"
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FEATURES

```
source
Location/Qualifiers
1. .44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_022894.23.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
```

```
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
ORIGIN
Query Match 55.4%; Score 14.4; DB 8; Length 35;
Best Local Similarity 75.0%; Pred. No. 2.5e+04; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 6;
QY 3 TCTTTCCAGATCGGTACCTCAAT 26
DB 5 TCGTACGTAGTCGACATGAT 28
```

```
RESULT 2
BZ289495/5 44 bp DNA linear GSS 24-OCT-2002
LOCUS SALK_022894.23.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_022894.23.05.x, genomic
survey sequence.
ACCESSION BZ289495
VERSION BZ289495.1 GI:24331195
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 44)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g17530.
Class: TDNA tagged.
```



```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL02839"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      52.3%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 6.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2  GTCTTTGCGAGATCGGTACC 21
      ||| ||| ||| ||| ||| |||
DB      26  GTCGTTGCCAGATCGGTGCC 45

RESULT 6
LOCUS      AUI07934      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI07934 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION  AUI07934
VERSION    AUI07934
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   21270072
PUBMED    11375929
CONTACT   Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HS101159"
                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      52.3%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 6.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  CGCTTTTCGAGATCGGTAC 20
      ||| ||| ||| ||| ||| |||
DB      23  CGGCTTTGCGAGCTCGGGAC 42

RESULT 7
TAJ344B09Q/c
LOCUS      TAJ344B09Q      37 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 344b09, reverse sequence,
            genomic survey sequence.
ACCESSION  AL495780
VERSION    AL495780.1  GI:11869820
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei

```


Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCCGAGATCGGTACTCAAT 26
|||||
Db 4 TCGTACCTAGATCGGAACATGAAT 27
|||||

RESULT 11
BX891607/c 43 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-553F11-023213,
DEFINITION genomic survey sequence.
ACCESSION BX891607
VERSION BX891607.1 GI:39924102
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL
MEDLINE 22755829
PUBMED 12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weissshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
MEDLINE
PUBMED 14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weissshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
14682050
PUBMED
4 (bases 1 to 43)
Strizhov, N., Rosso, M.G., Li, Y. and Weissshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At1g05140.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-kat/>.
Location/Qualifiers
1. .43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-553F11-023213"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 49.2%; Score 12.8; DB 9; Length 43;
Best Local Similarity 70.8%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCCGAGATCGGTACTCAAT 26
|||||
Db 25 TCATTATCTGCTGTTTCTCAAT 2
|||||

RESULT 12
AZ486826 44 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0315109R Mouse 10kb plasmid UUGClm library Mus musculus genomic
DEFINITION clone UUGClm0315109 R, genomic survey sequence.
ACCESSION AZ486826
VERSION AZ486826.1 GI:10653979
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: I column: 09
Seq primer: CACACAGGACACGATGATGACC
Class: Plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
1. .44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGClm0315109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClm library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```

Query Match      49.2%; Score 12.8; DB 8; Length 44;
Best Local Similarity 70.8%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCCTTCGCAGATCGGTACCTCAAT 26
Db 5 TCCTTCACTGTGTTTACCTCAAT 28

RESULT 13
LOCUS BH628960 45 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007075B10.1BL_y1 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence.
ACCESSION BH628960
VERSION BH628960
KEYWORDS BH628960.1 GI:18442211
SOURCE GSS.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 45)
REFERENCE Walbot, V.
AUTHORS Zea mays
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007075 column: 36
Class: transposon-tagged.
FEATURES
source
1. 45
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription web units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match      49.2%; Score 12.8; DB 8; Length 45;
Best Local Similarity 70.8%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCCTTCGCAGATCGGTACCTCAAT 26
Db 2 TCATCCTCAGATCCGACGCCCAAT 25

RESULT 14
BH846331/c

Query Match      49.2%; Score 12.8; DB 8; Length 49;
Best Local Similarity 70.8%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCCTTCGCAGATCGGTACCTCAAT 26
Db 37 TTTTTCGCAATCGTTAAGGCATT 14

RESULT 15
AA972865/c
LOCUS AA972865 34 bp mRNA linear EST 21-DEC-1998
DEFINITION OP20G03.s1 NCI CGAP Col2 Homo sapiens cDNA clone IMAGE:1576276 3, similar to TF:Q12905 Q12905 NF45 PROTEIN. ; mRNA sequence.
ACCESSION AA972865
VERSION AA972865.1 GI:3148045
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-romail.nih.gov

```

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Stratagene, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert length: 854 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES
source

Location/Qualifiers

1..34

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="IMAGE:1576276"

/sex="mixed"

/tissue type="colon tumor"

/lab host="SOLR (kanamycin resistant)"

/clone lib="NCI CGAP Col2"

/note="Organ: colon; Vector: Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. Pooled colon tumors. 5' adaptor sequence: 5'

GAATTCGACGAG 3' 3' adaptor sequence: 5'

CTCAGATTTTCTTTTCTTTTCTTTT 3' Average insert size: 1.2 kb."

ORIGIN

Query Match 47.7%; Score 12.4; DB 1; Length 34;

Best Local Similarity 72.7%; Pred. NO. 2.6e+05;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTCGACATCGGTACCT 22

||||| ||||| ||||| ||||| |||||

Db 25 CGTCTTCGCAATATCTACCT 4

RESULT 16

CR360589

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-821F03-025531,

genomic survey sequence.

ACCESSION CR360589

VERSION CR360589.1 GI:45543511

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.

GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis

thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

22755829

12874060

REFERENCE

2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

Weisshaar, B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

23117147

PUBMED

14756321

3 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and

Weisshaar, B.

High-throughput generation of sequence indexes from T-DNA

mutagenized Arabidopsis thaliana lines

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BioTechniques 35 (6), 1164-1168 (2003)

14682050

4 (bases 1 to 39)

Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004)

Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

K19B1. Details on the protocols used for generation of the sequence

are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program

designated 'GABI'. Information on line availability can be found

at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source

Location/Qualifiers

1..39

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-821F03-025531"

/clone lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/notes="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pAC106 (GenBank accession number: AJ537513). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN

Query Match 47.7%; Score 12.4; DB 9; Length 39;

Best Local Similarity 72.7%; Pred. NO. 2.6e+05;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTCGACATCGGTACCT 22

||||| ||||| ||||| ||||| |||||

Db 1 CGTCTTCGCAATCGCAACAT 22

RESULT 17

CA935542/c

LOCUS

DEFINITION

Gm-cl071-4929 5', mRNA sequence.

ACCESSION CA935542

VERSION CA935542.1 GI:27424022

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 49)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Putative full length read vector to vector length is 50
Seq primer: -40RP from Gibco.

FEATURES

Location/Qualifiers
1..49
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-ci071-4929"
/tissue_type="immature pods (~2cm long) of greenhouse grown plants"
/lab_host="DH10B"
/clone_lib="Gm-ci071"
/note="Vector: pSPOT1; Site 1: NotI; Site 2: SalI; The cDNA library was constructed from mRNA isolated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPOT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. email: l-vodkin@uiuc.edu"

ORIGIN

Query Match 47.7%; Score 12.4; DB 6; Length 49;
Best Local Similarity 72.7%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TTTCGAGATCGGTACTCAAT 26

Db 42 TTTTGCTGATGGCGATTCAT 21

RESULT 18

AU105437
LOCUS AU105437 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP15178, mRNA sequence.
ACCESSION AU105437
VERSION AU105437.1 GI:13554958
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE

EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers

source

1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP15178"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 47.7%; Score 12.4; DB 1; Length 50;
Best Local Similarity 72.7%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGTCTTTCGACATCGGTACTCT 22

Db 15 CGTCTTTCGCTTCGCGGGCCT 36

RESULT 19

AJ590848/c
LOCUS AJ590848 22 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 575G11, genomic survey sequence.
ACCESSION AJ590848
VERSION AJ590848.1 GI:37940472
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1

REFERENCE

1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

TITLE

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565

REFERENCE

2 (bases 1 to 22)

AUTHORS

Balzergue,S.

TITLE

Direct Submission

JOURNAL

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

COMMENT

Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1..22
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiliewskaja"
/db_xref="taxon:3702"
/clone="575G11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..22
/note="T-DNA flanking sequence left border"

ORIGIN

Query Match 46.9%; Score 12.2; DB 9; Length 22;
Best Local Similarity 82.4%; Pred. No. 3.2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCAGATCGGTACTCTCA 24

[illegible]

Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satchoascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers
 1. ..43
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="rcieg9sh13"
 /tissue_type="whole animal"
 /dev_stage="egg"
 /clone_lib="Nori Satcho unpublished cDNA library, egg"

FEATURES
 source

ORIGIN

Query Match	46.9%;	Score 12.2;	DB 1;	Length 43;
Best Local Similarity	82.4%;	Pred. No. 3.3e+05;		
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	10	CAGATCGGTACCTCAAT	26	
Db	20	CAGATGGGTACCGGAAI	4	

LOCUS	AL766296	45 bp	DNA	linear	GSS 01-APR-2000
DEFINITION	Arabidopsis thaliana. T-DNA flanking sequence GK-209D03-014556, genomic survey sequence.				
ACCESSION	AL766296				
VERSION	AL766296.1	GI:21519429			

KEYWORDS	GRS.
SOURCE	<i>Arabidopsis thaliana</i> (thale cress)
ORGANISM	<i>Arabidopsis thaliana</i>
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1.
AUTHORS	Li, Y., Rosso, M.G., Srizhov, N., Viehoever, P. and Weissshaar, B.

TITLE	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE	22755829
PUBMED	12874060
REFERENCE	2
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissenhaar, B.
TITLE	Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics

Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0281 row: B column: 06

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

FEATURES

source

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0281B06"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 46.2%; Score 12; DB 8; Length 26;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy

6 TTCGCAGATCGGTACTCTCA 25

Db

7 TACGTAGATCGGACATGAA 26

RESULT 23

CN973502/c

LOCUS

21001_45-39 Fundulus heteroclitus Heart Fundulus heteroclitus cDNA,

EST.

CN973502

Accession

Version

Source

Organism

Fundulus heteroclitus

(killifish)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthopterygii; Acanthopterygii; Percormorpha; Atherinomorpha;

Cyprinodontiformes; Fundulidae; Fundulus.

1 (bases 1 to 26)

Crawford,D.L., Oleksiak,M.F., Kellell,K.J., Paschall,J., VanWye,J.,

Rosch,J.L. and Whitehead,J.A.

Fundulus Functional Genomics: EST Database for Teleost Fish

Unpublished (2004)

Contact: Crawford, Douglas L.

Marine Genomics - Crawford Lab

Rosenstiel School of Marine and Atmospheric Science - University of

Miami

4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA

Tel: 305 361 4121

Email: dcrawford@rmas.miami.edu

Database Web Interface

http://genomics.rmas.miami.edu/funnybase/super_craw3/

Plate: 45 row: B column: 5.

Location/Qualifiers

1..28

/organism="Fundulus heteroclitus"

/mol_type="mRNA"

/db_xref="taxon:8078"

/tissue_type="Heart"

/clone_lib="Fundulus heteroclitus Heart"

/note="Organ: Heart"

ORIGIN

Query Match

Best Local Similarity 46.2%; Score 12; DB 7; Length 28;

Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy

3 TCTTTCCGACATCGGTACTCTCA 24

Db

22 TTTTACACAGATCGATNTCNCA 1

RESULT 24

TA383E12Q

LOCUS

DEFINITION

TA383E12Q

37 bp DNA linear

GSS

Accession

Version

Keywords

Source

Organism

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 37)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000)

Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..37

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="383e12"

Query Match

Best Local Similarity 46.2%; Score 12; DB 9; Length 37;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy

7 TCGCAGATCGGTACTCTCAAT 26

||||| ||||| ||||| ||||| |||||

Db	12	TCGCTGATAGGTTCTTGAAT	31	ORGANISM	Mus musculus
REFERENCE					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS					1 (bases 1 to 43)
TITLE					Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
JOURNAL					Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT					Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0014 row: P column: 03 Seq primer: CGGTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 43.
FEATURES					Location/Qualifiers
source					1. 43 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0014P03" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN					
Query Match		46.2%;	Score 12;	DB 8;	Length 43;
Best Local Similarity		75.0%;	Pred. No. 4.2e+05;		
Matches		15;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
QY	3	TCCTTTCGACATCGGTACCT	22		
Db	32	TCCTTCACAGTCCGTAGCT	13		
RESULT 27					
BZ664508					
LOCUS					
DEFINITION					Arabidopsis thaliana genomic clone SALK_075791.25.80.x Arabidopsis thaliana TDNA insertion lines
ACCESSION					BZ664508
VERSION					BZ664508.1
KEYWORDS					GI:28181208
SOURCE					GSS.
ORIGIN					
Query Match		46.2%;	Score 12;	DB 8;	Length 43;
Best Local Similarity		75.0%;	Pred. No. 4.2e+05;		
Matches		15;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
QY	2	GTCTTTTCGACATCGGTACC	21		
Db	20	GTCCGTCGATGTCAGTACC	1		
RESULT 26					
AZ778700/c					
LOCUS					
DEFINITION					2M0014P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0014P03 F, genomic survey sequence.
ACCESSION					AZ778700
VERSION					AZ778700.1
KEYWORDS					GI:12908611
SOURCE					GSS.
ORIGIN					
Query Match		46.2%;	Score 12;	DB 8;	Length 42;
Best Local Similarity		75.0%;	Pred. No. 4.2e+05;		
Matches		15;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
QY	2	GTCTTTTCGACATCGGTACC	21		
Db	20	GTCCGTCGATGTCAGTACC	1		
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atlg76710.
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_075791.25.80.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html."

ORIGIN
 Query Match 46.2%; Score 12; DB 8; Length 45;
 Best Local Similarity 75.0%; Pred. No. 4.2e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0

OY 4 CTTTCGCAGATCGGTACCTC 23
 | ||||| | | | | |
 Db 5 CGTTCGCAGATAGATATATC 24

RESULT 28
 CL5211995/c
 LOCUS
 DEFINITION CL5211995 45 bp DNA linear GSS 02-APR-2000
 SALK7C08 Flanking Sequence Tag of Oryza sativa T-DNA insertion line
 Oryza sativa (japonica cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL5211995
 VERSION CL5211995.1 GI:46148795
 KEYWORDS GSS.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegou,B., Droc,G., Regad,F., Bourgeois,B., Meynard,D., Perin,C., Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
 TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
 JOURNAL Plant J. (2004) In press
 COMMENT Contact: Guiderdoni
 UMR PIA Biotrop program
 CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629


```

Best Local Similarity 75.0%; Pred. No. 4.2e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTTTCGACAGATCGGTACCTC 23
    |||||
Db 28 CTTTCACAGAACGTGCCTC 9

RESULT 32
AZ805662
LOCUS 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0067K09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0067K09 F, genomic survey sequence.
ACCESSION AZ805662
VERSION AZ805662.1 GI:12966473
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: K column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
source
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0067K09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 27;

```

```

Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
    |||||
Db 12 GATCGGTACATGAAT 26

RESULT 33
AZ803827
LOCUS 28 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0064J20F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0064J20 F, genomic survey sequence.
ACCESSION AZ803827
VERSION AZ803827.1 GI:12956150
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: J column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUC2M0064J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 28;

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Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACTCAAT 26
Db 12 GATCGGTACTCAAT 26

RESULT 34
AZ9797143
LOCUS 30 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M053N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0053N07 F, genomic survey sequence.
ACCESSION AZ9797143
VERSION AZ9797143.1 GI:12945917
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 30)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: N column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0053N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203G18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 30;

Best Local Similarity 86.7%; Pred. No. 5.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACTCAAT 26
Db 12 GATCGGTACTCAAT 26

RESULT 35
AZ942892
LOCUS 32 bp DNA linear GSS 26-APR-2001
DEFINITION 2M0203G18F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0203G18 F, genomic survey sequence.
ACCESSION AZ942892
VERSION AZ942892.1 GI:13806539
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 32)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: G column: 18
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203G18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 32;

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Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACTCTCAAT 26
Db 13 GATCGGTACTATCAAT 27

RESULT 36
CL655958/c
LOCUS
DEFINITION
PR10125b.C09 - PR10125b.B21 (32) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
CL655958
VERSION
CL655958.1 GI:50135823
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
APPEND: an AcedB database for the nematode satellite organism
TITLE
Pristionchus pacificus
COMMENT
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@cuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
1..32
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/mol_type="genomic DNA"
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/db_xref="taxon:54126"
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/notes="Vector: pEpifos-5 Fosmid vector"
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Query Match 45.4%; Score 11.8; DB 9; Length 32;
Best Local Similarity 69.6%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACTCTCAAT 26
Db 29 CTCCTCAGGTCGCTATTTCAGT 7

RESULT 37
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LOCUS
DEFINITION
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2M0076C16F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0076C16 F, genomic survey sequence.
ACCESSION
AZ810604
VERSION
AZ810604.1 GI:12978019
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
1
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 16
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
FEATURES
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1..34
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/db_xref="taxon:10090"
/clone="UUGC2M0076C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 45.4%; Score 11.8; DB 8; Length 34;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACTCTCAAT 26
Db 12 GATCGGTACTATCAAT 26

RESULT 38
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LOCUS
DEFINITION
AZ803114 35 bp DNA linear GSS 16-FEB-2001
2M0063N14F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0063N14 F, genomic survey sequence.
ACCESSION
AZ803114
VERSION
AZ803114.1 GI:12955437
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE
1
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: G column: 15
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers

FEATURES
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [GII4732114|GB|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 35;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
|||||||
Db 11 GATCGGTACATGAAT 25

RESULT 40
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ810670
2M0076C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076C22 F, genomic survey sequence.
AZ810670
AZ810670.1 GI:12978150
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [GII4732114|GB|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 35;
Best Local Similarity 86.7%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GATCGGTACCTCAAT 26
|||||||
Db 9 GATCGGTACATGAAT 23

RESULT 39
AZ805718
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ805718
2M0067G15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0067G15 F, genomic survey sequence.
AZ805718
AZ805718.1 GI:12966529
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 22
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 36.

FEATURES
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/clone="UUCG2M0076C22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.4%; Score 11.8; DB 8; Length 36;
Best Local Similarity 86.7%; Pred. NO. 5.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAAT 26
|||
Db 12 GATCGGTACATGAAT 26

Search completed: November 23, 2004, 22:24:50
Job time : 1268.54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 504.21 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28
Sequence: 1 cgtcgtgggtagtcgcgtatgtgtt 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	100.0	28	6	BD181370
2	28	100.0	28	6	AX523950
3	28	100.0	28	6	AX524848
4	17	60.7	47	6	AR289945
5	15.4	55.0	36	6	AX710947
6	15.4	55.0	37	6	CO779042
7	15	53.6	15	6	BD244764
8	15	53.6	15	6	AX255271
9	15	53.6	19	6	AX645654
10	15	53.6	19	6	AX645658
11	14.6	52.1	21	6	AX097318
12	14.6	52.1	23	6	E31555
13	14.6	52.1	38	6	AR172071
14	14.6	52.1	38	6	AR173362
15	14.6	52.1	50	6	AR437662
16	14.6	52.1	50	6	AX026712
17	14.4	51.4	32	6	AR200549
18	14.4	51.4	38	6	AR082475
19	14.4	51.4	38	6	AR083603

38	6	AR111795	Sequence
38	6	AR124707	Sequence
38	6	AR171824	Sequence
38	6	BD267970	Inhibitor
38	6	BD270873	Inhibitor
38	6	BD272024	Inhibitor
38	6	BD272043	Inhibitor
38	6	BD274581	Inhibitor
38	6	BD274600	Inhibitor
38	6	AR181816	Sequence
38	6	AR195282	Sequence
38	6	AR199998	Sequence
38	6	AR201351	Sequence
38	6	AR201370	Sequence
38	6	AR216094	Sequence
38	6	AR224803	Sequence
38	6	AR317262	Sequence
38	6	AR337537	Sequence
38	6	AR366761	Sequence
38	6	AR368676	Sequence
38	6	AR383170	Sequence
38	6	AR409174	Sequence
38	6	AX029442	Sequence
38	6	BD075049	Method fo
38	6	BD075063	Method fo
20	6	AR053322	Sequence
20	6	I40941	Sequence 58
46	6	A98787	Sequence 20
47	6	AR242315	Sequence
48	6	BD264534	Compounds
48	6	BD264534	Compounds
48	6	AR229345	Sequence
48	6	AR321963	Sequence
48	6	AX155972	Sequence
48	6	AX361822	Sequence
48	6	AX361822	Sequence
25	6	CO830679	Sequence
25	6	AX196933	Sequence
26	6	I22747	Sequence 23
40	6	I47572	Sequence 23
41	6	AX020989	Sequence
41	6	AR153180	Sequence
20	6	AR163349	Sequence
20	6	BD242951	Method fo
20	6	AX247509	Sequence
25	6	AR071262	Sequence
26	6	AX455128	Sequence
27	6	AX455128	Sequence
35	6	A19074	oligonucleo
35	6	AR059409	Sequence
35	6	AR178490	Sequence
35	6	A91103	Sequence 6
36	6	AR130192	Sequence 5
39	6	A91102	Sequence 5
42	6	AR130191	Sequence
42	6	E36958	Human telom
42	6	AR243479	Sequence
42	6	AR390635	Sequence
42	6	AR393249	Sequence
42	6	AX810540	Sequence
42	6	BD011209	Human tel
42	6	MMB6B14	M. musculus
50	6	AR282232	Sequence
24	6	CQ754213	Sequence
31	6	AX248279	Sequence
48	6	AR208509	Sequence
48	6	AR473650	Sequence 13
18	6	I33520	Sequence 13
18	6	I33521	Sequence 14
26	6	AX022232	Sequence
26	6	BD009976	Human muc
37	6	BD243257	Variants
39	6	BD061606	Novel rec
39	6	BD102069	Novel rec
43	6	AR041126	Sequence
43	6	AX472654	Sequence

93	13.2	47.1	45	6	AR237994 Sequence	166	12.6	45.0	20	6	BD080533	BD080533 Large-sca
c 94	13.2	47.1	47	6	E37138 Method for	c 167	12.6	45.0	24	6	AX116463	AX116463 Sequence
c 95	13	46.4	21	6	BD144876 A method	168	12.6	45.0	25	6	BD169709	BD169709 Human gli
c 96	13	46.4	23	6	BD097354 Method fo	169	12.6	45.0	27	6	AX117876	AX117876 Sequence
c 97	13	46.4	25	6	AX500848 Sequence	c 170	12.6	45.0	30	6	AR220730	AR220730 Sequence
c 98	13	46.4	25	6	AX500849 Sequence	171	12.6	45.0	30	6	BD091353	BD091353 Method of
c 99	13	46.4	25	6	AX500850 Sequence	c 172	12.6	45.0	30	6	BD137054	BD137054 Method of
c 100	13	46.4	25	6	AX500851 Sequence	173	12.6	45.0	38	6	A26131	A26131 Artificial
c 101	13	46.4	25	6	AX500852 Sequence	174	12.6	45.0	38	6	A29558	A29558 K.lactis ge
c 102	13	46.4	26	6	BD078207 Modulator	175	12.6	45.0	38	6	AR045708	AR045708 Sequence
c 103	13	46.4	27	6	AX253011 Sequence	176	12.6	45.0	38	6	AR047595	AR047595 Sequence
c 104	13	46.4	30	6	I27669 Sequence 24	177	12.6	45.0	38	6	133669	133669 Sequence 12
c 105	13	46.4	32	6	A08190 Oligonucleo	178	12.6	45.0	38	6	143817	143817 Sequence 4
c 106	13	46.4	36	6	AR206961 Sequence	179	12.6	45.0	38	6	152760	152760 Sequence 50
c 107	13	46.4	36	6	AR206963 Sequence	180	12.6	45.0	38	6	154647	154647 Sequence 23
c 108	13	46.4	36	6	BD107722 Tissue pl	c 181	12.6	45.0	38	6	AX111341	AX111341 Sequence
c 109	13	46.4	36	6	BD107724 Tissue pl	c 182	12.6	45.0	39	6	AS1623	AS1623 Sequence 33
c 110	13	46.4	40	6	BD180768 Array of	c 183	12.6	45.0	39	9	HSC085717	HSC085717 Sequence m
c 111	13	46.4	43	6	AR034922 Sequence	c 184	12.6	45.0	41	6	BD249724	BD249724 Productio
c 112	13	46.4	47	6	AX590990 Sequence	c 185	12.6	45.0	41	6	AR316683	AR316683 Sequence
c 113	13	46.4	47	6	AX591143 Sequence	c 186	12.6	45.0	41	6	AX134748	AX134748 Sequence
c 114	13	46.4	47	6	AX717566 Sequence	c 187	12.6	45.0	42	6	BD249722	BD249722 Productio
c 115	12.8	45.7	20	6	AX294614 Sequence	c 188	12.6	45.0	42	6	AR306649	AR306649 Sequence
c 116	12.8	45.7	21	6	BD217310 Detection	c 189	12.6	45.0	42	6	AR316681	AR316681 Sequence
c 117	12.8	45.7	21	6	AX009459 Sequence	c 190	12.6	45.0	42	6	AR340084	AR340084 Sequence
c 118	12.8	45.7	24	6	AX173390 Sequence	c 191	12.6	45.0	42	6	AR412153	AR412153 Sequence
c 119	12.8	45.7	24	6	AX289981 Sequence	c 192	12.6	45.0	42	6	AX134745	AX134745 Sequence
c 120	12.8	45.7	27	6	AX356260 Sequence	c 193	12.6	45.0	42	6	AX301873	AX301873 Sequence
c 121	12.8	45.7	30	6	AX598040 Sequence	c 194	12.6	45.0	42	6	AX301890	AX301890 Sequence
c 122	12.8	45.7	38	6	AR082481 Sequence	c 195	12.6	45.0	45	6	AR262362	AR262362 Sequence
c 123	12.8	45.7	38	6	AR083609 Sequence	c 196	12.6	45.0	45	6	BD102842	BD102842 Sequence
c 124	12.8	45.7	38	6	AR111801 Sequence	c 197	12.6	45.0	47	6	AR289438	AR289438 Sequence
c 125	12.8	45.7	38	6	AR124713 Sequence	c 198	12.6	45.0	50	14	CXA5TERM	CXA5TERM Beta-Lipo
c 126	12.8	45.7	38	6	AR171830 Sequence	c 199	12.4	44.3	24	6	AX289693	AX289693 Sequence
c 127	12.8	45.7	38	6	BD267976 Inhibitor	c 200	12.4	44.3	24	6	AX290199	AX290199 Sequence
c 128	12.8	45.7	38	6	BD267979 Inhibitor	c 201	12.4	44.3	26	6	AX110367	AX110367 Sequence
c 129	12.8	45.7	38	6	BD270879 Inhibitor	c 202	12.4	44.3	30	6	A42452	A42452 Sequence 1
c 130	12.8	45.7	38	6	BD272030 Inhibitor	c 203	12.4	44.3	31	6	AX057066	AX057066 Sequence
c 131	12.8	45.7	38	6	BD272049 Inhibitor	c 204	12.4	44.3	31	6	AR142919	AR142919 Sequence
c 132	12.8	45.7	38	6	BD274587 Inhibitor	c 205	12.4	44.3	31	6	AR142935	AR142935 Sequence
c 133	12.8	45.7	38	6	BD274606 Inhibitor	c 206	12.4	44.3	32	6	AR065300	AR065300 Sequence
c 134	12.8	45.7	38	6	AR181822 Sequence	c 207	12.4	44.3	32	6	AR065301	AR065301 Sequence
c 135	12.8	45.7	38	6	AR195288 Sequence	c 208	12.4	44.3	33	6	AX427960	AX427960 Sequence
c 136	12.8	45.7	38	6	AR195291 Sequence	c 209	12.4	44.3	36	6	145574	145574 Sequence 2
c 137	12.8	45.7	38	6	AR200004 Sequence	c 210	12.4	44.3	36	6	AR481892	AR481892 Sequence
c 138	12.8	45.7	38	6	AR201357 Sequence	c 211	12.4	44.3	36	6	AX111714	AX111714 Sequence
c 139	12.8	45.7	38	6	AR201376 Sequence	c 212	12.4	44.3	36	6	AX167463	AX167463 Sequence
c 140	12.8	45.7	38	6	AR201379 Sequence	c 213	12.4	44.3	37	6	BD250410	BD250410 Methods f
c 141	12.8	45.7	38	6	AR216100 Sequence	c 214	12.4	44.3	37	6	BD269056	BD269056 Method fo
c 142	12.8	45.7	38	6	AR216103 Sequence	c 215	12.4	44.3	37	6	AR349544	AR349544 Sequence
c 143	12.8	45.7	38	6	AR224809 Sequence	c 216	12.4	44.3	37	6	AX097677	AX097677 Sequence
c 144	12.8	45.7	38	6	AR224812 Sequence	c 217	12.4	44.3	37	6	AX166879	AX166879 Sequence
c 145	12.8	45.7	38	6	AR317268 Sequence	c 218	12.4	44.3	37	6	AX167006	AX167006 Sequence
c 146	12.8	45.7	38	6	AR317271 Sequence	c 219	12.4	44.3	38	6	AX467362	AX467362 Sequence
c 147	12.8	45.7	38	6	AR337543 Sequence	c 220	12.4	44.3	39	6	AX197432	AX197432 Sequence
c 148	12.8	45.7	38	6	AR337546 Sequence	c 221	12.4	44.3	42	6	AR031539	AR031539 Sequence
c 149	12.8	45.7	38	6	AR366767 Sequence	c 222	12.4	44.3	42	6	AX052952	AX052952 Sequence
c 150	12.8	45.7	38	6	AR368682 Sequence	c 223	12.4	44.3	45	6	AX614307	AX614307 Sequence
c 151	12.8	45.7	38	6	AR383176 Sequence	c 224	12.4	44.3	47	6	AR290572	AR290572 Sequence
c 152	12.8	45.7	38	6	AR383179 Sequence	c 225	12.4	44.3	50	6	CQ008319	CQ008319 Sequence
c 153	12.8	45.7	38	6	AR409180 Sequence	c 226	12.4	44.3	50	6	AR218534	AR218534 Sequence
c 154	12.8	45.7	38	6	AX029448 Sequence	c 227	12.4	44.3	50	6	AR218535	AR218535 Sequence
c 155	12.8	45.7	38	6	BD075055 Method fo	c 228	12.4	44.3	50	6	AR218538	AR218538 Sequence
c 156	12.8	45.7	38	6	BD075058 Method fo	c 229	12.4	44.3	50	6	AR218539	AR218539 Sequence
c 157	12.8	45.7	43	6	A26231 MHC HGE pri	c 230	12.4	44.3	50	6	AR391615	AR391615 Sequence
c 158	12.8	45.7	43	6	A26233 MHC HGE pri	c 231	12.4	44.3	50	6	AR433565	AR433565 Sequence
c 159	12.8	45.7	43	6	AR208357 Sequence	c 232	12.4	44.3	50	6	AR433567	AR433567 Sequence
c 160	12.8	45.7	43	6	AR208359 Sequence	c 233	12.4	44.3	50	6	AR433571	AR433571 Sequence
c 161	12.8	45.7	45	6	AR030774 Sequence	c 234	12.4	44.3	50	6	AX411551	AX411551 Sequence
c 162	12.8	45.7	45	6	AR101078 Sequence	c 235	12.4	44.3	50	6	AX411552	AX411552 Sequence
c 163	12.8	45.7	45	6	AR228249 Sequence	c 236	12.4	44.3	50	6	AX411557	AX411557 Sequence
c 164	12.6	45.0	20	6	A98454 Sequence 1	c 237	12.4	44.3	50	6	AX411558	AX411558 Sequence
c 165	12.6	45.0	20	6	AR071285 Sequence	c 238	12.4	44.3	50	6	AX411559	AX411559 Sequence

C 239	12.4	44.3	50	6	AX411560 Sequence	AX411560 Sequence	312	12	42.9	20	6	BD272645	BD272645 Antisense
C 240	12.4	44.3	50	6	AX411565 Sequence	AX411565 Sequence	313	12	42.9	20	6	E12680	E12680 Anti-HTLV-1
C 241	12.4	44.3	50	6	AX657040 Sequence	AX657040 Sequence	314	12	42.9	20	6	AR367884	AR367884 Sequence
C 242	12.4	44.3	50	6	AX657041 Sequence	AX657041 Sequence	315	12	42.9	22	6	A80978	A80978 Sequence 30
C 243	12.4	44.3	50	6	AX657044 Sequence	AX657044 Sequence	316	12	42.9	22	6	A95357	A95357 Sequence 30
C 244	12.4	44.3	50	6	AX657045 Sequence	AX657045 Sequence	C 317	12	42.9	24	6	AX289027	AX289027 Sequence
C 245	12.4	44.3	50	6	AX773923 Sequence	AX773923 Sequence	C 318	12	42.9	25	6	AX500847	AX500847 Sequence
C 246	12.2	43.6	18	6	I26867 Sequence 90	I26867 Sequence 90	C 319	12	42.9	25	6	AX500853	AX500853 Sequence
C 247	12.2	43.6	18	6	I31608 Sequence 90	I31608 Sequence 90	C 320	12	42.9	25	6	AX609295	AX609295 Sequence
C 248	12.2	43.6	19	6	I30698 Sequence 13	I30698 Sequence 13	C 321	12	42.9	26	6	A36732	A36732 Sequence 3
C 249	12.2	43.6	19	6	I30699 Sequence 13	I30699 Sequence 13	C 322	12	42.9	27	6	CQ797777	CQ797777 Sequence
C 250	12.2	43.6	19	6	I46157 Sequence 13	I46157 Sequence 13	C 323	12	42.9	27	6	I44736	I44736 Sequence 3
C 251	12.2	43.6	19	6	I46158 Sequence 13	I46158 Sequence 13	C 324	12	42.9	29	6	BD227388	BD227388 Secreted
C 252	12.2	43.6	19	6	AR214558 Sequence	AR214558 Sequence	325	12	42.9	29	6	AX923503	AX923503 Sequence
C 253	12.2	43.6	20	6	AR230871 Sequence	AR230871 Sequence	326	12	42.9	30	6	E58660	E58660 Novel metal
C 254	12.2	43.6	21	6	AX224666 Sequence	AX224666 Sequence	327	12	42.9	32	6	A41180	A41180 Sequence 14
C 255	12.2	43.6	22	6	AX591616 Sequence	AX591616 Sequence	328	12	42.9	32	6	AR117410	AR117410 Sequence
C 256	12.2	43.6	22	6	BD088168	BD088168 A method	C 329	12	42.9	32	6	I69226	I69226 Sequence 49
C 257	12.2	43.6	22	12	AB068979	AB068979 Synthetic	C 330	12	42.9	32	6	AR253824	AR253824 Sequence
C 258	12.2	43.6	23	6	E40789	E40789 Antihuman F	331	12	42.9	32	6	AR309049	AR309049 Sequence
C 259	12.2	43.6	23	6	AR253010	AR253010 Sequence	C 332	12	42.9	32	6	AX696879	AX696879 Sequence
C 260	12.2	43.6	24	6	BD131526	BD131526 Heat shock	C 333	12	42.9	32	9	HUMCD1B6	M22173 Human corti
C 261	12.2	43.6	25	6	AR235165	AR235165 Sequence	334	12	42.9	33	6	AR098132	AR098132 Sequence
C 262	12.2	43.6	26	6	AR121161	AR121161 Sequence	335	12	42.9	33	6	AR428448	AR428448 Sequence
C 263	12.2	43.6	26	6	AX823459	AX823459 Sequence	336	12	42.9	33	6	AR428454	AR428454 Sequence
C 264	12.2	43.6	26	6	AX823462	AX823462 Sequence	337	12	42.9	33	6	BD080488	BD080488 Methods f
C 265	12.2	43.6	28	6	AR090254	AR090254 Sequence	C 338	12	42.9	34	6	AR211327	AR211327 Sequence
C 266	12.2	43.6	28	6	AR197289	AR197289 Sequence	C 339	12	42.9	35	6	A98633	A98633 Sequence 1
C 267	12.2	43.6	28	6	AR259443	AR259443 Sequence	C 340	12	42.9	35	6	AR121376	AR121376 Sequence
C 268	12.2	43.6	28	6	AX573803	AX573803 Sequence	C 341	12	42.9	35	6	AR124108	AR124108 Sequence
C 269	12.2	43.6	30	6	A52377	AX2377 Sequence 5	C 342	12	42.9	35	6	BD268671	BD268671 Isolation
C 270	12.2	43.6	30	6	AR171267	AR171267 Sequence	C 343	12	42.9	35	6	E12667	E12667 Anti-HTLV-1
C 271	12.2	43.6	30	6	AX548447	AX548447 Sequence	C 344	12	42.9	35	6	E36131	E36131 Chimeric se
C 272	12.2	43.6	30	10	MWHNF113A	X66551 M.musculus	C 345	12	42.9	35	6	AR269039	AR269039 Sequence
C 273	12.2	43.6	31	6	A59676	A59676 Sequence 7	C 346	12	42.9	35	6	AR437549	AR437549 Sequence
C 274	12.2	43.6	33	6	AR004878	AR004878 Sequence	C 347	12	42.9	35	6	AX022590	AX022590 Sequence
C 275	12.2	43.6	33	6	AR020560	AR020560 Sequence	C 348	12	42.9	35	6	BD073319	BD073319 Recombina
C 276	12.2	43.6	33	6	BD076373	BD076373 Recombina	C 349	12	42.9	35	6	BD080322	BD080322 Zymogen p
C 277	12.2	43.6	35	6	AR161464	AR161464 Sequence	C 350	12	42.9	36	6	A04622	A04622 Nucleotide
C 278	12.2	43.6	35	6	CQ774874	CQ774874 Sequence	C 351	12	42.9	36	6	A04623	A04623 Nucleotide
C 279	12.2	43.6	35	6	CQ774876	CQ774876 Sequence	C 352	12	42.9	36	6	A14074	A14074 Nucleotide
C 280	12.2	43.6	36	6	BD102124	BD102124 Method of	C 353	12	42.9	36	6	A14075	A14075 Nucleotide
C 281	12.2	43.6	36	6	BD102125	BD102125 Method of	C 354	12	42.9	36	6	AR116802	AR116802 Sequence
C 282	12.2	43.6	38	6	AR407787	AR407787 Sequence	C 355	12	42.9	36	6	BD181183	BD181183 Human che
C 283	12.2	43.6	38	6	AR411243	AR411243 Sequence	C 356	12	42.9	36	6	AR256434	AR256434 Sequence
C 284	12.2	43.6	38	6	AX190638	AX190638 Sequence	C 357	12	42.9	36	6	AR436691	AR436691 Sequence
C 285	12.2	43.6	38	6	AX370310	AX370310 Sequence	C 358	12	42.9	37	6	I69227	I69227 Sequence 49
C 286	12.2	43.6	39	6	AX516385	AX516385 Sequence	C 359	12	42.9	37	6	AR253825	AR253825 Sequence
C 287	12.2	43.6	40	6	AX060288	AX060288 Sequence	C 360	12	42.9	37	6	AR436900	AR436900 Sequence
C 288	12.2	43.6	41	6	AR061553	AR061553 Sequence	C 361	12	42.9	37	6	AX696880	AX696880 Sequence
C 289	12.2	43.6	41	6	AR108452	AR108452 Sequence	C 362	12	42.9	38	6	AR156817	AR156817 Sequence
C 290	12.2	43.6	41	6	I16409	I16409 Sequence 23	C 363	12	42.9	38	6	AR220212	AR220212 Sequence
C 291	12.2	43.6	41	6	I66895	I66895 Sequence 23	C 364	12	42.9	38	6	AR329755	AR329755 Sequence
C 292	12.2	43.6	41	6	I84989	I84989 Sequence 23	C 365	12	42.9	38	6	AR366635	AR366635 Sequence
C 293	12.2	43.6	41	6	AR263413	AR263413 Sequence	C 366	12	42.9	38	6	AX358372	AX358372 Sequence
C 294	12.2	43.6	41	6	AX516722	AX516722 Sequence	C 367	12	42.9	41	6	AX097532	AX097532 Sequence
C 295	12.2	43.6	41	6	AX518886	AX518886 Sequence	C 368	12	42.9	41	6	AX520201	AX520201 Sequence
C 296	12.2	43.6	42	6	AX497900	AX497900 Sequence	C 369	12	42.9	42	6	AX840438	AX840438 Sequence
C 297	12.2	43.6	43	6	AR061564	AR061564 Sequence	C 370	12	42.9	45	6	I17261	I17261 Sequence 27
C 298	12.2	43.6	43	6	AR108463	AR108463 Sequence	C 371	12	42.9	45	6	I17262	I17262 Sequence 28
C 299	12.2	43.6	43	6	I16420	I16420 Sequence 24	C 372	12	42.9	45	6	I55020	I55020 Sequence 44
C 300	12.2	43.6	43	6	I66906	I66906 Sequence 24	C 373	12	42.9	45	6	AR481915	AR481915 Sequence
C 301	12.2	43.6	43	6	I85000	I85000 Sequence 24	C 374	12	42.9	45	6	AR481916	AR481916 Sequence
C 302	12.2	43.6	43	6	AR263424	AR263424 Sequence	C 375	12	42.9	47	6	I17263	I17263 Sequence 29
C 303	12.2	43.6	44	6	AR4734	AR4734 Sequence 12	C 376	12	42.9	47	6	AR288962	AR288962 Sequence
C 304	12.2	43.6	44	6	BD107486	BD107486 Method of	C 377	12	42.9	47	6	AR291516	AR291516 Sequence
C 305	12.2	43.6	45	6	AR263588	AR263588 Sequence	C 378	12	42.9	47	6	AR481917	AR481917 Sequence
C 306	12.2	43.6	45	6	BD168552	BD168552 Cells pro	C 379	12	42.9	48	6	I17260	I17260 Sequence 26
C 307	12.2	43.6	48	6	BD191587	BD191587 Single-ch	C 380	12	42.9	48	6	AR444664	AR444664 Sequence
C 308	12.2	43.6	48	6	AR262537	AR262537 Sequence	C 381	12	42.9	48	6	AR481914	AR481914 Sequence
C 309	12.2	43.6	50	6	CQ813892	CQ813892 Sequence	C 382	12	42.9	48	6	AX076991	AX076991 Sequence
C 310	12.2	43.6	50	6	E40770	E40770 Antihuman F	C 383	12	42.9	48	6	AX426699	AX426699 Sequence
C 311	12	42.9	20	6	AR121024	AR121024 Sequence	C 384	12	42.9	49	6	BD175537	BD175537 Secretary

C 385	12	42.9	49	6	AR410793	Sequence	458	11.8	42.1	37	6	AR181189	Sequence
C 386	12	42.9	49	6	AR410917	Sequence	459	11.8	42.1	37	6	AR220213	Sequence
C 387	12	42.9	49	6	AR439157	Sequence	460	11.8	42.1	37	6	AR366636	Sequence
C 388	12	42.9	49	6	AR439281	Sequence	461	11.8	42.1	37	6	AR358373	Sequence
C 389	12	42.9	49	6	AR473177	Sequence	462	11.8	42.1	37	6	AR769572	Sequence
C 390	12	42.9	49	6	AR473301	Sequence	463	11.8	42.1	38	6	AR082478	Sequence
C 391	12	42.9	49	6	AR473301	Sequence	464	11.8	42.1	38	6	AR083606	Sequence
C 392	12	42.9	49	6	AR697789	Sequence	465	11.8	42.1	38	6	AR111798	Sequence
C 393	12	42.9	49	6	BD075686	Secretory	466	11.8	42.1	38	6	AR124710	Sequence
C 394	12	42.9	49	6	BD172546	Secreted	467	11.8	42.1	38	6	AR171827	Inhibitor
C 395	12	42.9	49	6	BD172865	Secreted	468	11.8	42.1	38	6	BD267973	Inhibitor
C 396	12	42.9	49	6	BD173184	Secreted	469	11.8	42.1	38	6	BD270876	Inhibitor
C 397	12	42.9	49	6	BD173503	Secreted	470	11.8	42.1	38	6	BD272027	Inhibitor
C 398	12	42.9	50	6	CQ005575	Sequence	471	11.8	42.1	38	6	BD272046	Inhibitor
C 399	12	42.9	50	6	I09225	Sequence 26	472	11.8	42.1	38	6	BD274584	Inhibitor
C 400	11.8	42.1	18	6	AR073370	Sequence	473	11.8	42.1	38	6	BD274603	Inhibitor
C 401	11.8	42.1	18	6	BD250694	Identific	474	11.8	42.1	38	6	AR181819	Sequence
C 402	11.8	42.1	19	6	AR242594	Sequence	475	11.8	42.1	38	6	AR195285	Sequence
C 403	11.8	42.1	19	6	AR242603	Sequence	476	11.8	42.1	38	6	AR200001	Sequence
C 404	11.8	42.1	19	6	AX080228	Sequence	477	11.8	42.1	38	6	AR201354	Sequence
C 405	11.8	42.1	19	6	AX080237	Sequence	478	11.8	42.1	38	6	AR216097	Sequence
C 406	11.8	42.1	20	6	AR084397	Sequence	479	11.8	42.1	38	6	AR224806	Sequence
C 407	11.8	42.1	20	6	AR156820	Sequence	480	11.8	42.1	38	6	AR317265	Sequence
C 408	11.8	42.1	20	6	AR220187	Sequence	481	11.8	42.1	38	6	AR337540	Sequence
C 409	11.8	42.1	20	6	AR366638	Sequence	482	11.8	42.1	38	6	AR366794	Sequence
C 410	11.8	42.1	20	6	AX167253	Sequence	483	11.8	42.1	38	6	AR368679	Sequence
C 411	11.8	42.1	20	6	AX358347	Sequence	484	11.8	42.1	38	6	AR383173	Sequence
C 412	11.8	42.1	21	6	BD227358	Secreted	485	11.8	42.1	38	6	AR409177	Sequence
C 413	11.8	42.1	21	6	AX922994	Sequence 2	486	11.8	42.1	38	6	AX029445	Sequence
C 414	11.8	42.1	21	6	AX3656	Sequence	487	11.8	42.1	38	6	BD075052	Method fo
C 415	11.8	42.1	22	6	AR003708	Sequence	488	11.8	42.1	39	6	BD083663	disulfide
C 416	11.8	42.1	22	6	AX504898	Sequence	489	11.8	42.1	40	6	BD185649	Methods f
C 417	11.8	42.1	23	6	AX504909	Sequence	490	11.8	42.1	40	6	BD185795	Methods f
C 418	11.8	42.1	23	6	AX504911	Sequence	491	11.8	42.1	40	6	BD187660	Methods f
C 419	11.8	42.1	23	6	AX959157	Sequence	492	11.8	42.1	40	6	BD187683	Methods f
C 420	11.8	42.1	23	6	AX959167	Sequence	493	11.8	42.1	40	6	BD189712	Methods f
C 421	11.8	42.1	24	6	I73496	Sequence 9	494	11.8	42.1	40	6	AR342178	Sequence
C 422	11.8	42.1	24	6	AX231696	Sequence	495	11.8	42.1	40	6	AX932208	Sequence
C 423	11.8	42.1	24	6	AX504899	Sequence	496	11.8	42.1	40	6	AX932208	Sequence
C 424	11.8	42.1	24	6	AX504911	Sequence	497	11.8	42.1	41	6	AR082473	Sequence
C 425	11.8	42.1	24	6	AX959157	Sequence	498	11.8	42.1	41	6	AR083601	Sequence
C 426	11.8	42.1	24	6	AX959169	Sequence	499	11.8	42.1	41	6	AR096931	Sequence
C 427	11.8	42.1	25	6	CQ628886	Sequence	500	11.8	42.1	41	6	AR111793	Sequence
C 428	11.8	42.1	25	6	CQ628887	Sequence	501	11.8	42.1	41	6	AR124705	Sequence
C 429	11.8	42.1	25	6	CQ628887	Sequence	502	11.8	42.1	41	6	AR171822	Sequence
C 430	11.8	42.1	25	6	CQ628888	Sequence	503	11.8	42.1	41	6	BD267968	Inhibitor
C 431	11.8	42.1	25	6	AR469949	Sequence	504	11.8	42.1	41	6	BD270871	Inhibitor
C 432	11.8	42.1	25	6	AR469950	Sequence	505	11.8	42.1	41	6	BD272022	Inhibitor
C 433	11.8	42.1	25	6	AR469951	Sequence	506	11.8	42.1	41	6	BD272041	Inhibitor
C 434	11.8	42.1	25	6	AX179680	Sequence	507	11.8	42.1	41	6	BD274579	Inhibitor
C 435	11.8	42.1	25	6	AX504900	Sequence	508	11.8	42.1	41	6	BD274598	Inhibitor
C 436	11.8	42.1	25	6	AX504914	Sequence	509	11.8	42.1	41	6	AR181814	Sequence
C 437	11.8	42.1	25	6	AX744587	Sequence	510	11.8	42.1	41	6	AR195280	Sequence
C 438	11.8	42.1	25	6	AX744588	Sequence	511	11.8	42.1	41	6	AR199996	Sequence
C 439	11.8	42.1	25	6	AX744589	Sequence	512	11.8	42.1	41	6	AR201349	Sequence
C 440	11.8	42.1	25	6	AX782929	Sequence	513	11.8	42.1	41	6	AR201368	Sequence
C 441	11.8	42.1	25	6	AX782930	Sequence	514	11.8	42.1	41	6	AR216092	Sequence
C 442	11.8	42.1	25	6	AX782931	Sequence	515	11.8	42.1	41	6	AR224801	Sequence
C 443	11.8	42.1	25	6	AX959158	Sequence	516	11.8	42.1	41	6	AR317260	Sequence
C 444	11.8	42.1	25	6	AX959171	Sequence	517	11.8	42.1	41	6	AR337535	Sequence
C 445	11.8	42.1	25	6	AX959172	Sequence	518	11.8	42.1	41	6	AR366759	Sequence
C 446	11.8	42.1	25	6	BD161089	RNA molec	519	11.8	42.1	41	6	AR368674	Sequence
C 447	11.8	42.1	25	6	BD161089	Sequence	520	11.8	42.1	41	6	AR383168	Sequence
C 448	11.8	42.1	26	6	AX351788	Sequence	521	11.8	42.1	41	6	AR409172	Sequence
C 449	11.8	42.1	26	6	AX3522603	Sequence	522	11.8	42.1	41	6	AX004513	Sequence
C 450	11.8	42.1	30	6	AX792831	Sequence	523	11.8	42.1	41	6	AX029440	Sequence
C 451	11.8	42.1	31	6	AX249623	Sequence	524	11.8	42.1	41	6	AX515248	Sequence
C 452	11.8	42.1	34	6	AX467532	Sequence	525	11.8	42.1	41	6	AX517745	Sequence
C 453	11.8	42.1	36	6	BD174700	Ribozyme	526	11.8	42.1	41	6	AX518216	Sequence
C 454	11.8	42.1	37	6	AR003401	Sequence	527	11.8	42.1	41	6	BD075047	Method fo
C 455	11.8	42.1	37	6	AR156818	Sequence	528	11.8	42.1	41	6	BD136126	Vaccines
C 456	11.8	42.1	37	6	I21190	Sequence 36	529	11.8	42.1	41	9	L39570 Homo sapien	
C 457	11.8	42.1	37	6	I74457	Sequence 36	530	11.8	42.1	43	6	HUMTCRWJ32	
												AX601642	Sequence

531	11.8	42.1	44	6	AR442669	Sequence	AR442669	Sequence	604	11.6	41.4	28	6	AX193528	Sequence
532	11.8	42.1	44	6	AX513493	Sequence	AX513493	Sequence	c	11.6	41.4	28	6	AX358202	Sequence
533	11.8	42.1	45	9	HUMIGHABH	L06994 Homo sapien	L06994	Homo sapien	606	11.6	41.4	30	6	AX135796	Sequence
534	11.8	42.1	47	6	AR161514	Sequence	AR161514	Sequence	607	11.6	41.4	30	6	AX791082	Sequence
535	11.8	42.1	47	6	AR161530	Sequence	AR161530	Sequence	c	11.6	41.4	30	6	AX791177	Sequence
536	11.8	42.1	47	6	AR284752	Sequence	AR284752	Sequence	c	11.6	41.4	30	6	BD107206	Base sequ
537	11.8	42.1	47	6	AR289051	Sequence	AR289051	Sequence	c	11.6	41.4	33	6	AX033184	Sequence
538	11.8	42.1	48	9	S82552	rearranged	S82552	rearranged	c	11.6	41.4	34	11	C75763	Sequence
539	11.8	42.1	50	6	CQ002681	Sequence	CQ002681	Sequence	c	11.6	41.4	35	6	BD264035	Sequence
540	11.8	42.1	50	6	CQ005437	Sequence	CQ005437	Sequence	613	11.6	41.4	35	6	I92423	Sequence 75
541	11.8	42.1	50	6	CQ006595	Sequence	CQ006595	Sequence	614	11.6	41.4	35	6	AX751490	Sequence
542	11.8	42.1	50	6	AR218536	Sequence	AR218536	Sequence	615	11.6	41.4	36	6	AR041542	Sequence
543	11.8	42.1	50	6	AR218537	Sequence	AR218537	Sequence	616	11.6	41.4	36	6	AR045320	Sequence
544	11.8	42.1	50	6	AR218540	Sequence	AR218540	Sequence	617	11.6	41.4	36	6	AR132686	Sequence
545	11.8	42.1	50	6	AR433566	Sequence	AR433566	Sequence	618	11.6	41.4	36	6	AR132687	Sequence
546	11.8	42.1	50	6	AR433568	Sequence	AR433568	Sequence	619	11.6	41.4	36	6	AR133762	Sequence
547	11.8	42.1	50	6	AR433570	Sequence	AR433570	Sequence	620	11.6	41.4	36	6	BD251317	Pancreas
548	11.8	42.1	50	6	AX411553	Sequence	AX411553	Sequence	621	11.6	41.4	36	6	I52372	Sequence 11
549	11.8	42.1	50	6	AX411554	Sequence	AX411554	Sequence	622	11.6	41.4	36	6	I77550	Sequence 25
550	11.8	42.1	50	6	AX411555	Sequence	AX411555	Sequence	623	11.6	41.4	36	6	I77974	Sequence 68
551	11.8	42.1	50	6	AX411556	Sequence	AX411556	Sequence	624	11.6	41.4	36	6	I78008	Sequence 71
552	11.8	42.1	50	6	AX657042	Sequence	AX657042	Sequence	625	11.6	41.4	36	6	AR200546	Sequence
553	11.8	42.1	50	6	AX657043	Sequence	AX657043	Sequence	626	11.6	41.4	36	6	AX421424	Sequence
554	11.8	42.1	50	6	AX657046	Sequence	AX657046	Sequence	627	11.6	41.4	36	6	AX573483	Sequence
555	11.8	42.1	50	8	N7A538887	Nicotiana	AJ538887	Nicotiana	628	11.6	41.4	36	6	AX637000	Sequence
556	11.6	41.4	18	6	AX254790	Sequence	AX254790	Sequence	629	11.6	41.4	36	6	AX638269	Sequence
557	11.6	41.4	18	6	AX254792	Sequence	AX254792	Sequence	630	11.6	41.4	36	6	AX638511	Sequence
558	11.6	41.4	19	6	AR166701	Sequence	AR166701	Sequence	631	11.6	41.4	36	6	AX638545	Sequence
559	11.6	41.4	19	6	BD084003	Diagnosi	BD084003	Diagnosi	632	11.6	41.4	37	6	BD266828	Human bra
560	11.6	41.4	20	6	AR310857	Sequence	AR310857	Sequence	633	11.6	41.4	37	6	BD266830	Human bra
561	11.6	41.4	20	6	AX512395	Sequence	AX512395	Sequence	c	11.6	41.4	37	6	AX278121	Sequence
562	11.6	41.4	21	6	AR225951	Sequence	AR225951	Sequence	635	11.6	41.4	38	6	AR045746	Sequence
563	11.6	41.4	21	6	AX096736	Sequence	AX096736	Sequence	636	11.6	41.4	38	6	AR046785	Sequence
564	11.6	41.4	21	6	AX145813	Sequence	AX145813	Sequence	637	11.6	41.4	38	6	AR047653	Sequence
565	11.6	41.4	21	6	BD094209	Genes for	BD094209	Genes for	638	11.6	41.4	38	6	AR047787	Sequence
566	11.6	41.4	22	6	AR303962	Sequence	AR303962	Sequence	639	11.6	41.4	38	6	I52798	Sequence 53
567	11.6	41.4	22	6	AX551577	Sequence	AX551577	Sequence	640	11.6	41.4	38	6	I53837	Sequence 15
568	11.6	41.4	23	6	AR148148	Sequence	AR148148	Sequence	641	11.6	41.4	38	6	I54705	Sequence 24
569	11.6	41.4	23	6	BD179348	Insulin-1	BD179348	Insulin-1	642	11.6	41.4	38	6	I54839	Sequence 25
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571	11.6	41.4	23	6	E30554	Neurogenesi	E30554	Neurogenesi	644	11.6	41.4	38	6	AX776711	Sequence
572	11.6	41.4	23	6	AR217407	Sequence	AR217407	Sequence	c	11.6	41.4	38	6	BD143241	Fucose-ep
573	11.6	41.4	23	6	AR256813	Sequence	AR256813	Sequence	c	11.6	41.4	39	6	CQ778839	Sequence
574	11.6	41.4	23	6	AR268842	Sequence	AR268842	Sequence	c	11.6	41.4	39	6	CQ778871	Sequence
575	11.6	41.4	23	6	AR369300	Sequence	AR369300	Sequence	c	11.6	41.4	39	6	AX081636	Sequence
576	11.6	41.4	23	6	AR435618	Sequence	AR435618	Sequence	c	11.6	41.4	39	6	AX374817	Sequence
577	11.6	41.4	23	6	AR453219	Sequence	AR453219	Sequence	c	11.6	41.4	40	6	A05823	Oligonucleo
578	11.6	41.4	23	6	BD000539	Formation	BD000539	Formation	c	11.6	41.4	40	6	AR302069	Sequence
579	11.6	41.4	23	6	BD105356	Novel ins	BD105356	Novel ins	c	11.6	41.4	40	6	AR338170	Sequence
580	11.6	41.4	24	6	AR066370	Sequence	AR066370	Sequence	c	11.6	41.4	40	6	AR343087	Sequence
581	11.6	41.4	24	6	AR130356	Sequence	AR130356	Sequence	c	11.6	41.4	40	6	BD137947	Antigen 1
582	11.6	41.4	24	6	E11684	PCR primer.	E11684	PCR primer.	c	11.6	41.4	40	9	S80819	gamma delta
583	11.6	41.4	24	6	E13116	Oligonucleo	E13116	Oligonucleo	c	11.6	41.4	41	6	A40462	Sequence 8
584	11.6	41.4	25	6	CQ619815	Sequence	CQ619815	Sequence	c	11.6	41.4	41	6	BD249710	Productio
585	11.6	41.4	25	6	CQ619816	Sequence	CQ619816	Sequence	c	11.6	41.4	41	6	AR316670	Sequence
586	11.6	41.4	25	6	CQ619817	Sequence	CQ619817	Sequence	c	11.6	41.4	41	6	AX134733	Sequence
587	11.6	41.4	25	6	CQ619818	Sequence	CQ619818	Sequence	c	11.6	41.4	41	6	AX278092	Sequence
588	11.6	41.4	25	6	CQ619819	Sequence	CQ619819	Sequence	c	11.6	41.4	41	6	AX301861	Sequence
589	11.6	41.4	25	6	CQ619820	Sequence	CQ619820	Sequence	c	11.6	41.4	41	6	AX16543	Sequence
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591	11.6	41.4	25	6	CQ619822	Sequence	CQ619822	Sequence	c	11.6	41.4	43	6	AX268517	Sequence
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593	11.6	41.4	25	6	AR460879	Sequence	AR460879	Sequence	c	11.6	41.4	45	6	A40463	Sequence 9
594	11.6	41.4	25	6	AR460880	Sequence	AR460880	Sequence	c	11.6	41.4	47	6	AR284532	Sequence
595	11.6	41.4	25	6	AR460881	Sequence	AR460881	Sequence	c	11.6	41.4	47	6	AR284697	Sequence
596	11.6	41.4	25	6	AR460882	Sequence	AR460882	Sequence	c	11.6	41.4	47	6	AR291148	Sequence
597	11.6	41.4	25	6	AR460883	Sequence	AR460883	Sequence	c	11.6	41.4	47	6	AR292047	Sequence
598	11.6	41.4	25	6	AR460884	Sequence	AR460884	Sequence	c	11.6	41.4	47	6	AX252287	Sequence
599	11.6	41.4	25	6	AR460885	Sequence	AR460885	Sequence	c	11.6	41.4	48	6	A49833	Sequence 6
600	11.6	41.4	27	6	CQ771800	Sequence	CQ771800	Sequence	c	11.6	41.4	48	6	CQ767217	Sequence
601	11.6	41.4	28	6	CQ797707	Sequence	CQ797707	Sequence	c	11.6	41.4	48	6	AX222314	Sequence
602	11.6	41.4	28	6	AR428335	Sequence	AR428335	Sequence	c	11.6	41.4	48	6	AX426278	Sequence
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686	11.6	41.4	50	6	AX987950	AR454201 Sequence
687	11.6	41.4	50	6	BD015910	AR317221 Sequence
688	11.6	41.4	50	6	BD016278	BD224796 Novel pla
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693	11.4	40.7	22	6	E13354	AX601756 Sequence
694	11.4	40.7	22	6	I17617	AX601757 Sequence
695	11.4	40.7	22	6	I17623	AX601758 Sequence
696	11.4	40.7	22	6	I38399	AX601762 Sequence
697	11.4	40.7	22	6	I38405	AX601763 Sequence
698	11.4	40.7	22	6	AX776584	AX601764 Sequence
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702	11.4	40.7	24	6	AX444442	AX59387 Sequence 37
703	11.4	40.7	25	6	AR049774	AR036051 Sequence
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ALIGNMENTS

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LOCUS A method for determination of a nucleic acid using a control.
DEFINITION
ACCESSION BD181370.1 GI:30792288
VERSION JP 2002335981-A/9.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 28)
Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: JP 2002335981-A 9 26-NOV-2002;
JOURNAL F.HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/9
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/566,G01N33/58,
CC C12N15/00
CC Description of Artificial Sequence: ST778pc Primer parallel-
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RESULT 2
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LOCUS Sequence 9 from Patent EP1236804.
DEFINITION
ACCESSION AX523950
VERSION AX523950.1 GI:25168881
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
Jaeger,S.
AUTHORS A method for determination of a nucleic acid using a control
TITLE Patent: EP 1236804-A 9 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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AX524848 28 bp DNA linear PAT 21-NOV-2002
LOCUS Sequence 9 from Patent EP1236805.
DEFINITION
ACCESSION AX524848
VERSION AX524848.1 GI:25169942
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
Jaeger,S.
AUTHORS A method for the determination of a nucleic acid using a control
TITLE Patent: EP 1236805-A 9 04-SEP-2002;
JOURNAL Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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ACCESSION    AR289945
VERSION      AR289945.1  GI:31677229
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 47)
AUTHORS      Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE        Biallelic markers for use in constructing a high density
JOURNAL      disequilibrium map of the human genome
FEATURES     Patent: US 6537751-A 1680 25-MAR-2003;
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DEFINITION   Sequence 247 from Patent EP1288296.
ACCESSION    AX710947
VERSION      AX710947.1  GI:29787328
KEYWORDS     Human herpesvirus 5
SOURCE       Human herpesvirus 5
ORGANISM     Human herpesvirus 5
REFERENCE    1
AUTHORS      Draper,K.G., Mcswiggen,J.A., Holecck,J.J., Dudycz,L.W.,
TITLE        Macejak,D.G. and Mamone,J.A.
JOURNAL      Method and reagent for inhibiting HBV viral replication
              Patent: EP 1288296-A 247 05-MAR-2003;
              RIBOZYME PHARMACEUTICALS, INC. (US)
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DEFINITION   Sequence 30 from Patent WO2004015117.
ACCESSION    CQ779042
VERSION      CQ779042.1  GI:45381689
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.

REFERENCE    1
AUTHORS      te.Rigle,H.P.
TITLE        Targeted gene modification by single-stranded dna oligonucleotides
JOURNAL      Patent: WO 2004015117-A 30 19-FEB-2004;
              Het Nederlands Kanker Instituut (NL)
FEATURES     Location/Qualifiers
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DEFINITION   Isolation method of primer extension products by modular
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ACCESSION    BD244764
VERSION      BD244764.1  GI:33054534
KEYWORDS     JP 2002525076-A/43.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Lundeberg,J. and Uhlen,M.
TITLE        Isolation method of primer extension products by modular
JOURNAL      Patent: JP 2002525076-A 43 13-AUG-2002;
              DYNAL AS
COMMENT       OS Artificial Sequence
              PN JP 2002525076-A/43
              PD 13-AUG-2002
              PF 15-SEP-1999 JP 2000570369
              PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
              PC C12N15/09,C12Q1/68,C12N15/00
              JOAKIM LUNDEBERG, MATHIAS UHLEN
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Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  15 TCGTGGGATAGTCCG 1

RESULT 8
LOCUS       AR255271/c                    15 bp    DNA
DEFINITION   Sequence 37 from patent US 6482592.
ACCESSION    AR255271
VERSION      AR255271.1  GI:27304320
KEYWORDS     Sequence 37 from patent US 6482592.
SOURCE       AR255271
ORGANISM     AR255271.1  GI:27304320

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using modular oligonucleotides
JOURNAL Patent: US 6482592-A 37 19-NOV-2002;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Query Match 53.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TCGTGGGATGTCG 18
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Db 15 TCGTGGGATGTCG 1

RESULT 9
AX645654/c
LOCUS AX645654 19 bp DNA linear PAT 03-MAR-2003
DEFINITION Sequence 8 from Patent EP1270738.
ACCESSION AX645654
VERSION AX645654.1 GI:28798009
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Niemeyer,C.M., Wacker,R. and Adler,M.
TITLE Method for detecting substances in liquids
JOURNAL Patent: EP 1270738-A 8 02-JAN-2003;
Chimera Biotech GmbH (DE)
FEATURES Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="F nger-Oligonucleotid cK-Es"

misc_feature 1
/note="biotinylert"

ORIGIN
Query Match 53.6%; Score 15; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCGTGGGATAGT 15
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Db 15 CGTTCGTGGGATAGT 1

RESULT 10
AX645658
LOCUS AX645658 19 bp DNA linear PAT 03-MAR-2003
DEFINITION Sequence 12 from Patent EP1270738.
ACCESSION AX645658
VERSION AX645658.1 GI:28798013
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Niemeyer,C.M., Wacker,R. and Adler,M.
TITLE Method for detecting substances in liquids
JOURNAL Patent: EP 1270738-A 12 02-JAN-2003;
Chimera Biotech GmbH (DE)

FEATURES source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Erkennungssequenz K-Es"

ORIGIN
Query Match 53.6%; Score 15; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCGTGGGATAGT 15
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Db 5 CGTTCGTGGGATAGT 19

RESULT 11
AX097318/c
LOCUS AX097318 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 2496 from Patent WO0118250.
ACCESSION AX097318
VERSION AX097318.1 GI:13513795
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 2496 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 52.1%; Score 14.6; DB 6; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.5e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GTTCGTGGGATAGTCCGTGAT 22
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Db 21 GTTCGTGGGATAGTCCGTGAT 1

RESULT 12
E31555/c
LOCUS E31555 Cecropin gene.
DEFINITION E31555
ACCESSION E31555.1 GI:13017395
VERSION JP 1999313680-A/6.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Yoshio,M., Kazumi,S., Tomohisa,K., Yasushi,H. and Keiko,N.
TITLE Cecropin gene
JOURNAL Patent: JP 1999313680-A 6 16-NOV-1999;
IWATE PREF
COMMENT
OS Unidentified
PN JP 1999313680-A/6
PD 16-NOV-1999
PF 30-APR-1998 JP 1998121309
PR
PI YOSHIO MIURA, KAZUMI SUZUKI, TOMOHISA KURODA, YASUSHI HIKIJI, PI KEIKO NASU

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PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//A01N63/00,C12N15/00,
PC C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key 1..23 /organism='Unidentified'.
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FT Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTTCGTGGGATAGTCCGTCAT 22
Db 22 GATAGTGGGATTGTGCGTCAT 2
RESULT 13
AR172071/c
LOCUS AR172071 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6297425.
ACCESSION AR172071
VERSION AR172071.1 GI:17911021
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 38)
    Unclassified.
AUTHORS Scelongo,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6297425-A 25 02-OCT-2001;
FEATURES
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            /mol_type='unassigned DNA'
ORIGIN
Query Match
Best Local Similarity 52.1%; Score 14.6; DB 6; Length 38;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTTCGTGGGATAGTCCGTCAT 22
Db 22 GATAGTGGGATTGTGCGTCAT 2
RESULT 14
AR173362/c
LOCUS AR173362 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6303846.
ACCESSION AR173362
VERSION AR173362.1 GI:17912853
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 38)
    Unclassified.
AUTHORS Scelongo,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6303846-A 25 16-OCT-2001;
FEATURES
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            /mol_type='unassigned DNA'
ORIGIN
Query Match
Best Local Similarity 52.1%; Score 14.6; DB 6; Length 38;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Best Local Similarity 81.0%; Pred. No. 3.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTTCGTGGGATAGTCCGTCAT 22
Db 22 GATAGTGGGATTGTGCGTCAT 2
RESULT 15
AR437662/c
LOCUS AR437662 50 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6660524.
ACCESSION AR437662
VERSION AR437662.1 GI:40202820
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 50)
    Unclassified.
AUTHORS Turck,J.A. and Archer,J.A.C.
TITLE Control of gene expression in eukaryotes
JOURNAL Patent: US 6660524-A 14 09-DEC-2003;
FEATURES
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            /mol_type='genomic DNA'
ORIGIN
Query Match
Best Local Similarity 52.1%; Score 14.6; DB 6; Length 50;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTTCGTGGGATAGTCCGTCAT 22
Db 37 GATAGTGGGATTGTGCGTCAT 17
RESULT 16
AX026712/c
LOCUS AX026712 50 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 14 from Patent WO0039300.
ACCESSION AX026712
VERSION AX026712.1 GI:10187879
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1
    synthetic construct
    artificial sequences.
AUTHORS Archer,J.A. and Tuerck,J.A.
TITLE Control of gene expression in eukaryotes
JOURNAL Patent: WO 0039300-A 14 06-JUL-2000;
FEATURES
    source
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            /db_xref='taxon:32630'
            /note='CaMVop2'
ORIGIN
Query Match
Best Local Similarity 52.1%; Score 14.6; DB 6; Length 50;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTTCGTGGGATAGTCCGTCAT 22
Db 37 GATAGTGGGATTGTGCGTCAT 17
RESULT 17
AR200549/c
LOCUS AR200549 32 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 78 from patent US 6358505.
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[illegible]

LOCUS AR171824 38 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6297239.
ACCESSION AR171824
VERSION AR171824.1 GI:17910774
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Desolms,S.Jane., Hutchinson,J.H., Shaw,A.W., Graham,S.L. and Ciccarone,T.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6297239-A 18 02-OCT-2001;
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1..38 /organism="unknown"
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ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13
RESULT 23
BD267970/c
LOCUS BD267970 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD267970
VERSION BD267970.1 GI:33077738
KEYWORDS JP 2002519376-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 38)
AUTHORS Bell,I.M., Dinsmore,C.J., Stokker,G.E., Anthony,N.J., Beshore,D.C., Ciccarone,T.M. and Desolms,J.S.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002519376-A 11 02-JUL-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002519376-A/11
PD 02-JUL-2002
PF 29-JUN-1999 JP 2000557828
PR 02-JUL-1998 US 60/091513
PI IAN M BELL,CHRISTOPHER J DINSMORE,GERALD E STOKKER,NEVILLE J PI ANTHONY,
PI DOUGLAS C BRESHORE,TERRENCE M CICCARONE,JANE S DESOLMS PC
C07D498/08,A61K31/337,A61K31/4188,A61P9/00,A61P9/10,A61P13/12, PC
A61P27/02,
PC A61P31/10,A61P31/12,A61P31/14,A61P35/00,A61P43/00,A61P43/00,
PC C07D515/08
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FH Key Location/Qualifiers
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Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13
RESULT 25
BD272024/c
LOCUS BD272024 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD272024
VERSION BD272024.1 GI:33081792
KEYWORDS JP 2002538120-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 38)
AUTHORS Jr.W.C.L., Sisko,J.T., Smith,A.M., Tucker,T.J., Dinsmore,C.J. and Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002538120-A 11 12-NOV-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002538120-A/11
PD 12-NOV-2002
PF 01-MAR-2000 JP 2000602080
PR 03-MAR-1999 US 60/122771,31-MAR-1999 US 60/127257 PI
WILLIAM C LUMMA JR,JOHN T SISCO,ANTHONY M SMITH,THOMAS J PI
TUCKER,
PI CHRISTOPHER J DINSMORE,JEFFREY M BERGMAN
PC C07D233/64,A61K31/496,A61P9/10,A61P13/12,A61P27/02,A61P31/12,
PC A61P35/00,

Db 28 ATATTCGTCATGGTG 13
RESULT 24
BD270873/c
LOCUS BD270873 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD270873
VERSION BD270873.1 GI:33080641
KEYWORDS JP 2002528504-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 38)
AUTHORS Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002528504-A 11 03-SEP-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002528504-A/11
PD 03-SEP-2002
PF 26-OCT-1999 JP 2000579229
PR 29-OCT-1998 US 60/106177,05-JAN-1999 GB 9900148.9 PI
JEFFREY M BERGMAN
PC C07D498/18,A61P1/16,A61P9/10,A61P13/12,A61P25/00,A61P27/02, PC
A61P31/12,
PC A61P35/00,A61P43/00//A61K31/4985
CC completely synthesized
FH Key Location/Qualifiers
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Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 ATAGTCCGTCATGGTG 26
Db 28 ATATTCGTCATGGTG 13
RESULT 25
BD272024/c
LOCUS BD272024 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD272024
VERSION BD272024.1 GI:33081792
KEYWORDS JP 2002538120-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 38)
AUTHORS Jr.W.C.L., Sisko,J.T., Smith,A.M., Tucker,T.J., Dinsmore,C.J. and Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002538120-A 11 12-NOV-2002;
COMMENT MERCK AND CO INC
OS Artificial Sequence
PN JP 2002538120-A/11
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000602080
PR 01-MAR-1999 US 60/122771,31-MAR-1999 US 60/127257 PI
WILLIAM C LUMMA JR,JOHN T SISCO,ANTHONY M SMITH,THOMAS J PI
TUCKER,
PI CHRISTOPHER J DINSMORE,JEFFREY M BERGMAN
PC C07D233/64,A61K31/496,A61P9/10,A61P13/12,A61P27/02,A61P31/12,
PC A61P35/00,

PC A61P43/00
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FH Key Location/Qualifiers
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FT Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCGCGTCATGGTG 26
DB 28 ATATTCGTCATGGTG 13

RESULT 26
BD272043/c
LOCUS BD272043 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferases.
ACCESSION BD272043
VERSION JP 2002538121-A/11.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stump,C.A. and Williams,T.M.
TITLE Inhibitors of prenyl-protein transferases
JOURNAL Patent: JP 2002538121-A 11 12-NOV-2002;
MERCK AND CO INC
OS Artificial Sequence
PN JP 2002538121-A/11
PD 12-NOV-2002
PF 01-MAR-2000 JP 2000602082
PR 03-MAR-1999 US 60/122971,31-MAR-1999 US 60/127252 PI
CRAIG A. STUMP,THERESA M WILLIAMS
PC C07D233/64, A61K31/4164, A61K31/4709, A61K31/4725, A61K31/496, PC
A61P9/10, A61P31/12, A61P35/00, A61P43/00, C07D401/12, C07D403/12,
PC C07D405/12
CC completely synthetic sequence
FH Key Location/Qualifiers
FT source 1..38 /organism='Artificial Sequence'.
FT Location/Qualifiers
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/db_xref='taxon:32630'

ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCGCGTCATGGTG 26
DB 28 ATATTCGTCATGGTG 13

RESULT 27
BD274581/c
LOCUS BD274581 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD274581
VERSION JP 2002542155-A/11.
KEYWORDS

synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 38)
AUTHORS Jr,W.C.L., Smith,A.M. and Sisko,J.T.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002542155-A 11 10-DEC-2002;
MERCK AND CO INC
OS Artificial Sequence
PN JP 2002542155-A/11
PD 10-DEC-2002
PF 01-MAR-2000 JP 2000602019
PR 03-MAR-1999 US 60/122970,31-MAR-1999 US 60/127259 PI
WILLIAM C LUMMA JR,ANTHONY M SMITH,JOHN T SISCO PC
C07D233/64, A61K31/454, A61P1/16, A61P9/10, A61P13/12, PC
A61P27/02, A61P31/10, A61P31/12, A61P35/00, A61P35/02, A61P43/00, C07D401/06//
PC A61P31/10, A61P31/12, A61P35/00, A61P35/02, A61P43/00, C07D401/06//
CC completely synthetic sequence
FH Key Location/Qualifiers
FT source 1..38 /organism='Artificial Sequence'.
FT Location/Qualifiers
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ORIGIN
Query Match 51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATAGTCGCGTCATGGTG 26
DB 28 ATATTCGTCATGGTG 13

RESULT 28
BD274600/c
LOCUS BD274600 38 bp DNA linear PAT 17-JUL-2003
DEFINITION Inhibitors of prenyl-protein transferase.
ACCESSION BD274600
VERSION BD274600.1 GI:33084368
KEYWORDS JP 2002540072-A/11.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hartman,G.D., Jr,W.C.L., Sisko,J.T., Smith,A.M., Tucker,T.J. and
Stokker,G.E.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: JP 2002540072-A 11 26-NOV-2002;
MERCK AND CO INC
OS Artificial Sequence
PN JP 2002540072-A/11
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602079
PR 03-MAR-1999 US 60/122768,31-MAR-1999 US 60/127253 PI
GEORGE D HARTMAN,WILLIAM C LUMMA JR,JOHN T SISCO,ANTHONY M PI
SMITH,
PC C07D233/64, A61K31/496, A61P1/16, A61P9/00, A61P13/12, PC
A61P27/02, A61P31/10, A61P31/12, A61P35/00, A61P35/02, A61P43/00, C07D401/12,
PC C07D405/12
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FH Key Location/Qualifiers
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FT Location/Qualifiers
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ORIGIN
Query Match          51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGCGTCATGGTG 26
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Db 28 ATATTCGCGTCATGGTG 13

RESULT 29
AR181816/c
LOCUS          AR181816          38 bp          DNA          linear          PAT 20-APR-2002
DEFINITION     Sequence 13 from patent US 6335343.
ACCESSION      AR181816
VERSION        AR181816.1 GI:20224030
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Lumma,W.C. Jr., Smith,A.M. and Sisko,J.T.
TITLE          Inhibitors of prenyl-protein transferase
JOURNAL        Patent: US 6335343-A 13 01-JAN-2002;
FEATURES       Location/Qualifiers
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                /mol_type="unassigned DNA"

ORIGIN
Query Match          51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGCGTCATGGTG 26
    ||| ||||| ||||| |||||
Db 28 ATATTCGCGTCATGGTG 13

RESULT 30
AR195282/c
LOCUS          AR195282          38 bp          DNA          linear          PAT 20-APR-2002
DEFINITION     Sequence 14 from patent US 6350755.
ACCESSION      AR195282
VERSION        AR195282.1 GI:20244719
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 38)
AUTHORS        deSolms,S.Jane. and Shaw,A.W.
TITLE          Inhibitors of prenyl-protein transferase
JOURNAL        Patent: US 6350755-A 14 26-FEB-2002;
FEATURES       Location/Qualifiers
                source
                1..38
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match          51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGCGTCATGGTG 26
    ||| ||||| ||||| |||||
Db 28 ATATTCGCGTCATGGTG 13

RESULT 31
AR199998/c
LOCUS          AR199998          38 bp          DNA          linear          PAT 20-APR-2002
DEFINITION     Sequence 13 from patent US 6355643.
ACCESSION      AR199998
VERSION        AR199998.1 GI:20250072
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Lumma,W.C., Sisko,J.T., Smith,A.M., Tucker,T.J., Dinsmore,C.J. and Bergman,J.M.
TITLE          Inhibitors of prenyl-protein transferase
JOURNAL        Patent: US 6355643-A 13 12-MAR-2002;
FEATURES       Location/Qualifiers
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ORIGIN
Query Match          51.4%; Score 14.4; DB 6; Length 38;
Best Local Similarity 93.8%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGCGTCATGGTG 26
    ||| ||||| ||||| |||||
Db 28 ATATTCGCGTCATGGTG 13

RESULT 32
AR201351/c
LOCUS          AR201351          38 bp          DNA          linear          PAT 20-APR-2002
DEFINITION     Sequence 13 from patent US 6358956.
ACCESSION      AR201351
VERSION        AR201351.1 GI:20252239
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Hartman,G.D., Lumma,W.C. Jr., Sisko,J.T., Smith,A.M., Tucker,T.J. and Stokker,G.E.
TITLE          Inhibitors of prenyl-protein transferase
JOURNAL        Patent: US 6358956-A 13 19-MAR-2002;
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DEFINITION     Sequence 14 from patent US 6358985.
ACCESSION      AR201370
VERSION        AR201370.1 GI:20252258
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Anthony,N.J., Bell,I.M., Beshore,D.C., Ciccarone,T.M., de Solms,S.Jane, Dinsmore,C.J. and Stokker,G.E.
TITLE          Inhibitors of prenyl-protein transferase
JOURNAL        Patent: US 6358985-A 14 19-MAR-2002;
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DEFINITION Sequence 14 from patent US 6410534.
ACCESSION AR216094
VERSION AR216094.1 GI:23314382
KEYWORDS
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ORGANISM
REFERENCE 1 (bases 1 to 38)
AUTHORS Dinmore,C.J., Bell,I.M., Beshore,D.C. and Williams,T.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6410534-A 14 25-JUN-2002;
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RESULT 35
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DEFINITION Sequence 13 from patent US 6441017.
ACCESSION AR224803
VERSION AR224803.1 GI:23333713
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 38)
AUTHORS Bell,I.M., Beshore,D.C., Gallicchio,S.N. and Zartman,C.B.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6441017-A 13 27-AUG-2002;
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ACCESSION AR317262
VERSION AR317262.1 GI:33698226
KEYWORDS
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REFERENCE 1 (bases 1 to 38)
AUTHORS Dinmore,C.J., Bergman,J.M., Graham,S.L., Nguyen,D.N.,
Stokker,G.E., Williams,T.M. and Zartman,C.B.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6562823-A 14 13-MAY-2003;
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RESULT 37
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VERSION AR337537.1 GI:33723589
KEYWORDS
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REFERENCE 1 (bases 1 to 38)
AUTHORS deSolms,S.J., Stokker,G.E. and Shaw,A.W.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6566385-A 14 20-MAY-2003;
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DEFINITION Sequence 13 from patent US 6329376.
ACCESSION AR366761
VERSION AR366761.1 GI:34599663
KEYWORDS
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REFERENCE 1 (bases 1 to 38)
AUTHORS Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6329376-A 13 11-DEC-2001;
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ACCESSION AR368676
VERSION AR368676.1 GI:34602827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hartman,G.D., Lumma,W.C. Jr., Sisko,J.T., Smith,A.M., Tucker,T.J.
and Bergman,J.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6376496-A 13 23-APR-2002;
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ACCESSION AR383170
VERSION AR383170.1 GI:40092623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stump,C.A. and Williams,T.M.
TITLE Inhibitors of prenyl-protein transferase
JOURNAL Patent: US 6610722-A 14 26-AUG-2003;
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GenCore version 5.1.6
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Perfect score: 26

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Listing first 1000 summaries

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C 239 10.8 41.5 50 1 AU103378 AU103378
C 240 10.8 41.5 50 1 AU103763 AU103763
C 241 10.8 41.5 50 1 AU104255 AU104255
C 242 10.8 41.5 50 1 AU106985 AU106985
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AJ668956 AJ668956
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AU106985 AU106985
AU107257 AU107257

244	10.8	41.5	50	1	AU107258	AU107258	317	10.6	40.8	50	1	AU105176	AU105176
245	10.8	41.5	50	1	AU107260	AU107260	C 318	10.6	40.8	50	1	AU105235	AU105235
246	10.8	41.5	50	1	AU107261	AU107261	C 319	10.6	40.8	50	1	AU107879	AU107879
247	10.8	41.5	50	1	AU107537	AU107537	C 320	10.6	40.8	50	8	BH905285	SALK 1058
248	10.8	41.5	50	7	CK225906	701613105	C 321	10.6	40.8	50	8	CH019705	3591_1_16
249	10.8	41.5	50	9	CG808002	1118088F1	C 322	10.4	40.0	19	6	CF293217	30DGS--02
250	10.6	40.8	21	8	AZ581771	1M0370F10	C 323	10.4	40.0	19	8	AZ450851	1M0249113
251	10.6	40.8	23	8	AZ609364	1M0434004	C 324	10.4	40.0	21	4	BM400238	5009-0-7-
252	10.6	40.8	23	8	AZ609364	1M0434004	C 325	10.4	40.0	21	4	BM400238	5009-0-7-
253	10.6	40.8	26	8	AZ620208	1M0420K07	C 326	10.4	40.0	24	8	AZ811574	T. brucei
254	10.6	40.8	27	8	BH904657	SALK 1048	C 327	10.4	40.0	24	8	AZ811574	T. brucei
255	10.6	40.8	28	8	BH789687	SALK 0444	C 328	10.4	40.0	25	1	AU257461	AU257461
256	10.6	40.8	29	8	AZ609543	1M0434C15	C 329	10.4	40.0	28	8	AZ621815	1M0455A08
257	10.6	40.8	31	9	BX656964	ArabiDops	C 330	10.4	40.0	28	8	AZ665590	1M0547D08
258	10.6	40.8	31	9	AZ620458	Pan trogl	C 331	10.4	40.0	28	8	BH813863	SALK 0653
259	10.6	40.8	32	15	AJ648311	AJ648311	C 332	10.4	40.0	30	8	AZ623794	1M0461C19
260	10.6	40.8	32	15	AJ648311	AJ648311	C 333	10.4	40.0	31	1	AA980782	u45e10_r
261	10.6	40.8	34	1	A1200149	BZ424912	C 334	10.4	40.0	32	9	AJ590509	ArabiDops
262	10.6	40.8	34	8	BH854533	KG02257-3	C 335	10.4	40.0	32	9	AJ590509	ArabiDops
263	10.6	40.8	34	8	BH854533	KG02257-3	C 336	10.4	40.0	32	9	AJ590509	ArabiDops
264	10.6	40.8	35	8	BH854533	KG02257-3	C 337	10.4	40.0	32	9	AJ590509	ArabiDops
265	10.6	40.8	37	8	BZ358957	SALK 1335	C 338	10.4	40.0	36	8	BH911899	SALK 0727
266	10.6	40.8	37	9	CG722986	1119074C0	C 339	10.4	40.0	36	8	BH911899	SALK 0727
267	10.6	40.8	38	1	AA054107	zf50f06_r	C 340	10.4	40.0	36	8	BH911899	SALK 0727
268	10.6	40.8	38	8	AZ785016	2M0028D05	C 341	10.4	40.0	37	8	AZ811748	2M0087C04
269	10.6	40.8	39	8	AZ603310	1M0422N12	C 342	10.4	40.0	37	8	AZ811748	2M0087C04
270	10.6	40.8	43	1	AA926972	Om26a12_s	C 343	10.4	40.0	37	9	CL653059	PR10116C
271	10.6	40.8	43	1	A1047023	uh57e09_r	C 344	10.4	40.0	37	9	CL653059	PR10116C
272	10.6	40.8	43	1	AV962349	AV962349	C 345	10.4	40.0	38	8	AZ643994	1M0507B14
273	10.6	40.8	43	1	AV962349	AV962349	C 346	10.4	40.0	38	8	AZ643994	1M0507B14
274	10.6	40.8	43	8	AZ623767	1M0461K16	C 347	10.4	40.0	40	1	AL657570	fc15c02.y
275	10.6	40.8	43	8	AZ623767	1M0461K16	C 348	10.4	40.0	40	9	BX663464	ArabiDops
276	10.6	40.8	43	9	CG797401	SALK 1448	C 349	10.4	40.0	40	9	CL639694	1M07075B1
277	10.6	40.8	45	4	BG527007	602556245	C 350	10.4	40.0	41	8	BH080690	P028E11 G
278	10.6	40.8	45	7	H67715	Y72C07_81	C 351	10.4	40.0	42	6	CA966788	CcLX06a23
279	10.6	40.8	45	8	AZ952610	2M0217E06	C 352	10.4	40.0	42	6	CA966788	CcLX06a23
280	10.6	40.8	45	8	CL182796	KG533 Bay	C 353	10.4	40.0	43	1	AL669008	AL669008
281	10.6	40.8	45	8	CL182796	KG533 Bay	C 354	10.4	40.0	43	7	W20560	mc20C04_r1
282	10.6	40.8	45	9	TA379D04Q	TA379D04Q	C 355	10.4	40.0	43	8	AZ949460	2M0212P24
283	10.6	40.8	45	9	CL256726	XS0211 Sa	C 356	10.4	40.0	43	9	TA114C01P	T. brucei
284	10.6	40.8	45	9	CL256726	XS0211 Sa	C 357	10.4	40.0	44	5	BX548721	BX548721
285	10.6	40.8	45	9	AG215618	Drosophi	C 358	10.4	40.0	44	9	AL771069	ArabiDops
286	10.6	40.8	45	9	AG215618	Drosophi	C 359	10.4	40.0	44	9	CG892045	10S0561-0
287	10.6	40.8	46	9	CL525775	AG0018 Sa	C 360	10.4	40.0	44	8	BH628960	1007075B1
288	10.6	40.8	47	1	AG557740	AJ657740	C 361	10.4	40.0	45	8	BZ385312	SALK 1370
289	10.6	40.8	47	9	BX533076	BX533076	C 362	10.4	40.0	45	8	CC183529	XE347 Bay
290	10.6	40.8	47	9	AG192238	Pan trogl	C 363	10.4	40.0	45	9	DME547098	ArabiDops
291	10.6	40.8	48	8	AZ427432	1M0209F20	C 364	10.4	40.0	46	1	AA828568	od74b11.s
292	10.6	40.8	48	8	BH790348	SALK 0568	C 365	10.4	40.0	46	1	AL935210	wpl17b09.x
293	10.6	40.8	48	8	BH910594	BZ288754	C 366	10.4	40.0	46	8	BH865495	SALK 0986
294	10.6	40.8	48	8	BZ288754	SALK 0221	C 367	10.4	40.0	46	8	CC178563	NPX460 Ba
295	10.6	40.8	48	9	TA372F02Q	TA372F02Q	C 368	10.4	40.0	46	9	TA281A04Q	T. brucei
296	10.6	40.8	48	9	AG217828	Drosophi	C 369	10.4	40.0	47	8	BH901057	KG08638-5
297	10.6	40.8	49	1	AA427743	zw25h01.s	C 370	10.4	40.0	48	6	CO1973	HUMG000398
298	10.6	40.8	49	8	AZ500008	1M0338E09	C 371	10.4	40.0	48	7	R44463	Yg28f03.81
299	10.6	40.8	49	9	CG427099	01S0723-0	C 372	10.4	40.0	48	8	AZ412179	1M0185H06
300	10.6	40.8	49	9	CL233809	01S0638-0	C 373	10.4	40.0	48	8	CC044288	3591_1_16
301	10.6	40.8	49	9	CL674014	PR10111a	C 374	10.4	40.0	48	9	AG218724	Drosophi
302	10.6	40.8	50	1	AU103015	AU103015	C 375	10.4	40.0	49	1	AA588107	nk10e04.s
303	10.6	40.8	50	1	AU103753	AU103753	C 376	10.4	40.0	49	3	BX036579	Single re
304	10.6	40.8	50	1	AU104339	AU104339	C 377	10.4	40.0	49	4	BI753840	603027521
305	10.6	40.8	50	1	AU104344	AU104344	C 378	10.4	40.0	49	6	C20876	HUMG000494
306	10.6	40.8	50	1	AU104345	AU104345	C 379	10.4	40.0	49	8	BH800310	1008124B0
307	10.6	40.8	50	1	AU104354	AU104354	C 380	10.4	40.0	49	8	BH912865	3526_1_37
308	10.6	40.8	50	1	AU104359	AU104359	C 381	10.4	40.0	49	8	CC020451	3591_1_1
309	10.6	40.8	50	1	AU104360	AU104360	C 382	10.4	40.0	50	1	AU102827	AU102827
310	10.6	40.8	50	1	AU104361	AU104361	C 383	10.4	40.0	50	1	AU104332	AU104332
311	10.6	40.8	50	1	AU104362	AU104362	C 384	10.4	40.0	50	1	AU105349	AU105349
312	10.6	40.8	50	1	AU105169	AU105169	C 385	10.4	40.0	50	1	AU106596	AU106596
313	10.6	40.8	50	1	AU105170	AU105170	C 386	10.4	40.0	50	1	AU107637	AU107637
314	10.6	40.8	50	1	AU105171	AU105171	C 387	10.4	40.0	50	4	BI416796	hasp002xf
315	10.6	40.8	50	1	AU105174	AU105174	C 388	10.4	40.0	50	8	BH215111	1006025D0
316	10.6	40.8	50	1	AU105175	AU105175	C 389	10.4	40.0	50	9	CR027504	Forward s

C 390	10.4	40.0	50	9	CR059583	Forward s	CR059583	Forward s	C 463	10.2	39.2	49	1	AA497509	vh29ei2.r
C 391	10.4	40.0	50	9	TA34605Q	AL496230	T. brucei	AL496230	C 464	10.2	39.2	49	4	BG222669	nah36d07.
C 392	10.2	39.2	15	4	BM398834	5009-0-5-	BM398834	5009-0-5-	C 465	10.2	39.2	49	4	BG222669	nah40b02.
C 393	10.2	39.2	19	8	AZ481008	1M0302M15	AZ481008	1M0302M15	C 466	10.2	39.2	49	4	BG223065	nah42g11.
C 394	10.2	39.2	22	6	CD535018	54P20 Ara	CD535018	54P20 Ara	C 467	10.2	39.2	49	4	BG223113	nah43f03.
C 395	10.2	39.2	25	8	AZ818242	2M0088G12	AZ818242	2M0088G12	C 468	10.2	39.2	49	4	BG231002	nah43b01.
C 396	10.2	39.2	26	8	AZ626835	1M0467L14	AZ626835	1M0467L14	C 469	10.2	39.2	49	4	BG231030	nah43h01.
C 397	10.2	39.2	27	8	AZ989590	2M0273D03	AZ989590	2M0273D03	C 470	10.2	39.2	49	4	BG236496	nah44a12.
C 398	10.2	39.2	27	9	CG723757	1119077H0	CG723757	1119077H0	C 471	10.2	39.2	49	4	BG271392	nah50a04.
C 399	10.2	39.2	27	9	CL681352	PR10130d	CL681352	PR10130d	C 472	10.2	39.2	49	4	BG271415	nah50d11.
C 400	10.2	39.2	28	8	AZ615744	1M0445B15	AZ615744	1M0445B15	C 473	10.2	39.2	49	4	BG271439	nah50h06.
C 401	10.2	39.2	28	9	TA297B09Q	AL489564	T. brucei	AL489564	C 474	10.2	39.2	49	4	BG271529	nah58f01.
C 402	10.2	39.2	29	9	CG714953	1119039C0	CG714953	1119039C0	C 475	10.2	39.2	49	4	BG271560	nah59a07.
C 403	10.2	39.2	30	8	BZ352917	SALK_1194	BZ352917	SALK_1194	C 476	10.2	39.2	49	4	BG271601	nah59f08.
C 404	10.2	39.2	31	9	DR430BT	Danio rer	DR430BT	Danio rer	C 477	10.2	39.2	49	4	BG271654	nah51e08.
C 405	10.2	39.2	31	9	CG719530	1119058A0	CG719530	1119058A0	C 478	10.2	39.2	49	4	BG271663	nah51g06.
C 406	10.2	39.2	33	4	BJ039102	BJ039102	BJ039102	BJ039102	C 479	10.2	39.2	49	4	BG271686	nah52b05.
C 407	10.2	39.2	33	8	AZ660655	1M0538D20	AZ660655	1M0538D20	C 480	10.2	39.2	49	4	BG271865	nah52b05.
C 408	10.2	39.2	33	9	DR23D20T	AL978858	Danio rer	AL978858	C 481	10.2	39.2	49	4	BG272235	nah31g07.
C 409	10.2	39.2	34	4	BJ064751	BJ064751	BJ064751	BJ064751	C 482	10.2	39.2	49	4	BG272662	nah35b08.
C 410	10.2	39.2	34	4	BJ066450	BJ066450	BJ066450	BJ066450	C 483	10.2	39.2	49	4	BG370431	nah33e05.
C 411	10.2	39.2	34	9	TA227B06Q	AL479989	T. brucei	AL479989	C 484	10.2	39.2	49	7	H55111	CHR220050 C
C 412	10.2	39.2	34	9	CL438623	FST7894-N	CL438623	FST7894-N	C 485	10.2	39.2	49	7	R08243	YF18f06.r1
C 413	10.2	39.2	35	8	BH852495	SALK_0747	BH852495	SALK_0747	C 486	10.2	39.2	50	1	AA948106	ons1a04.s
C 414	10.2	39.2	36	9	DR43A15T	AL973794	Danio rer	AL973794	C 487	10.2	39.2	50	1	AJ650056	AJ650056
C 415	10.2	39.2	37	1	AI118163	ue38f01.x	AI118163	ue38f01.x	C 488	10.2	39.2	50	1	AU102316	AU102316
C 416	10.2	39.2	37	1	BM400556	5009-0-75	BM400556	5009-0-75	C 489	10.2	39.2	50	1	AU102529	AU102529
C 417	10.2	39.2	37	7	H53607	YQ87h08.81	H53607	YQ87h08.81	C 490	10.2	39.2	50	1	AU102733	AU102733
C 418	10.2	39.2	37	8	BH901965	BH901965	BH901965	BH901965	C 491	10.2	39.2	50	1	AU103795	AU103795
C 419	10.2	39.2	37	8	CG712023	1119023G0	CG712023	1119023G0	C 492	10.2	39.2	50	1	AU104346	AU104346
C 420	10.2	39.2	38	2	BF144195	601786804	BF144195	601786804	C 493	10.2	39.2	50	1	AU104959	AU104959
C 421	10.2	39.2	38	9	TA128E05P	AL464359	T. brucei	AL464359	C 494	10.2	39.2	50	1	AU105238	AU105238
C 422	10.2	39.2	39	1	AV970688	AV970688	AV970688	AV970688	C 495	10.2	39.2	50	1	AU105314	AU105314
C 423	10.2	39.2	39	8	AZ391588	AZ391588	AZ391588	AZ391588	C 496	10.2	39.2	50	1	AU105549	AU105549
C 424	10.2	39.2	39	8	AZ836176	2M0130I22	AZ836176	2M0130I22	C 497	10.2	39.2	50	1	AU106767	AU106767
C 425	10.2	39.2	39	8	CC060550	EX04745-5	CC060550	EX04745-5	C 498	10.2	39.2	50	1	AU107095	AU107095
C 426	10.2	39.2	40	8	AZ862112	2M0169F03	AZ862112	2M0169F03	C 499	10.2	39.2	50	1	AU107467	AU107467
C 427	10.2	39.2	41	2	BF572131	602076910	BF572131	602076910	C 500	10.2	39.2	50	1	AU107468	AU107468
C 428	10.2	39.2	41	8	AZ345445	1M0080H07	AZ345445	1M0080H07	C 501	10.2	39.2	50	1	AU107552	AU107552
C 429	10.2	39.2	41	8	AZ788255	2M0035A16	AZ788255	2M0035A16	C 502	10.2	39.2	50	1	AU107634	AU107634
C 430	10.2	39.2	41	9	AZ936284	Arabidops	AZ936284	Arabidops	C 503	10.2	39.2	50	1	AU107952	AU107952
C 431	10.2	39.2	41	9	BX943466	Arabidops	BX943466	Arabidops	C 504	10.2	39.2	50	1	AA503797	ne51c06.s
C 432	10.2	39.2	42	6	CD029192	mgns017XP	CD029192	mgns017XP	C 505	10.2	39.2	50	2	AW248365	2820706.5
C 433	10.2	39.2	42	6	AQ026241	1(3)L1233	AQ026241	1(3)L1233	C 506	10.2	39.2	50	4	BG222716	nah27e07.
C 434	10.2	39.2	42	9	AL765117	Arabidops	AL765117	Arabidops	C 507	10.2	39.2	50	4	BG223051	nah28b01.
C 435	10.2	39.2	42	9	BX157082	Danio rer	BX157082	Danio rer	C 508	10.2	39.2	50	4	BG271426	nah28f06.
C 436	10.2	39.2	43	1	AA126556	AA126556	AA126556	AA126556	C 509	10.2	39.2	50	4	BG271427	nah28f06.
C 437	10.2	39.2	43	7	H14006	EST00032 Ch	H14006	EST00032 Ch	C 510	10.2	39.2	50	4	BG271665	nah28f06.
C 438	10.2	39.2	43	8	AZ588007	1M0396P08	AZ588007	1M0396P08	C 511	10.2	39.2	50	4	BG271710	nah28f06.
C 439	10.2	39.2	44	8	AZ376080	1M0129I13	AZ376080	1M0129I13	C 512	10.2	39.2	50	4	BG271931	nah28f06.
C 440	10.2	39.2	44	8	AZ830256	2M0109H20	AZ830256	2M0109H20	C 513	10.2	39.2	50	4	BG272024	nah28f06.
C 441	10.2	39.2	44	8	AZ834721	2M0117L04	AZ834721	2M0117L04	C 514	10.2	39.2	50	4	BG272395	nah28f06.
C 442	10.2	39.2	44	9	BX221218	Danio rer	BX221218	Danio rer	C 515	10.2	39.2	50	4	BG272610	nah28f06.
C 443	10.2	39.2	44	9	BX893266	Arabidops	BX893266	Arabidops	C 516	10.2	39.2	50	4	BG272631	nah28f06.
C 444	10.2	39.2	44	9	CG718685	1119054A1	CG718685	1119054A1	C 517	10.2	39.2	50	4	BG272640	nah28f06.
C 445	10.2	39.2	45	8	AZ473700	1M0289P11	AZ473700	1M0289P11	C 518	10.2	39.2	50	4	BG272691	nah28f06.
C 446	10.2	39.2	45	8	BH814770	SALK_0669	BH814770	SALK_0669	C 519	10.2	39.2	50	4	BG272917	nah28f06.
C 447	10.2	39.2	45	9	BX287479	Arabidops	BX287479	Arabidops	C 520	10.2	39.2	50	4	BG273145	nah28f06.
C 448	10.2	39.2	46	1	AA987637	or-93d11.s	AA987637	or-93d11.s	C 521	10.2	39.2	50	4	BG370313	nah28f06.
C 449	10.2	39.2	46	8	AZ784657	AA787637	AA787637	AA787637	C 522	10.2	39.2	50	4	BG370398	nah28f06.
C 450	10.2	39.2	46	9	CG784706	RRR527 Ba	CG784706	RRR527 Ba	C 523	10.2	39.2	50	4	BI416779	hasp002xd
C 451	10.2	39.2	47	8	AZ481406	1M0303E09	AZ481406	1M0303E09	C 524	10.2	39.2	50	4	BM514736	ky07f07.y
C 452	10.2	39.2	47	8	AZ665018	1M0545B15	AZ665018	1M0545B15	C 525	10.2	39.2	50	7	H41744	yo06b09.b1
C 453	10.2	39.2	47	8	AZ776409	2M0010D06	AZ776409	2M0010D06	C 526	10.2	39.2	50	8	AZ326669	1M0049108
C 454	10.2	39.2	47	8	BH623585	1007077H0	BH623585	1007077H0	C 527	10.2	39.2	50	8	AG189033	Pan trogl
C 455	10.2	39.2	47	8	BZ580301	3590.1.27	BZ580301	3590.1.27	C 528	10.2	39.2	50	9	AG194535	Pan trogl
C 456	10.2	39.2	48	8	BH623937	1M0071F09	BH623937	1M0071F09	C 529	10.2	39.2	50	9	AG194535	Pan trogl
C 457	10.2	39.2	48	8	BH624836	1007089A0	BH624836	1007089A0	C 530	10.2	39.2	50	9	AG194535	Pan trogl
C 458	10.2	39.2	48	8	CC050390	01S0536-0	CC050390	01S0536-0	C 531	10.2	39.2	50	9	AG194535	Pan trogl
C 459	10.2	39.2	48	1	AA792088	VP47b08.r	AA792088	VP47b08.r	C 532	10.2	39.2	50	9	AG194535	Pan trogl
C 460	10.2	39.2	49	1	AI048774	ub32d01.f	AI048774	ub32d01.f	C 533	10.2	39.2	50	9	AG194535	Pan trogl
C 461	10.2	39.2	49	1	AI475242	t180f10.x	AI475242	t180f10.x	C 534	10.2	39.2	50	9	AG194535	Pan trogl
C 462	10.2	39.2	49	1	AI958154	fc91d08.y	AI958154	fc91d08.y	C 535	10.2	39.2	50	9	AG194535	Pan trogl

C 536	10	38.5	29	8	AZ598862	AZ598862	1M0413G23	C 609	10	38.5	47	1	AA199768	AA199768	zq7f609.r
C 537	10	38.5	29	8	AZ598897	AZ598897	1M0413N20	C 610	10	38.5	47	7	R07222	R07222	yf14b07.r1
C 538	10	38.5	30	4	BM395434	BM395434	50072-2-9	C 611	10	38.5	47	8	AZ634688	AZ634688	1M0490D09
C 539	10	38.5	30	4	BM396904	BM396904	5009-0-26	C 612	10	38.5	47	8	AZ765062	AZ765062	2M0561K15
C 540	10	38.5	30	8	AZ74529	AZ74529	1M0292B13	C 613	10	38.5	47	8	AZ805158	AZ805158	2M0066K14
C 541	10	38.5	31	1	AA868659	AA868659	ak4902.s	C 614	10	38.5	47	8	BZ354183	BZ354183	SALK_1233
C 542	10	38.5	31	1	AA917290	AA917290	SWOVL3CAN	C 615	10	38.5	47	9	BX182559	BX182559	Danilo rer
C 543	10	38.5	31	7	HA1262	HA1262	YH89D01.B1	C 616	10	38.5	47	9	CL214121	CL214121	G016E06 G
C 544	10	38.5	31	7	HA1491	HA1491	YD94C02.B1	C 617	10	38.5	48	8	AQ026170	AQ026170	1(3101470
C 545	10	38.5	32	9	DR1E11T	AL732743	Danilo rer	C 618	10	38.5	48	9	BX533275	BX533275	Arabidops
C 546	10	38.5	33	4	BJ081548	BJ081548		C 619	10	38.5	49	1	AA909940	AA909940	om32g02.s
C 547	10	38.5	33	4	BM398846	BM398846	5009-0-5-	C 620	10	38.5	49	1	AI956143	AI956143	wt35601.x
C 548	10	38.5	33	8	AZ784186	AZ784186	2M0026F12	C 621	10	38.5	49	7	D12406	D12406	HUM00FW129
C 549	10	38.5	33	8	BH846998	BH846998	SALK_0125	C 622	10	38.5	49	8	AQ025458	AQ025458	EP(X)1427
C 550	10	38.5	33	9	BX533337	BX533337	Arabidops	C 623	10	38.5	49	8	BH130349	BH130349	G-6p13.f
C 551	10	38.5	34	1	AI192873	AI192873	qe68b12.x	C 624	10	38.5	50	1	AI708455	AI708455	as97e06.x
C 552	10	38.5	34	8	AZ462024	AZ462024	1M0269E12	C 625	10	38.5	50	1	AL874998	AL874998	AL874998
C 553	10	38.5	35	4	BM395896	BM395896	5009-0-13	C 626	10	38.5	50	1	AU103076	AU103076	
C 554	10	38.5	35	9	CL213092	CL213092	F032F01 G	C 627	10	38.5	50	1	AU103192	AU103192	
C 555	10	38.5	36	1	AU283358	AU283358		C 628	10	38.5	50	1	AU103739	AU103739	
C 556	10	38.5	36	1	AV832509	AV832509		C 629	10	38.5	50	1	AU103745	AU103745	
C 557	10	38.5	36	1	BI869626	BI869626	603393580	C 630	10	38.5	50	1	AU104027	AU104027	
C 558	10	38.5	36	7	R84783	R84783	yt66c02.r1	C 631	10	38.5	50	1	AU104437	AU104437	
C 559	10	38.5	36	8	AZ439912	AZ439912	1M0230E15	C 632	10	38.5	50	1	AU106331	AU106331	
C 560	10	38.5	36	9	CR360542	CR360542	Arabidops	C 633	10	38.5	50	1	AU106339	AU106339	
C 561	10	38.5	37	1	AI384342	AI384342	fb07h06.y	C 634	10	38.5	50	1	AU106340	AU106340	
C 562	10	38.5	37	5	BM3927309	BM3927309		C 635	10	38.5	50	1	AU106680	AU106680	
C 563	10	38.5	37	8	AZ583188	AZ583188	1M0376P20	C 636	10	38.5	50	1	AU106744	AU106744	
C 564	10	38.5	38	4	BM704291	BM704291	602687674	C 637	10	38.5	50	1	AU106745	AU106745	
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C 566	10	38.5	39	1	AL768941	AL768941	Arabidops	C 639	10	38.5	50	1	AU106750	AU106750	
C 567	10	38.5	39	1	AV834166	AV834166		C 640	10	38.5	50	1	AU107846	AU107846	
C 568	10	38.5	39	7	H84235	H84235	ys65f06.B1	C 641	10	38.5	50	1	AU107847	AU107847	
C 569	10	38.5	39	8	AZ493934	AZ493934	1M0328F19	C 642	10	38.5	50	1	AU107851	AU107851	
C 570	10	38.5	39	8	AZ659162	AZ659162		C 643	10	38.5	50	1	AU107854	AU107854	
C 571	10	38.5	40	1	AZ206107	AI206107	q528d01.x	C 644	10	38.5	50	1	AU107855	AU107855	
C 572	10	38.5	40	8	AZ606449	AZ606449	1M0428B15	C 645	10	38.5	50	1	AU108090	AU108090	
C 573	10	38.5	41	4	BI659995	BI659995	503302286	C 646	10	38.5	50	2	BB616279	BB616279	
C 574	10	38.5	41	7	HA14824	HA14824	ym25d07.B1	C 647	10	38.5	50	8	AZ853478	AZ853478	2M0156M11
C 575	10	38.5	41	8	AZ658005	AZ658005	1M0534J03	C 648	9	37.7	14	9	AJ593881	AJ593881	Arabidops
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C 578	10	38.5	42	4	BG252356	BG252356	602365945	C 651	9	37.7	21	8	AZ462622	AZ462622	1M0269C08
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C 582	10	38.5	43	4	BG250039	BG250039	602362124	C 655	9	37.7	25	8	AZ815351	AZ815351	2M0083I02
C 583	10	38.5	43	4	BG259962	BG259962	602371733	C 656	9	37.7	25	9	TA6E12Q	TA6E12Q	
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C 585	10	38.5	44	2	BE252118	BE252118	601113681	C 658	9	37.7	28	9	TA30F12Q	TA30F12Q	
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C 587	10	38.5	44	6	CF3211982	CF3211982	HD--13-G1	C 660	9	37.7	30	9	TA263H06Q	TA263H06Q	
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C 589	10	38.5	44	8	CC046354	CC046354	3591_1_18	C 662	9	37.7	31	9	CR361271	CR361271	Arabidops
C 590	10	38.5	44	9	CR405063	CR405063	Arabidops	C 663	9	37.7	32	8	AZ834299	AZ834299	2M016N24
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C 594	10	38.5	45	2	BE256638	BE256638	601110972	C 667	9	37.7	33	9	AJ596521	AJ596521	Arabidops
C 595	10	38.5	45	4	BU034411	BU034411	BJ034411	C 668	9	37.7	34	7	TA115B10Q	TA115B10Q	
C 596	10	38.5	45	6	CB209994	CB209994	OML00274	C 669	9	37.7	34	7	T60701	T60701	YB69F02.B1
C 597	10	38.5	45	6	CB211074	CB211074	OML01354	C 670	9	37.7	34	8	AZ648259	AZ648259	1M0517M11
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C 602	10	38.5	46	1	AA129426	AA129426	zn78d03.s	C 675	9	37.7	35	8	BH846699	BH846699	SALK_0098
C 603	10	38.5	46	1	AI861936	AI861936	td18a12.x	C 676	9	37.7	36	8	AZ514452	AZ514452	1M0361N13
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CL658173 PRI0130C
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AL473175 T. brucei
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AU587914 Arabidops
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AZ839538 2M0135P10
BH861733 SALK_0879
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C 830	9.6	36.9	33	9	BX945822	BX945822	Arabidops	903	9.6	36.9	44	8	BH850740	BH850740	SALK 0717
C 831	9.6	36.9	33	9	TA204F11P	TA204F11P	T. brucei	C 904	9.6	36.9	44	9	CR297276	CR297276	Medicago
C 832	9.6	36.9	34	1	AA717376	AA717376	VP42h10.r	C 905	9.6	36.9	44	9	DR71117S	DR71117S	Danio rer
C 833	9.6	36.9	34	1	AA908764	AA908764	ol06a05.s	906	9.6	36.9	44	9	CG802823	CG802823	1118035A0
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C 839	9.6	36.9	36	1	AV833092	AV833092	Arabidops	C 912	9.6	36.9	45	8	AJ600711	AJ600711	Arabidops
C 840	9.6	36.9	36	8	AZ781971	AZ781971	2M0021K14	C 913	9.6	36.9	45	9	EX893660	EX893660	Arabidops
C 841	9.6	36.9	36	8	BH854787	BH854787	SALK 0885	914	9.6	36.9	45	9	EX944839	EX944839	Arabidops
C 842	9.6	36.9	36	8	BZ381819	BZ381819	SALK 1173	915	9.6	36.9	45	9	TA247807Q	TA247807Q	T. brucei
C 843	9.6	36.9	36	9	AL760306	AL760306	Arabidops	916	9.6	36.9	45	9	TA372A04P	TA372A04P	T. brucei
C 844	9.6	36.9	36	9	CL681770	CL681770	PR10132a	917	9.6	36.9	45	9	CL212732	CL212732	G049E09 G
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C 847	9.6	36.9	37	8	AQ025345	AQ025345	EP(X)0491	C 920	9.6	36.9	46	1	AV959402	AV959402	AV959402
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C 851	9.6	36.9	38	8	BH902425	BH902425	SALK 0918	C 924	9.6	36.9	46	7	W69845	W69845	zd48b04.r1
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C 855	9.6	36.9	39	9	DME547534	DME547534	Drosophil	928	9.6	36.9	46	9	BI126315	BI126315	Danio rer
C 856	9.6	36.9	40	1	AA916980	AA916980	ol54g07.s	929	9.6	36.9	47	6	CJ0881	CJ0881	HUMGS000495
C 857	9.6	36.9	40	1	AA137304	AA137304	mq80b07.r	930	9.6	36.9	47	8	BH865116	BH865116	SALK_0974
C 858	9.6	36.9	40	8	BZ761528	BZ761528	SALK 0008	931	9.6	36.9	47	8	BH893272	BH893272	3526_1_24
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C 862	9.6	36.9	40	9	AG192612	AG192612	Pan trogl	935	9.6	36.9	47	9	CG799430	CG799430	1118002D1
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C 865	9.6	36.9	41	4	BI602229	BI602229	603244161	C 938	9.6	36.9	48	1	AA423295	AA423295	603244161
C 866	9.6	36.9	41	4	BJ040593	BJ040593	BJ040593	C 939	9.6	36.9	48	4	BI764981	BI764981	603051127
C 867	9.6	36.9	41	6	CF281514	CF281514	14ETL--08	940	9.6	36.9	48	8	AZ443664	AZ443664	1M0238A03
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C 869	9.6	36.9	41	7	CO788347	CO788347	NT004A.A0	C 942	9.6	36.9	48	8	BH636387	BH636387	1008011A0
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C 872	9.6	36.9	41	9	CC882364	CC882364	01S0576-0	945	9.6	36.9	48	9	AJ597909	AJ597909	Arabidops
C 873	9.6	36.9	41	9	CG730875	CG730875	1119130B0	C 946	9.6	36.9	48	9	AL752055	AL752055	Arabidops
C 874	9.6	36.9	42	8	AZ575712	AZ575712	AST-T31A0	C 947	9.6	36.9	48	9	TA194C12Q	TA194C12Q	T. brucei
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C 876	9.6	36.9	42	9	DME545593	DME545593	Drosophil	C 949	9.6	36.9	48	9	AG203889	AG203889	Pan trogl
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C 878	9.6	36.9	43	1	AA994992	AA994992	ou09b09.s	C 951	9.6	36.9	49	1	AV856631	AV856631	AV856631
C 879	9.6	36.9	43	1	AI301796	AI301796	qn08e06.x	C 952	9.6	36.9	49	4	AA429584	AA429584	zw77h05.r
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C 881	9.6	36.9	43	1	AJ233964	AJ233964	AJ233964	C 954	9.6	36.9	49	6	CA341266	CA341266	PK13c02.x
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C 883	9.6	36.9	43	2	AA247576	AA247576	2819553.s	C 956	9.6	36.9	49	7	W97994	W97994	mg07b01.r1
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C 885	9.6	36.9	43	8	BZ355522	BZ355522	SALK 1268	958	9.6	36.9	49	8	AQ254822	AQ254822	EP(2)1132
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C 887	9.6	36.9	43	8	BZ769930	BZ769930	SALK_1428	C 960	9.6	36.9	49	9	TA235H07Q	TA235H07Q	T. brucei
C 888	9.6	36.9	43	9	AJ587489	AJ587489	Arabidops	961	9.6	36.9	49	9	CG779221	CG779221	1123032D0
C 889	9.6	36.9	43	9	BX228681	BX228681	Danio rer	962	9.6	36.9	49	9	CL640727	CL640727	M012C08 G
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C 899	9.6	36.9	44	6	CF332083	CF332083	NACL--08-	C 972	9.6	36.9	50	1	AU104487	AU104487	AU104487
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ALIGNMENTS

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EST.
Homosapiens (human)
Homosapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
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Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

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FEATURES source

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Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 53.8% Score 14; DB 1; Length 31;
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Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 GAAAGCGCTAGCCATGGCGTT 25
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Db 28 GAATACGCTACCCATTGCTTT 7

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genomic survey sequence.
AUI759390
AUI759390.1 GI:21497738
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 46)
Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar, B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
It indicates an insertion within the locus defined by the T-DNA.
f6f22. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German plant genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiiz-koeln.mpg.de/GABI-Kat/.
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (rl) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

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Query Match      53.1%; Score 13.8; DB 9; Length 46;
Best Local Similarity 72.0%; Pred. No. 5.9e+04;
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QY      2  CAGAAACGGTCTAGCCATGGCGTTA 26
db      14  CAGAAGACGCTGTCTTGGCGTTA 38

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ORIGIN

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Best Local Similarity	93.3%;	Pred. NO. 8.e+04;		
Matches 14; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
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Dh	5	GTCTACCCATGGCGT	19	

ORIGIN

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Best Local Similarity	83.3%;	Pred. No. 1.2e+05;		
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
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Db	20	CACAAAGCATCTAGTCAT	3	

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ACCESSION
  AUI06301
VERSION
  AUI06301.1 GI:13555922
KEYWORDS
  EST.
SOURCE
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ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 50)
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
  EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
  21270072
MEDLINE
  11375929
PUBMED
  11375929
COMMENT
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: ysuzuki@ims.u-tokyo.ac.jp
  Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
  Sugano,S. Construction and characterization of a full
  length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
  149-156 (1997).
FEATURES
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  Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
  Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
  Db 15 GCAGAGCGCGTGTAGCGTGCCTGTTA 40
  RESULT 6
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  DEFINITION
    AUI07857 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
    KAT02325, mRNA sequence.
  ACCESSION
    AUI07857
  VERSION
    AUI07857.1 GI:13557379
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 50)
    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
    Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
    Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
    Diverse transcriptional initiation revealed by fine, large-scale
    mapping of mRNA start sites
    EMBO Rep. 2 (5), 388-393 (2001)
  JOURNAL
    21270072
  MEDLINE
    11375929
  PUBMED
    11375929
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp
    Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
    Sugano,S. Construction and characterization of a full
    length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
    149-156 (1997).
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    Best Local Similarity 69.2%; Pred. No. 1.2e+05;
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    Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
    Db 27 GCGGGAGAGCCCCAGCGGTGCGGTTA 2
    RESULT 7
    AUI07861
    LOCUS
    DEFINITION
      AUI07861 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
      KAT02084, mRNA sequence.
    ACCESSION
      AUI07861
    VERSION
      AUI07861.1 GI:13557383
    KEYWORDS
      EST.
    SOURCE
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    ORGANISM
      Homo sapiens
      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
      Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
      Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
      Diverse transcriptional initiation revealed by fine, large-scale
      mapping of mRNA start sites
      EMBO Rep. 2 (5), 388-393 (2001)
    JOURNAL
      21270072
    MEDLINE
      11375929
    PUBMED
      11375929
    COMMENT
      Contact: Yutaka Suzuki
      Department of Virology
      Institute of Medical Science, University of Tokyo
      4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
      Email: ysuzuki@ims.u-tokyo.ac.jp
      Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
      Sugano,S. Construction and characterization of a full
      length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
      149-156 (1997).
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      Best Local Similarity 69.2%; Pred. No. 1.2e+05;
      Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
      Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
      Db 17 GCAGAGCGCGTGTAGCGTGCCTGTTA 42
  
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Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

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  Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
  Db 15 GCAGAGCGCGTGTAGCGTGCCTGTTA 40
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  LOCUS
  DEFINITION
    AUI07861 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
    KAT02084, mRNA sequence.
  ACCESSION
    AUI07861
  VERSION
    AUI07861.1 GI:13557383
  KEYWORDS
    EST.
  SOURCE
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  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 50)
    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
    Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
    Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
    Diverse transcriptional initiation revealed by fine, large-scale
    mapping of mRNA start sites
    EMBO Rep. 2 (5), 388-393 (2001)
  JOURNAL
    21270072
  MEDLINE
    11375929
  PUBMED
    11375929
  COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: ysuzuki@ims.u-tokyo.ac.jp
    Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
    Sugano,S. Construction and characterization of a full
    length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
    149-156 (1997).
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    Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
    Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
    Db 17 GCAGAGCGCGTGTAGCGTGCCTGTTA 42
  
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Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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  Best Local Similarity 69.2%; Pred. No. 1.2e+05;
  Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
  Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
  Db 17 GCAGAGCGCGTGTAGCGTGCCTGTTA 42
  
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RESULT 8
AUI07875
LOCUS
DEFINITION AUI07875 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZYR6C825, mRNA sequence.
ACCESSION AUI07875
VERSION AUI07875.1 GI:13557397
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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/db_xref="taxon:9606"
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Query Match 50.8%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCCATGCGGTTA 26
||||| ||| ||| ||| ||| |||
Db 15 GGAGAAGCGGTAGCGTGGCGGTTA 40
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Arabidopsis thaliana genomic clone SALK_084531.41.35.x, genomic
survey sequence.
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VERSION BH855809.1 GI:21705399
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
REFERENCE
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

```

```

Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atlg16730 and 300 bases of the 5' end of Atlg16740.
Class: TDNA tagged.
FEATURES
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each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
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Best Local Similarity 70.8%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 AGAAAGCGTCTAGCCATGCGGTTA 26
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Db 5 AGGACAGTGTGCGCATGTCATTA 28
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DEFINITION BH855815 44 bp DNA linear GSS 08-JUL-2002
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Arabidopsis thaliana genomic clone SALK_084523.40.30.x, genomic
survey sequence.
ACCESSION BH855815
VERSION BH855815.1 GI:21705405
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 44)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atlg16730 and 300 bases of the 5' end of Atlg16740.
Class: TDNA tagged.
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KEYWORDS
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g57230.
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 : /organism="Arabidopsis thaliana"
 : /mol_type="genomic DNA"
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 : /clone_lib="Arabidopsis thaliana TDNA insertion lines"
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 : each of which contains one or more TDNA insertion
 : elements. The resultant fragment for each line was
 : directly sequenced to determine the genomic sequence at
 : the site of insertion. Details of the protocols used can
 : be found at http://signal.salk.edu/tdna_protocols.html"
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 Best Local Similarity 78.9%; Pred. No. 2.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 Db 19 CACAAATGCTCTAGACATG 1
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 ACCESSION BZ762449
 VERSION BZ762449.1 GI:28935002
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g57230.
FEATURES
 source : Location/Qualifiers
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 : /organism="Arabidopsis thaliana"
 : /mol_type="genomic DNA"
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 : each of which contains one or more TDNA insertion
 : elements. The resultant fragment for each line was
 : directly sequenced to determine the genomic sequence at
 : the site of insertion. Details of the protocols used can
 : be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
 Query Match 48.5%; Score 12.6; DB 8; Length 30;
 Best Local Similarity 78.9%; Pred. No. 2.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 CAGAAAGCGTCTAGCCATG 20
 ||||| ||||| |||||
 Db 19 CACAAATGCTCTAGACATG 1
 RESULT 14
 BZ762449/c
 LOCUS BZ762449.1 GI:28935002
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 Arabidopsis thaliana genomic clone SALK_104714.34.65.x, genomic
 survey sequence.
 ACCESSION BZ762449
 VERSION BZ762449.1 GI:28935002
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g57230.
FEATURES
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 : /organism="Arabidopsis thaliana"
 : /mol_type="genomic DNA"
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 : /clone_lib="Arabidopsis thaliana TDNA insertion lines"
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 : each of which contains one or more TDNA insertion
 : elements. The resultant fragment for each line was
 : directly sequenced to determine the genomic sequence at
 : the site of insertion. Details of the protocols used can
 : be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
 Query Match 48.5%; Score 12.6; DB 8; Length 30;
 Best Local Similarity 78.9%; Pred. No. 2.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 Db 19 CACAAATGCTCTAGACATG 1
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 LOCUS BH915541
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 genomic survey sequence.
 ACCESSION BH915541
 VERSION BH915541.1 GI:22803175
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526.1.48.1 row: 13
 Class: transposon-tagged.
FEATURES
 source : Location/Qualifiers
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 : /db_xref="taxon:4577"
 : /tissue_type="leaf"
 : /dev_stage="adult"
 : /lab_host="DH10B"
 : /clone_lib="3526 - RescueMu Grid K"
 : /note="Organ: leaf; Vector: RescueMu (engineered from
 : pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
 : RescueMu is a 4.9 Kb, modified maize Mu transposon
 : designed to allow plasmid rescue from total genomic DNA."

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g57230.
FEATURES
 source : Location/Qualifiers
 : 1..30
 : /organism="Arabidopsis thaliana"
 : /mol_type="genomic DNA"
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 : /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 : /note="PCR was performed on Arabidopsis thaliana lines
 : each of which contains one or more TDNA insertion
 : elements. The resultant fragment for each line was
 : directly sequenced to determine the genomic sequence at
 : the site of insertion. Details of the protocols used can
 : be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
 Query Match 48.5%; Score 12.6; DB 8; Length 30;
 Best Local Similarity 78.9%; Pred. No. 2.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 CAGAAAGCGTCTAGCCATG 20
 ||||| ||||| |||||
 Db 19 CACAAATGCTCTAGACATG 1
 RESULT 15
 BH915541
 LOCUS BH915541
 DEFINITION 3526.1.48.1.A10.2EL_x.1 3526 - RescueMu Grid K Zea mays genomic,
 genomic survey sequence.
 ACCESSION BH915541
 VERSION BH915541.1 GI:22803175
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526.1.48.1 row: 13
 Class: transposon-tagged.
FEATURES
 source : Location/Qualifiers
 : 1..42
 : /organism="Zea mays"
 : /mol_type="genomic DNA"
 : /cultivar="mixed background W23/A188/B73"
 : /db_xref="taxon:4577"
 : /tissue_type="leaf"
 : /dev_stage="adult"
 : /lab_host="DH10B"
 : /clone_lib="3526 - RescueMu Grid K"
 : /note="Organ: leaf; Vector: RescueMu (engineered from
 : pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
 : RescueMu is a 4.9 Kb, modified maize Mu transposon
 : designed to allow plasmid rescue from total genomic DNA."

JOURNAL
MEDLINE
PUBMED
COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: 0 column: 13
Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
1. .38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0062013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 47.7%; Score 12.4; DB 8; Length 38;
Best Local Similarity 92.9%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TAGCCATGGCGTTA 26
|||||
Db 37 TAGCCATGGCATT 24
|||||

RESULT 19
AQ073861
LOCUS
DEFINITION
EP(3)3258-3prime Drosophila melanogaster EP line Drosophila melanogaster genomic sequence.
genomic survey sequence.
AQ073861
AQ073861.1 GI:3403903
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 46)
Liao,G.-C., Rehm,E.J. and Rubin,G.M.
Insertion site preferences of the P transposable element in Drosophila melanogaster

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
20202638
10716700
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P element

FEATURES
source
1. .46
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Lavery T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

ORIGIN

Query Match 47.7%; Score 12.4; DB 8; Length 46;
Best Local Similarity 72.7%; Pred. No. 2.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGCC 22
|||||
Db 25 GCAAAAACGCTCTGCCAGCGC 46
|||||

RESULT 20
CF281394/c
LOCUS
DEFINITION
14ETL--08-G23.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-G23,
mRNA sequence.
CF281394
CF281394.1 GI:33658781
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

```

source
1. .29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14EFL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
Query Match 46.9%; Score 12.2; DB 6; Length 29;
Best Local Similarity 68.0%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGCTAGCCATGGCGTT 25
   ||| ||| ||| ||| ||| ||| |||
Db 26 GCTGCGGCGCTCTGCGCGCTGCTT 2

RESULT 21
LOCUS AZ959267/c 33 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0226D21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0226D21 R, genomic survey sequence.
ACCESSION AZ959267
VERSION AZ959267.1 GI:13830494
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: D column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0226D21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```

Query Match 46.9%; Score 12.2; DB 8; Length 33;
Best Local Similarity 82.4%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 5 AAAGCGTCTAGCCATGG 21
   ||| ||| ||| ||| ||| ||| |||
Db 31 AAAGTGTTTACCAATGG 15

```

RESULT 22

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LOCUS TAI175A01P 48 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 175a01, forward sequence, genomic survey sequence.
ACCESSION AL475152
VERSION AL475152.1 GI:11840164
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 48)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .48
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="175a01"

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FEATURES

source

ORIGIN

```

Query Match 46.9%; Score 12.2; DB 9; Length 48;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 4 GAAAGCGTCTAGCCATG 20
   ||| ||| ||| ||| ||| ||| |||

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Db      13  GAAAGCATTGGCCCATG 29

RESULT 23
CC888361
LOCUS   SALK_151752.40.50.x Arabidopsis thaliana DNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_151752.40.50.x, genomic survey sequence.
ACCESSION CC888361
VERSION   CC888361.1 GI:33364915
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 48)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE     A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL   Unpublished (2001)
COMMENT   Contact: Joseph R. Ecker
           Salk Institute Genomic Analysis Laboratory (SIGnAL)
           The Salk Institute for Biological Studies
           10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
           Tel: 858 453 4100 x1752
           Fax: 858 558 6379
           Email: ecker@salk.edu
           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g46430.
           Class: TDNA tagged.

FEATURES             Location/Qualifiers
     source            1..48
     /organism="Arabidopsis thaliana"
     /mol_type="genomic DNA"
     /ecotype="Col-0"
     /db_xref="taxon:3702"
     /clone="SALK_151752.40.50.x"
     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
     /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      46.9%; Score 12.2; DB 9; Length 48;
Best Local Similarity 68.0%; Pred. No. 3.7e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1  GCAGAACGGTCTAGCCATGGCGTT 25
    |||||
Db 7  GGAGAGAGCTTCTACCTAGACGTT 31

RESULT 24
AU104593
LOCUS   AU104593 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAE01245, mRNA sequence.
ACCESSION AU104593
VERSION   AU104593.1 GI:13554114
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT   Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: ysuzuki@ims.u-tokyo.ac.jp
           Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
           Location/Qualifiers
           source            1..50
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clones="CAE01245"
           /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9  CGTCTAGCCATGGCGTT 25
    |||||
Db 30 CGTCTAGGGATGGCGCT 46

RESULT 25
AU105172
LOCUS   AU105172 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS10704, mRNA sequence.
ACCESSION AU105172
VERSION   AU105172.1 GI:13554693
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT   Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: ysuzuki@ims.u-tokyo.ac.jp
           Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
           Location/Qualifiers
           source            1..50
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clones="CAS10704"
           /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

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```

Query Match      46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AGCGTCTAGCCATGGCG 23
    ||||| ||||| |||||
Db 6 AGCGGCCAGCCAGGGCG 22

RESULT 26
AUI06560/c
LOCUS AUI06560 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT00167, mRNA sequence.
ACCESSION AUI06560
VERSION AUI06560.1 GI:13556081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
    ||||| ||||| |||||
Db 7 CACGGAGCTGCTGGCCAGCGGTTA 31

RESULT 28
AUI07873
LOCUS AUI07873 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ZRVC724, mRNA sequence.
ACCESSION AUI07873
VERSION AUI07873.1 GI:13557395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.9%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AGCGTCTAGCCATGGCG 23
    ||||| ||||| |||||
Db 20 AGTGTCCAGGCATGGCG 4

RESULT 27
AUI07015
LOCUS AUI07015 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION REC00563, mRNA sequence.
ACCESSION AUI07015
VERSION AUI07015.1 GI:13556536
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
```


Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 ||||| ||||| ||||| ||||| |||||
 Db 17 GGAGAGCGCGTGTAGCGTGGCGTTA 42

RESULT 29
 AJ622111 50 bp DNA linear GSS 28-JAN-2004
 LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
 DEFINITION P[RS5]5-HA-2310, clone library P[RS5], genomic survey sequence.
 ACCESSION AJ622111 GI:41366324
 VERSION GSS; genome survey sequence.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 AUTHORS Ryder,E.J., Ashburner,M., Bagunya,J., Blows,F., Bucheton,A.,
 Coulson,D., Dickson,B., Drummond,J., Glover,D., Gunton,N.,
 Hafen,E., Hall,S., Heisenberg,M., Lepesant,J.A., Maroy,P.,
 Mechler,B., O'Kane,C., Pflugfelder,G., Rasmuson-Lestander,A.,
 Reuter,G., Roote,J., Szidonya,J., Wang,S., Webster,J. and
 Russell,S.
 TITLE Mapping of RS P element insertions in Drosophila melanogaster for
 the DrosDel second generation deficiency kit
 JOURNAL Unpublished
 AUTHORS Ryder,E.J.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
 University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
 COMMENT The insertion point of the P element is before base 1 of the
 sequence. Further information about this P element insertion line
 can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES
 source
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 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="3R"
 /clone="P[RS5]5-HA-2310"
 /clone_lib="P[RS5]"
 /note="read=5' end"

misc_feature 1..50
 /note="P element insertion in the 5' to 3' orientation"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CGTCTAGCCATGGCGTT 25
 ||||| ||||| ||||| ||||| |||||
 Db 1 CGTAAACCATGGCGTT 17

RESULT 30
 AJ622124 50 bp DNA linear GSS 28-JAN-2004
 LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
 DEFINITION P[RS5]5-HA-2407, clone library P[RS5], genomic survey sequence.
 ACCESSION AJ622124 GI:41366337
 VERSION GSS; genome survey sequence.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 AUTHORS Ryder,E.J., Ashburner,M., Bagunya,J., Blows,F., Bucheton,A.,
 Coulson,D., Dickson,B., Drummond,J., Glover,D., Gunton,N.,
 Hafen,E., Hall,S., Heisenberg,M., Lepesant,J.A., Maroy,P.,
 Mechler,B., O'Kane,C., Pflugfelder,G., Rasmuson-Lestander,A.,
 Reuter,G., Roote,J., Szidonya,J., Wang,S., Webster,J. and
 Russell,S.
 TITLE Mapping of RS P element insertions in Drosophila melanogaster for
 the DrosDel second generation deficiency kit
 JOURNAL Unpublished
 AUTHORS Ryder,E.J.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
 University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
 COMMENT The insertion point of the P element is before base 1 of the
 sequence. Further information about this P element insertion line
 can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES
 source
 1..50
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="3R"
 /clone="P[RS5]5-HA-2407"
 /clone_lib="P[RS5]"
 /note="read=5' end"

misc_feature 1..50
 /note="P element insertion in the 5' to 3' orientation"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CGTCTAGCCATGGCGTT 25
 ||||| ||||| ||||| ||||| |||||
 Db 1 CGTAAACCATGGCGTT 17

RESULT 31
 CR014420/c 50 bp DNA linear GSS 05-JUL-2004
 LOCUS Forward strand read from insert in 5'HPT insertion targeting and
 DEFINITION chromosome engineering clone MHPN315g04, genomic survey sequence.
 ACCESSION CR014420.1 GI:49747475
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (Bases 1 to 50)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu.Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>
 FEATURES
 source
 1..50
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN315g04"
 /clone_lib="MHPN"

ORIGIN
 Query Match 46.9%; Score 12.2; DB 9; Length 50;
 Best Local Similarity 82.4%; Pred. No. 3.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dgunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0584 row: 0 column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0584024"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [g14732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 46.2%; Score 12; DB 8; Length 26;
Best Local Similarity 75.0%; Pred. No. 4.3e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 4 GAAAGCGTCTAGCCATGCCG 23
||||| ||||| ||||| ||||| |||||
DB 22 GAAAGCAACAAGCCATAGAG 3

RESULT 34
BG973659/c
LOCUS
DEFINITION
602844696F1 NC1_CGAP Mam4 Mus musculus cDNA clone IMAGE:4980358 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM10979 row: p column: 23

High quality sequence start: 2

High quality sequence stop: 7.

FEATURES

Location/Qualifiers

1..34

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NMRI"

/db_xref="taxon:10090"

/clone="IMAGE:4980358"

/tissue_type="tumor, gross tissue"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam4"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Priscilla Furth,

NIH Reference for transgenic model: Li et al., Cell Growth

and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 46.2%; Score 12; DB 4; Length 34;

Best Local Similarity 75.0%; Pred. NO. 4.5e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 AAAGCGCTAGCCATGCGGT 24

Db 34 ACAGCGTCAGCCATGCGGT 15

RESULT 35

N49007/c

LOCUS Yy78h06.s1 Soares multiple sclerosis 2NBHSP Homo sapiens cDNA

clone IMAGE:279707 3' similar to gb:U03626 URIDINE 5'-MONOPHOSPHATE

SYNTHASE (HUMAN); mRNA sequence.

ACCESSION N49007

VERSION N49007.1 GI:1190173

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 37)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Roca, T., Soares, M., Tan, F.,

Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: ml3 -40 forward

High quality sequence stop: 1.

Location/Qualifiers

1..37

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3898083"

/db_xref="taxon:9606"

/clone="IMAGE:279707"

/sex="male"

/tissue_type="multiple sclerosis lesions"

/dev_stage="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares multiple sclerosis 2NBHSP"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V-type phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5,

TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH). "

ORIGIN

Query Match 46.2%; Score 12; DB 7; Length 37;

Best Local Similarity 75.0%; Pred. NO. 4.5e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATG 20

Db 33 GGAGATGGGCTTTGCCATG 14

RESULT 36

CL528415/c

LOCUS CL528415.1

DEFINITION CL528415.1

ACCESSION CL528415.1

VERSION CL528415.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 38)

Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H.,

Berry, C.C., Ecker, J.R. and Bushman, F.

Retroviral DNA integration: ASLV, HIV and MLV Show Distinct Target

Site Preferences

Unpublished (2004)

Contact: Frederic Bushman

Salk Institute Infectious Disease Laboratory

The Salk Institute for Biological Studies

10010 Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1630

Fax: 858 554 0341

Email: bushman@alk.edu

Class: PCR with specific primers.

Location/Qualifiers

1..38

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="ASV10806.fwd"

/clone_lib="ASLV-vector integration sites in human

293T-TVA cells"

/note="Human 293T cells expressing the subgroup A avian

retrovirus receptor (293T-TVA) were infected with an

ASLV-based vector. DNA was isolated and cleaved with

restriction enzymes; linkers were ligated onto the cleaved

DNA and DNAs were amplified using one primer that bound to


```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0541 row: 0 column: 22
            Seq primer: CACACAGGAACAGTATGACC
            Class: plasmid ends
            High quality sequence stop: 41.
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            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0541022"
            /sex="Male"
            /lab_host="E. Coli strain Xl10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli Xl10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
Query Match      46.2%; Score 12; DB 8; Length 41;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCCATG 20
      |||||
Db      23 GCAGCAAGCATGTTACCATG 4

RESULT 40
AZ447207/c
LOCUS      AZ447207
DEFINITION 1M0244K09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244K09 F, genomic survey sequence.
ACCESSION AZ447207
VERSION    AZ447207.1 GI:10598964

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0244 row: K column: 09
            Seq primer: CGTGTAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 47.
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source      1. .47
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            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0244K09"
            /sex="Male"
            /lab_host="E. Coli strain Xl10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli Xl10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
Query Match      46.2%; Score 12; DB 8; Length 47;
Best Local Similarity 75.0%; Pred. No. 4.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCCATG 20
      |||||
Db      23 GTAGAAGCAATAGTCATG 4

Search completed: November 23, 2004, 22:23:59
Job time : 1272.54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 38.191 Seconds
(without alignments)
614.177 Million cell updates/

Title: US-10-087-631B-5
 Perfect score: 33
 Sequence: 1 qccacatgaatggcaagcctctggtatccg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

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Minimum DB seq length: 0
Maximum DB seq length: 50
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	15.4	46.7	30	4	US-09-438-954-8	Sequence 8, Appl	
C 2	15.4	46.7	33	3	US-09-233-493-28	Sequence 28, Appl	
C 3	15.4	46.7	33	3	US-09-005-476-28	Sequence 28, Appl	
C 4	15.4	46.7	33	3	US-09-233-492-28	Sequence 28, Appl	
C 5	15.4	46.7	33	3	US-09-296-280-28	Sequence 28, Appl	
C 6	15.4	46.7	33	4	US-09-498-074-28	Sequence 28, Appl	
C 7	15.4	46.7	33	4	US-09-498-074-28	Sequence 28, Appl	
C 8	15.4	46.7	33	5	PCT-US96-10082A-28	Sequence 28, Appl	
9	15.4	46.7	34	1	US-08-323-192D-23	Sequence 23, Appl	
10	15.4	46.7	34	1	US-08-323-192D-25	Sequence 25, Appl	
11	15.4	46.7	34	1	US-08-470-887A-22	Sequence 22, Appl	
12	15.4	46.7	34	1	US-08-470-887A-24	Sequence 24, Appl	
13	15.4	46.7	34	2	US-08-316-439A-20	Sequence 20, Appl	
14	15.4	46.7	34	2	US-08-316-439A-22	Sequence 22, Appl	
15	15.4	46.7	34	2	US-08-252-508B-22	Sequence 22, Appl	
16	15.4	46.7	34	3	US-08-252-508B-24	Sequence 24, Appl	
17	15.4	46.7	34	3	US-09-106-377-22	Sequence 22, Appl	
18	15.4	46.7	34	3	US-09-106-377-24	Sequence 24, Appl	
19	15.4	46.7	34	6	5166057-35	Patent No. 5166057	
C 20	15.4	46.7	38	1	US-08-323-192D-24	Sequence 24, Appl	
C 21	15.4	46.7	38	1	US-08-323-192D-26	Sequence 26, Appl	
C 22	15.4	46.7	38	1	US-08-470-887A-23	Sequence 23, Appl	
C 23	15.4	46.7	38	1	US-08-470-887A-25	Sequence 25, Appl	
C 24	15.4	46.7	38	2	US-08-316-439A-23	Sequence 23, Appl	
C 25	15.4	46.7	38	2	US-08-252-508B-23	Sequence 23, Appl	
C 26	15.4	46.7	38	3	US-08-252-508B-25	Sequence 25, Appl	
C 27	15.4	46.7	38	3	US-09-106-377-23	Sequence 23, Appl	

C 101	13.2	40.0	38	4	US-09-371-772B-10592	Sequence 10592, A	174	12.6	38.2	38	1	US-08-390-850-824	Sequence 824, App
C 102	13.2	40.0	39	4	US-09-002-443-7	Sequence 7, Appl	175	12.6	38.2	38	1	US-08-435-634-824	Sequence 824, App
C 103	13.2	40.0	42	2	US-08-840-887-4	Sequence 4, Appl	176	12.6	38.2	38	4	US-09-371-772B-7848	Sequence 7848, App
C 104	13.2	40.0	44	3	US-09-672-609-30	Sequence 30, Appl	177	12.6	38.2	39	2	US-08-561-521-24	Sequence 24, Appl
C 105	13.2	40.0	44	3	US-09-025-403A-30	Sequence 30, Appl	C 178	12.6	38.2	39	4	US-09-060-299-217	Sequence 217, App
C 106	13.2	40.0	44	2	US-08-379-057-34	Sequence 34, Appl	C 179	12.6	38.2	39	4	US-09-402-923A-217	Sequence 217, App
C 107	13.2	40.0	45	2	US-08-687-355A-12	Sequence 12, Appl	C 180	12.6	38.2	39	5	PCT-US95-01219-24	Sequence 24, Appl
C 108	13.2	40.0	45	2	US-09-407-367-12	Sequence 12, Appl	181	12.6	38.2	40	1	US-08-050-132A-10	Sequence 10, Appl
C 109	13.2	40.0	47	4	US-09-671-317-972	Sequence 972, App	182	12.6	38.2	40	3	US-08-815-652B-10	Sequence 10, Appl
C 110	13.2	40.0	47	4	US-09-422-978-1458	Sequence 1458, App	183	12.6	38.2	42	3	US-08-284-516C-38	Sequence 38, Appl
C 111	13	39.4	16	3	US-09-509-565-16	Sequence 16, Appl	C 184	12.6	38.2	42	3	US-08-284-516C-39	Sequence 39, Appl
C 112	13	39.4	17	3	US-09-509-565-36	Sequence 36, Appl	185	12.6	38.2	42	4	US-09-537-911A-38	Sequence 38, Appl
C 113	13	39.4	18	4	US-09-153-242-41	Sequence 41, Appl	186	12.6	38.2	42	4	US-09-537-911A-39	Sequence 39, Appl
C 114	13	39.4	22	1	US-08-433-783-23	Sequence 23, Appl	187	12.6	38.2	44	4	US-09-155-106-42	Sequence 42, Appl
C 115	13	39.4	22	1	US-08-337-358-23	Sequence 23, Appl	C 188	12.6	38.2	45	3	US-09-199-737-45	Sequence 45, Appl
C 116	13	39.4	22	5	PCT-US93-12144-23	Sequence 23, Appl	189	12.6	38.2	47	4	US-09-058-333A-45	Sequence 45, Appl
C 117	13	39.4	22	5	PCT-US95-07537A-23	Sequence 23, Appl	C 190	12.6	38.2	47	4	US-09-422-978-1500	Sequence 1500, App
C 118	13	39.4	25	1	PCT-US95-07537-23	Sequence 23, Appl	191	12.6	38.2	47	4	US-09-422-978-1512	Sequence 1512, App
C 119	13	39.4	25	1	US-08-317-432A-45	Sequence 45, Appl	192	12.6	38.2	48	1	US-07-834-539A-64	Sequence 64, Appl
C 120	13	39.4	33	4	US-09-041-886-65	Sequence 65, Appl	193	12.6	38.2	48	1	US-08-053-131-112	Sequence 112, App
C 121	13	39.4	33	4	US-09-477-392-23	Sequence 23, Appl	194	12.6	38.2	48	1	US-07-853-408B-112	Sequence 112, App
C 122	13	39.4	35	3	US-09-275-850-278	Sequence 278, App	195	12.6	38.2	48	1	US-08-096-762-112	Sequence 112, App
C 123	13	39.4	38	2	US-08-460-529B-7	Sequence 7, Appl	196	12.6	38.2	48	2	US-08-800-353-64	Sequence 64, Appl
C 124	13	39.4	38	4	US-09-361-736B-7	Sequence 7, Appl	197	12.6	38.2	48	2	US-08-308-865-112	Sequence 112, App
C 125	13	39.4	39	3	US-09-423-439-4	Sequence 4, Appl	198	12.6	38.2	48	3	US-09-042-353-305	Sequence 305, App
C 126	13	39.4	41	1	US-08-317-432A-46	Sequence 46, Appl	199	12.6	38.2	48	3	US-08-758-417A-153	Sequence 153, App
C 127	13	39.4	41	1	US-08-317-432A-50	Sequence 50, Appl	200	12.6	38.2	48	3	PCT-US92-06185-64	Sequence 64, Appl
C 128	13	39.4	42	2	US-08-790-963-17	Sequence 17, Appl	201	12.6	38.2	48	5	PCT-US92-10983-112	Sequence 112, App
C 129	13	39.4	42	3	US-09-371-774-17	Sequence 17, Appl	202	12.6	38.2	48	5	US-08-171-389-494	Sequence 494, App
C 130	13	39.4	42	3	US-08-393-171-15	Sequence 15, Appl	203	12.6	38.2	50	1	US-08-123-936-494	Sequence 494, App
C 131	13	39.4	46	3	US-08-871-483-1	Sequence 1, Appl	204	12.6	38.2	50	1	US-08-475-228A-494	Sequence 494, App
C 132	12.8	38.8	21	4	US-09-657-472-1010	Sequence 1010, App	205	12.6	38.2	50	3	US-08-482-080A-494	Sequence 494, App
C 133	12.8	38.8	24	3	US-09-553-231-38	Sequence 38, Appl	206	12.6	38.2	50	3	US-09-046-247-38	Sequence 38, App
C 134	12.8	38.8	25	4	US-09-672-609-34	Sequence 34, Appl	C 207	12.6	38.2	50	3	US-09-354-947-494	Sequence 494, App
C 135	12.8	38.8	25	4	US-09-025-403A-34	Sequence 34, Appl	208	12.6	38.2	50	3	PCT-US93-12388-494	Sequence 494, App
C 136	12.8	38.8	29	1	US-08-356-287-22	Sequence 22, Appl	209	12.6	38.2	50	5	US-08-951-648-12	Sequence 12, Appl
C 137	12.8	38.8	29	5	PCT-US93-04863-22	Sequence 22, Appl	210	12.4	37.6	18	3	US-09-174-437-12	Sequence 12, Appl
C 138	12.8	38.8	30	2	US-08-481-658B-29	Sequence 29, Appl	211	12.4	37.6	18	3	US-09-686-055A-12	Sequence 12, Appl
C 139	12.8	38.8	30	2	US-08-477-504A-29	Sequence 29, Appl	212	12.4	37.6	18	3	US-07-988-430-18	Sequence 18, Appl
C 140	12.8	38.8	30	2	US-08-486-756A-29	Sequence 29, Appl	C 213	12.4	37.6	21	4	US-07-988-430-18	Sequence 18, Appl
C 141	12.8	38.8	30	2	US-08-485-862B-29	Sequence 29, Appl	C 214	12.4	37.6	21	4	US-09-001-052-4	Sequence 4, Appl
C 142	12.8	38.8	30	3	US-08-787-739-29	Sequence 29, Appl	C 215	12.4	37.6	22	4	US-07-901-707-18	Sequence 18, Appl
C 143	12.8	38.8	30	3	US-08-487-077A-29	Sequence 29, Appl	C 216	12.4	37.6	23	1	PCT-US92-09487-18	Sequence 18, Appl
C 144	12.8	38.8	30	3	US-08-485-863A-29	Sequence 29, Appl	C 217	12.4	37.6	23	5	US-09-614-034-204	Sequence 204, App
C 145	12.8	38.8	30	3	US-08-485-049D-29	Sequence 29, Appl	C 218	12.4	37.6	25	4	US-08-466-033-244	Sequence 244, App
C 146	12.8	38.8	30	3	US-09-178-115-29	Sequence 29, Appl	C 219	12.4	37.6	26	1	US-08-444-733-244	Sequence 244, App
C 147	12.8	38.8	30	3	US-09-177-776-29	Sequence 29, Appl	220	12.4	37.6	26	2	US-08-461-134-244	Sequence 244, App
C 148	12.8	38.8	30	4	US-09-772-719B-29	Sequence 29, Appl	221	12.4	37.6	26	2	US-08-461-134-244	Sequence 244, App
C 149	12.8	38.8	34	3	US-09-243-374-10	Sequence 10, Appl	222	12.4	37.6	26	2	US-08-485-910-244	Sequence 244, App
C 150	12.8	38.8	34	3	US-08-973-131-67	Sequence 67, Appl	223	12.4	37.6	26	2	US-08-859-998-65	Sequence 65, Appl
C 151	12.8	38.8	34	6	5188642-13	Patent No. 5188642	224	12.4	37.6	26	3	US-09-225-928-65	Sequence 65, Appl
C 152	12.8	38.8	34	6	5310667-16	Patent No. 5310667	225	12.4	37.6	26	4	US-09-225-928-65	Sequence 65, Appl
C 153	12.8	38.8	35	4	US-09-565-808-19	Sequence 19, Appl	226	12.4	37.6	29	1	US-08-700-186-10	Sequence 10, Appl
C 154	12.8	38.8	36	2	US-08-292-620A-846	Sequence 846, App	227	12.4	37.6	29	2	US-09-116-115-10	Sequence 10, Appl
C 155	12.8	38.8	36	3	US-09-071-845-846	Sequence 846, App	228	12.4	37.6	29	2	US-09-116-115-10	Sequence 10, Appl
C 156	12.8	38.8	38	4	US-09-371-772B-9407	Sequence 9407, App	229	12.4	37.6	29	3	US-09-578-656A-13	Sequence 13, Appl
C 157	12.8	38.8	38	4	US-09-371-772B-11578	Sequence 11578, A	C 230	12.4	37.6	29	3	US-09-541-762-10	Sequence 10, Appl
C 158	12.8	38.8	38	4	US-09-371-772B-12629	Sequence 12629, A	231	12.4	37.6	29	3	US-09-304-232-91	Sequence 91, Appl
C 159	12.8	38.8	39	5	PCT-US92-10430-1	Sequence 1, Appl	232	12.4	37.6	29	4	US-08-444-818-180	Sequence 180, App
C 160	12.8	38.8	41	4	US-09-825-561A-56	Sequence 56, Appl	C 233	12.4	37.6	30	3	US-10-123-170-10	Sequence 10, Appl
C 161	12.8	38.8	50	4	US-08-956-171B-2367	Sequence 2367, App	234	12.4	37.6	32	4	US-09-813-781-79	Sequence 79, Appl
C 162	12.8	38.8	50	4	US-08-781-986A-2367	Sequence 2367, App	C 235	12.4	37.6	32	4	US-08-934-494-10	Sequence 10, Appl
C 163	12.6	38.2	30	1	US-08-384-708A-15	Sequence 15, Appl	236	12.4	37.6	33	3	US-09-143-068-10	Sequence 10, Appl
C 164	12.6	38.2	30	4	US-08-687-421-15	Sequence 15, Appl	237	12.4	37.6	33	3	US-09-143-068-10	Sequence 10, Appl
C 165	12.6	38.2	30	4	US-08-442-423-15	Sequence 15, Appl	238	12.4	37.6	33	3	US-09-202-089-10	Sequence 10, Appl
C 166	12.6	38.2	31	4	US-09-555-889A-7	Sequence 7, Appl	C 239	12.4	37.6	33	3	US-09-511-133-10	Sequence 10, Appl
C 167	12.6	38.2	35	3	US-09-042-353-348	Sequence 348, App	240	12.4	37.6	33	3	US-09-511-133-10	Sequence 10, Appl
C 168	12.6	38.2	35	3	US-08-758-417A-196	Sequence 196, App	241	12.4	37.6	33	4	US-09-690-169-10	Sequence 10, Appl
C 169	12.6	38.2	36	1	US-08-319-492B-261	Sequence 261, App	242	12.4	37.6	33	4	US-09-511-631-10	Sequence 10, Appl
C 170	12.6	38.2	36	1	US-08-334-847-175	Sequence 175, App	243	12.4	37.6	33	4	US-09-690-189-10	Sequence 10, Appl
C 171	12.6	38.2	36	1	US-08-647-928-6	Sequence 6, Appl	244	12.4	37.6	34	2	US-09-560-098A-36	Sequence 36, Appl
C 172	12.6	38.2	36	1	US-08-311-486C-414	Sequence 414, App	245	12.4	37.6	39	4	US-09-396-154-85	Sequence 85, Appl
C 173	12.6	38.2	36	1	US-08-311-486C-924	Sequence 924, App	246	12.4	37.6	42	3	US-09-070-251-7	Sequence 7, Appl

C 247	12.4	37.6	43	4	US-10-001-052-18	Sequence 18, Appl	320	12.2	37.0	38	4	US-09-476-387-1324	Sequence 1324, Ap
C 248	12.4	37.6	45	3	US-08-495-695B-25	Sequence 25, Appl	321	12.2	37.0	40	2	US-08-425-684-98	Sequence 98, Appl
C 249	12.4	37.6	45	3	US-09-210-896-7	Sequence 7, Appl	322	12.2	37.0	40	2	US-08-628-422-38	Sequence 38, Appl
C 250	12.4	37.6	45	4	US-09-206-942-14	Sequence 14, Appl	323	12.2	37.0	40	2	US-08-675-502-98	Sequence 98, Appl
C 251	12.4	37.6	45	5	PCT-US94-14436-25	Sequence 25, Appl	324	12.2	37.0	40	3	US-09-411-687A-10	Sequence 10, Appl
C 252	12.2	37.0	18	2	US-08-951-648-19	Sequence 19, Appl	325	12.2	37.0	40	4	US-09-245-802-98	Sequence 98, Appl
C 253	12.2	37.0	18	3	US-09-280-409-134	Sequence 134, Appl	326	12.2	37.0	41	3	US-08-813-507-165	Sequence 165, Appl
C 254	12.2	37.0	18	3	US-09-174-437-19	Sequence 19, Appl	327	12.2	37.0	41	3	US-09-262-773-172	Sequence 172, Appl
C 255	12.2	37.0	18	4	US-09-686-055A-19	Sequence 19, Appl	328	12.2	37.0	41	3	US-09-464-453-165	Sequence 165, Appl
C 256	12.2	37.0	20	1	US-08-233-005-7	Sequence 7, Appl	329	12.2	37.0	43	3	US-08-983-564A-8	Sequence 8, Appl
C 257	12.2	37.0	20	1	US-08-428-943-7	Sequence 7, Appl	330	12.2	37.0	45	1	US-08-475-000-12	Sequence 12, Appl
C 258	12.2	37.0	20	3	US-09-016-649-7	Sequence 7, Appl	331	12.2	37.0	45	2	US-08-483-159-12	Sequence 12, Appl
C 259	12.2	37.0	20	3	US-09-330-330-7	Sequence 7, Appl	332	12.2	37.0	45	2	US-08-484-508-12	Sequence 12, Appl
C 260	12.2	37.0	20	4	PCT-US10-044-671-10	Sequence 10, Appl	333	12.2	37.0	46	1	US-08-271-880A-111	Sequence 111, Appl
C 261	12.2	37.0	20	5	PCT-US95-04858-7	Sequence 7, Appl	334	12.2	37.0	46	1	US-08-910-408-111	Sequence 111, Appl
C 262	12.2	37.0	22	3	US-09-069-886-18	Sequence 18, Appl	335	12.2	37.0	46	3	US-09-249-215-111	Sequence 111, Appl
C 263	12.2	37.0	25	4	US-09-313-458-41	Sequence 41, Appl	336	12.2	37.0	47	4	US-09-422-978-1500	Sequence 1500, Ap
C 264	12.2	37.0	25	4	US-09-866-108A-4846	Sequence 4846, Ap	337	12.2	37.0	47	4	US-09-422-978-2025	Sequence 2025, Ap
C 265	12.2	37.0	26	2	US-08-859-998-530	Sequence 530, App	338	12.2	37.0	47	4	US-08-422-978-2249	Sequence 2249, Ap
C 266	12.2	37.0	26	2	US-08-859-998-530	Sequence 530, App	339	12.2	37.0	48	3	US-08-675-566-103	Sequence 103, App
C 267	12.2	37.0	26	3	US-09-092-077-53	Sequence 53, Appl	340	12.2	37.0	49	2	US-08-053-451B-141	Sequence 141, App
C 268	12.2	37.0	26	3	US-09-092-077-53	Sequence 53, Appl	341	12.2	37.0	49	2	US-08-053-451B-141	Sequence 141, App
C 269	12.2	37.0	26	3	US-09-275-850-220	Sequence 220, App	342	12.2	37.0	50	2	US-08-053-451B-140	Sequence 140, App
C 270	12.2	37.0	26	3	US-09-225-928-530	Sequence 530, App	343	12.2	37.0	50	4	US-09-554-929-91	Sequence 91, Appl
C 271	12.2	37.0	26	4	US-09-225-201B-530	Sequence 530, App	344	12.2	37.0	50	4	US-08-068-945A-53	Sequence 53, Appl
C 272	12.2	37.0	27	1	US-08-468-347-5	Sequence 5, Appl	345	12.2	37.0	15	1	US-08-442-806-33	Sequence 33, Appl
C 273	12.2	37.0	27	1	US-08-467-389-5	Sequence 5, Appl	346	12.2	37.0	15	1	US-08-442-806-33	Sequence 33, Appl
C 274	12.2	37.0	27	2	US-08-779-379-5	Sequence 5, Appl	347	12.2	37.0	20	3	US-09-792-594-45	Sequence 45, Appl
C 275	12.2	37.0	27	2	US-08-469-219-5	Sequence 5, Appl	348	12.2	37.0	21	1	US-08-136-118-3	Sequence 3, Appl
C 276	12.2	37.0	27	3	US-09-228-152-5	Sequence 5, Appl	349	12.2	37.0	21	1	US-08-317-432A-23	Sequence 23, Appl
C 277	12.2	37.0	27	3	US-07-956-483-19	Sequence 19, Appl	350	12.2	37.0	22	4	US-09-707-938-3	Sequence 3, Appl
C 278	12.2	37.0	27	3	US-08-918-148-17	Sequence 17, Appl	351	12.2	37.0	24	2	US-08-572-447C-5	Sequence 5, Appl
C 279	12.2	37.0	27	4	US-09-184-418C-19	Sequence 19, Appl	352	12.2	37.0	24	3	US-09-267-747-5	Sequence 5, Appl
C 280	12.2	37.0	27	4	US-09-138-091A-17	Sequence 17, Appl	353	12.2	37.0	25	4	US-09-538-709-62	Sequence 62, Appl
C 281	12.2	37.0	28	4	US-09-519-232-21	Sequence 21, Appl	354	12.2	37.0	27	3	US-09-253-396A-121	Sequence 121, App
C 282	12.2	37.0	29	4	US-09-733-042-32	Sequence 32, Appl	355	12.2	37.0	28	4	US-09-894-799-23	Sequence 23, Appl
C 283	12.2	37.0	30	2	US-08-860-882A-23	Sequence 23, Appl	356	12.2	37.0	29	4	US-08-260-629-3	Sequence 3, Appl
C 284	12.2	37.0	30	3	US-08-840-466A-16	Sequence 16, Appl	357	12.2	37.0	30	3	US-09-275-850-173	Sequence 173, App
C 285	12.2	37.0	30	4	US-09-696-188B-16	Sequence 16, Appl	358	12.2	37.0	31	3	US-08-586-039B-42	Sequence 42, Appl
C 286	12.2	37.0	30	4	US-09-011-769A-19	Sequence 19, Appl	359	12.2	37.0	31	4	US-09-699-769-42	Sequence 42, Appl
C 287	12.2	37.0	31	1	US-08-647-584-27	Sequence 27, Appl	360	12.2	37.0	33	3	US-09-310-463-27	Sequence 27, Appl
C 288	12.2	37.0	32	3	US-09-091-219-16	Sequence 16, Appl	361	12.2	37.0	34	1	US-08-842-248A-27	Sequence 27, Appl
C 289	12.2	37.0	32	4	US-09-479-479-14	Sequence 14, Appl	362	12.2	37.0	34	1	US-08-347-792-22	Sequence 22, Appl
C 290	12.2	37.0	32	4	US-09-297-851-14	Sequence 14, Appl	363	12.2	37.0	34	1	US-08-431-357-22	Sequence 22, Appl
C 291	12.2	37.0	32	4	US-08-459-354-2	Sequence 2, Appl	364	12.2	37.0	34	5	PCT-US95-15353-22	Sequence 22, Appl
C 292	12.2	37.0	33	2	US-08-077-253-2	Sequence 2, Appl	365	12.2	37.0	36	1	US-08-433-037-5	Sequence 5, Appl
C 293	12.2	37.0	33	2	US-08-333-840-2	Sequence 2, Appl	366	12.2	37.0	37	4	US-09-894-799-1	Sequence 1, Appl
C 294	12.2	37.0	33	3	US-08-347-792-34	Sequence 34, Appl	367	12.2	37.0	38	1	US-08-390-850-805	Sequence 805, App
C 295	12.2	37.0	35	1	US-08-431-357-34	Sequence 34, Appl	368	12.2	37.0	38	1	US-08-373-124A-1217	Sequence 1217, Ap
C 296	12.2	37.0	35	5	PCT-US95-15353-34	Sequence 34, Appl	369	12.2	37.0	38	1	US-08-373-124A-1217	Sequence 1217, Ap
C 297	12.2	37.0	36	1	US-08-291-932A-653	Sequence 653, App	370	12.2	37.0	38	1	US-08-435-634-805	Sequence 805, App
C 298	12.2	37.0	36	1	US-08-569-806-16	Sequence 16, Appl	371	12.2	37.0	38	1	US-08-435-628-1217	Sequence 1217, Ap
C 299	12.2	37.0	36	1	US-08-311-486C-409	Sequence 409, App	372	12.2	37.0	38	1	US-08-435-628-1217	Sequence 1217, Ap
C 300	12.2	37.0	36	2	US-08-585-684B-1453	Sequence 1453, Ap	373	12.2	37.0	38	3	US-09-233-086-59	Sequence 59, Appl
C 301	12.2	37.0	36	2	US-08-585-684B-1891	Sequence 1891, Ap	374	12.2	37.0	38	4	US-09-474-432B-1260	Sequence 1260, Ap
C 302	12.2	37.0	36	2	US-08-585-684B-1892	Sequence 1892, Ap	375	12.2	37.0	38	4	US-09-474-432B-1452	Sequence 1452, Ap
C 303	12.2	37.0	36	2	US-08-585-684B-1893	Sequence 1893, Ap	376	12.2	37.0	38	4	US-09-371-772B-7428	Sequence 7428, Ap
C 304	12.2	37.0	36	3	US-09-038-073-1453	Sequence 1453, Ap	377	12.2	37.0	38	4	US-09-371-772B-7681	Sequence 7681, Ap
C 305	12.2	37.0	36	3	US-09-038-073-1453	Sequence 1453, Ap	378	12.2	37.0	38	4	US-09-371-772B-8235	Sequence 8235, Ap
C 306	12.2	37.0	36	3	US-09-038-073-1891	Sequence 1891, Ap	379	12.2	37.0	38	4	US-09-371-772B-8235	Sequence 8235, Ap
C 307	12.2	37.0	36	3	US-09-038-073-1892	Sequence 1892, Ap	380	12.2	37.0	38	4	US-09-371-772B-8235	Sequence 8235, Ap
C 308	12.2	37.0	36	3	US-09-038-073-1893	Sequence 1893, Ap	381	12.2	37.0	38	4	US-09-371-772B-9682	Sequence 9682, Ap
C 309	12.2	37.0	37	4	US-08-641-294-4	Sequence 4, Appl	382	12.2	37.0	38	4	US-09-371-772B-9682	Sequence 9682, Ap
C 310	12.2	37.0	38	1	US-08-390-850-766	Sequence 766, App	383	12.2	37.0	38	4	US-09-371-772B-10176	Sequence 10176, A
C 311	12.2	37.0	38	1	US-08-373-124A-1242	Sequence 1242, Ap	384	12.2	37.0	38	4	US-09-371-772B-10176	Sequence 10176, A
C 312	12.2	37.0	38	1	US-08-435-634-766	Sequence 766, App	385	12.2	37.0	38	4	US-09-371-772B-10854	Sequence 10854, A
C 313	12.2	37.0	38	4	US-08-435-628-1242	Sequence 1242, Ap	386	12.2	37.0	38	4	US-09-371-772B-10854	Sequence 10854, A
C 314	12.2	37.0	38	4	US-09-474-432B-1325	Sequence 1325, Ap	387	12.2	37.0	38	4	US-09-371-772B-11848	Sequence 11848, A
C 315	12.2	37.0	38	4	US-09-371-772B-9193	Sequence 9193, Ap	388	12.2	37.0	38	4	US-09-371-772B-12036	Sequence 12036, A
C 316	12.2	37.0	38	4	US-09-371-772B-10032	Sequence 10032, A	389	12.2	37.0	38	4	US-09-371-772B-12582	Sequence 12582, A
C 317	12.2	37.0	38	4	US-09-371-772B-11410	Sequence 11410, A	390	12.2	37.0	38	4	US-09-371-772B-12582	Sequence 12582, A
C 318	12.2	37.0	38	4	US-09-371-772B-11852	Sequence 11852, A	391	12.2	37.0	38	4	US-09-371-772B-13636	Sequence 13636, A
C 319	12.2	37.0	38	4	US-09-371-772B-11999	Sequence 11999, A	392	12.2	37.0	38	4	US-09-476-387-1259	Sequence 1259, Ap

C 393	12	36.4	40	2	US-08-628-422-28	Sequence 28, Appl	C 466	11.8	35.8	38	3	US-09-564-805-104	Sequence 104, App
C 394	12	36.4	40	2	US-08-483-695-20	Sequence 20, Appl	C 467	11.8	35.8	38	4	US-09-371-772B-7405	Sequence 7405, Ap
C 395	12	36.4	40	2	US-07-965-285-20	Sequence 20, Appl	C 468	11.8	35.8	38	4	US-09-371-772B-7597	Sequence 7597, Ap
C 396	12	36.4	40	2	US-08-487-231-20	Sequence 20, Appl	C 469	11.8	35.8	38	4	US-09-371-772B-10361	Sequence 10361, A
C 397	12	36.4	40	3	US-09-201-912-20	Sequence 20, Appl	C 470	11.8	35.8	38	4	US-09-371-772B-10365	Sequence 10365, A
C 398	12	36.4	41	3	US-08-864-473-69	Sequence 69, Appl	C 471	11.8	35.8	38	4	US-09-371-772B-10520	Sequence 10520, A
C 399	12	36.4	41	3	US-09-440-523-65	Sequence 69, Appl	C 472	11.8	35.8	38	4	US-09-371-772B-11889	Sequence 11889, A
C 400	12	36.4	41	4	US-09-823-823-45	Sequence 45, Appl	C 473	11.8	35.8	38	4	US-09-371-772B-12447	Sequence 12447, A
C 401	12	36.4	41	4	US-09-918-156-69	Sequence 69, Appl	C 474	11.8	35.8	38	4	US-09-371-772B-13790	Sequence 13790, A
C 402	12	36.4	42	4	US-08-749-852-12	Sequence 12, Appl	C 475	11.8	35.8	40	1	US-08-446-924-11	Sequence 11, Appl
C 403	12	36.4	42	4	US-09-459-133-19	Sequence 19, Appl	C 476	11.8	35.8	40	1	US-08-788-665-11	Sequence 11, Appl
C 404	12	36.4	45	4	US-09-579-625-21	Sequence 21, Appl	C 477	11.8	35.8	40	3	US-08-982-987A-11	Sequence 11, Appl
C 405	12	36.4	46	1	US-08-171-389-188	Sequence 188, App	C 478	11.8	35.8	40	3	US-09-363-970-14	Sequence 3, Appl
C 406	12	36.4	46	1	US-08-123-936-188	Sequence 188, App	C 479	11.8	35.8	45	4	US-08-928-592-3	Sequence 7, Appl
C 407	12	36.4	46	1	US-08-475-228A-188	Sequence 188, App	C 480	11.8	35.8	45	4	US-08-997-918-7	Sequence 1709, Ap
C 408	12	36.4	46	3	US-08-482-080A-478	Sequence 188, App	C 481	11.8	35.8	47	4	US-09-422-978-1709	Sequence 3761, Ap
C 409	12	36.4	46	3	US-09-354-947-188	Sequence 188, App	C 482	11.8	35.8	47	4	US-08-422-978-1761	Sequence 96, Appl
C 410	12	36.4	46	5	PCT-US93-12388-188	Sequence 1, Appl	C 483	11.8	35.8	49	3	US-08-706-945D-96	Sequence 34163, A
C 411	12	36.4	49	2	US-08-793-717-1	Sequence 1, Appl	C 484	11.8	35.8	50	4	US-08-513-999C-34163	Sequence 12, Appl
C 412	12	36.4	50	1	US-08-171-389-478	Sequence 478, App	C 485	11.6	35.2	17	1	US-08-275-983B-12	Sequence 20, Appl
C 413	12	36.4	50	1	US-08-123-936-478	Sequence 478, App	C 486	11.6	35.2	17	3	US-08-794-002-20	Sequence 20, Appl
C 414	12	36.4	50	2	US-08-475-228A-478	Sequence 478, App	C 487	11.6	35.2	17	3	US-08-854-039B-20	Sequence 20, Appl
C 415	12	36.4	50	3	US-08-482-080A-478	Sequence 478, App	C 488	11.6	35.2	17	4	US-08-765-702B-20	Sequence 13, Appl
C 416	12	36.4	50	3	US-09-354-947-478	Sequence 478, App	C 489	11.6	35.2	18	1	US-08-275-983B-13	Sequence 21, Appl
C 417	12	36.4	50	4	US-09-605-558B-22	Sequence 22, Appl	C 490	11.6	35.2	18	3	US-08-794-002-21	Sequence 21, Appl
C 418	12	36.4	50	4	US-09-605-558B-34	Sequence 34, Appl	C 491	11.6	35.2	18	3	US-08-854-039B-21	Sequence 21, Appl
C 419	12	36.4	50	5	PCT-US93-12388-478	Sequence 40, Appl	C 492	11.6	35.2	20	1	US-08-255-892-96	Sequence 96, Appl
C 420	11.8	35.8	18	4	US-09-153-242-40	Sequence 40, Appl	C 493	11.6	35.2	20	1	US-08-317-432A-22	Sequence 3, Appl
C 421	11.8	35.8	19	1	US-08-315-695-13	Sequence 13, Appl	C 494	11.6	35.2	20	1	US-08-499-048-3	Sequence 72, Appl
C 422	11.8	35.8	20	1	US-08-484-192-71	Sequence 71, Appl	C 495	11.6	35.2	20	4	US-10-027-983-72	Sequence 14, Appl
C 423	11.8	35.8	20	1	US-08-484-192-135	Sequence 135, App	C 496	11.6	35.2	21	1	US-08-017-570-14	Sequence 14, Appl
C 424	11.8	35.8	20	4	US-09-657-452A-46	Sequence 46, Appl	C 497	11.6	35.2	21	1	US-08-471-426-14	Sequence 416, App
C 425	11.8	35.8	20	4	US-09-866-451-45	Sequence 45, Appl	C 498	11.6	35.2	21	3	US-09-461-697-416	Sequence 30, Appl
C 426	11.8	35.8	21	2	US-08-680-326-20	Sequence 20, Appl	C 499	11.6	35.2	21	4	US-09-393-858-30	Sequence 30, Appl
C 427	11.8	35.8	21	3	US-09-254-325-3	Sequence 3, Appl	C 500	11.6	35.2	21	4	US-09-657-472-1731	Sequence 1731, Ap
C 428	11.8	35.8	21	4	US-09-657-472-1633	Sequence 1633, Ap	C 501	11.6	35.2	21	4	US-10-190-279-30	Sequence 30, Appl
C 429	11.8	35.8	23	4	US-10-192-369-3	Sequence 3, Appl	C 502	11.6	35.2	21	5	PCT-US94-01709-14	Sequence 14, Appl
C 430	11.8	35.8	24	1	US-08-337-268A-22	Sequence 22, Appl	C 503	11.6	35.2	22	3	US-09-240-918-41	Sequence 41, Appl
C 431	11.8	35.8	24	1	US-08-484-570A-22	Sequence 22, Appl	C 504	11.6	35.2	22	3	US-09-462-606-41	Sequence 41, Appl
C 432	11.8	35.8	24	4	US-09-854-140-14	Sequence 14, Appl	C 505	11.6	35.2	22	4	US-09-462-606-45	Sequence 45, Appl
C 433	11.8	35.8	25	1	US-08-752-238-8	Sequence 8, Appl	C 506	11.6	35.2	22	4	US-09-866-108A-15109	Sequence 43, Appl
C 434	11.8	35.8	25	3	US-09-085-603B-8	Sequence 8, Appl	C 507	11.6	35.2	25	1	US-08-317-432A-43	Sequence 43, Appl
C 435	11.8	35.8	25	4	US-09-866-108A-4847	Sequence 4847, Ap	C 508	11.6	35.2	25	4	US-09-866-108A-15107	Sequence 15107, A
C 436	11.8	35.8	25	4	US-09-866-108A-4848	Sequence 4848, Ap	C 509	11.6	35.2	25	4	US-09-866-108A-15108	Sequence 15108, A
C 437	11.8	35.8	26	1	US-08-239-256-22	Sequence 22, Appl	C 510	11.6	35.2	25	4	US-09-866-108A-15109	Sequence 15109, A
C 438	11.8	35.8	26	1	US-08-383-750-8	Sequence 8, Appl	C 511	11.6	35.2	25	4	US-09-866-108A-15110	Sequence 15110, A
C 439	11.8	35.8	26	2	US-08-225-488-8	Sequence 8, Appl	C 512	11.6	35.2	25	4	US-09-866-108A-15111	Sequence 15111, A
C 440	11.8	35.8	26	4	US-09-719-919A-8	Sequence 8, Appl	C 513	11.6	35.2	25	4	US-09-866-108A-15112	Sequence 15112, A
C 441	11.8	35.8	26	4	US-09-733-741C-5	Sequence 5, Appl	C 514	11.6	35.2	25	4	US-09-866-108A-15113	Sequence 15113, A
C 442	11.8	35.8	27	3	US-08-985-162-1509	Sequence 1509, Ap	C 515	11.6	35.2	26	3	US-08-859-998-685	Sequence 685, App
C 443	11.8	35.8	27	4	US-09-401-063-1509	Sequence 1509, Ap	C 516	11.6	35.2	26	3	US-09-225-201B-685	Sequence 685, App
C 444	11.8	35.8	29	2	US-08-457-254-12	Sequence 12, Appl	C 517	11.6	35.2	27	1	US-08-399-412A-97	Sequence 97, Appl
C 445	11.8	35.8	29	4	US-07-971-834-9	Sequence 9, Appl	C 518	11.6	35.2	27	1	US-08-640-517A-87	Sequence 87, Appl
C 446	11.8	35.8	29	5	PCT-US94-08806-24	Sequence 24, Appl	C 519	11.6	35.2	27	1	US-09-689-065B-45	Sequence 45, Appl
C 447	11.8	35.8	29	5	PCT-US95-16626-12	Sequence 12, Appl	C 520	11.6	35.2	27	6	5229496-10	Patent No. 5229496
C 448	11.8	35.8	33	3	US-09-243-374-11	Sequence 11, Appl	C 521	11.6	35.2	27	6	5391485-10	Patent No. 5391485
C 449	11.8	35.8	33	4	US-09-622-439-16	Sequence 16, Appl	C 522	11.6	35.2	28	1	US-08-468-036-22	Sequence 22, Appl
C 450	11.8	35.8	34	1	US-08-091-569-24	Sequence 24, Appl	C 523	11.6	35.2	28	1	US-08-376-843-22	Sequence 22, Appl
C 451	11.8	35.8	34	1	US-08-185-232A-17	Sequence 17, Appl	C 524	11.6	35.2	28	2	US-08-590-897A-29	Sequence 29, Appl
C 452	11.8	35.8	34	1	US-08-203-676-24	Sequence 24, Appl	C 525	11.6	35.2	29	3	US-08-902-623-28	Sequence 28, Appl
C 453	11.8	35.8	34	2	US-08-416-523-17	Sequence 17, Appl	C 526	11.6	35.2	30	2	US-08-259-609-1	Sequence 1, Appl
C 454	11.8	35.8	34	2	US-08-822-238-24	Sequence 24, Appl	C 527	11.6	35.2	30	2	US-09-263-944-1	Sequence 1, Appl
C 455	11.8	35.8	34	3	US-08-789-478-17	Sequence 17, Appl	C 528	11.6	35.2	30	3	US-09-305-483-1	Sequence 1, Appl
C 456	11.8	35.8	35	3	US-08-961-083-431	Sequence 431, App	C 529	11.6	35.2	30	4	US-09-638-649-9	Sequence 9, Appl
C 457	11.8	35.8	35	4	US-09-536-784-431	Sequence 431, App	C 530	11.6	35.2	30	4	US-09-556-390A-1	Sequence 1, Appl
C 458	11.8	35.8	35	4	US-08-757-207-16	Sequence 16, Appl	C 531	11.6	35.2	31	2	US-08-859-998-162	Sequence 162, App
C 459	11.8	35.8	36	1	US-08-291-932A-640	Sequence 640, App	C 532	11.6	35.2	31	3	US-08-777-708C-22	Sequence 22, Appl
C 460	11.8	35.8	36	1	US-08-334-847-395	Sequence 395, App	C 533	11.6	35.2	31	3	US-09-161-466-7	Sequence 7, Appl
C 461	11.8	35.8	36	2	US-08-585-684B-1953	Sequence 1953, Ap	C 534	11.6	35.2	31	3	US-09-225-928-162	Sequence 162, App
C 462	11.8	35.8	36	2	US-08-585-684B-1954	Sequence 1954, Ap	C 535	11.6	35.2	31	4	US-09-225-201B-162	Sequence 162, App
C 463	11.8	35.8	36	3	US-09-038-073-1953	Sequence 1953, Ap	C 536	11.6	35.2	31	4	US-08-246-373-5	Sequence 5, Appl
C 464	11.8	35.8	36	3	US-08-038-073-1954	Sequence 1954, Ap	C 537	11.6	35.2	33	1	US-08-802-191-4	Sequence 4, Appl
C 465	11.8	35.8	38	2	US-08-537-811-2	Sequence 2, Appl	C 538	11.6	35.2	33	3		

539	11.6	35.2	33	4	US-09-170-496D-137	Sequence 137, App	612	11.6	35.2	40	1	US-07-714-131C-277	Sequence 277, App
c 540	11.6	35.2	33	6	5180811-8	Patent No. 5180811	613	11.6	35.2	40	1	US-07-714-131C-279	Sequence 279, App
c 541	11.6	35.2	35	1	US-07-885-970A-33	Sequence 33, Appl	614	11.6	35.2	40	1	US-08-412-110-277	Sequence 277, App
c 542	11.6	35.2	35	1	US-08-298-687A-33	Sequence 33, Appl	615	11.6	35.2	40	1	US-08-412-110-279	Sequence 279, App
c 543	11.6	35.2	35	1	US-08-298-829-33	Sequence 33, Appl	616	11.6	35.2	40	1	US-08-409-442A-277	Sequence 277, App
c 544	11.6	35.2	35	3	US-08-096-181A-5	Sequence 5, Appl	617	11.6	35.2	40	1	US-08-409-442A-279	Sequence 279, App
c 545	11.6	35.2	35	5	PCT-US94-08326-5	Sequence 5, Appl	618	11.6	35.2	40	2	US-08-469-609A-277	Sequence 277, App
546	11.6	35.2	36	1	US-08-182-530-1	Sequence 11, Appl	619	11.6	35.2	40	2	US-08-469-609A-279	Sequence 279, App
547	11.6	35.2	36	1	US-08-182-530-11	Sequence 11, Appl	620	11.6	35.2	40	3	US-09-143-190-277	Sequence 277, App
548	11.6	35.2	36	1	US-08-334-847-410	Sequence 410, App	621	11.6	35.2	40	3	US-09-143-190-279	Sequence 279, App
549	11.6	35.2	36	1	US-08-363-240A-443	Sequence 443, App	c 622	11.6	35.2	40	3	US-09-153-310-35	Sequence 35, Appl
550	11.6	35.2	36	1	US-08-050-058B-1	Sequence 1, Appl	623	11.6	35.2	40	3	US-09-502-344-277	Sequence 277, App
551	11.6	35.2	36	1	US-08-050-058B-11	Sequence 11, Appl	624	11.6	35.2	40	3	US-09-502-344-279	Sequence 279, App
552	11.6	35.2	36	2	US-08-463-587A-1	Sequence 1, Appl	625	11.6	35.2	40	4	US-09-164-714-20	Sequence 20, Appl
553	11.6	35.2	36	2	US-08-463-667A-1	Sequence 1, Appl	626	11.6	35.2	41	1	US-07-931-473B-278	Sequence 278, App
554	11.6	35.2	36	2	US-08-441-871-5	Sequence 5, Appl	627	11.6	35.2	41	1	US-07-714-131C-278	Sequence 278, App
555	11.6	35.2	36	2	US-08-441-871-15	Sequence 15, Appl	628	11.6	35.2	41	1	US-08-412-110-278	Sequence 278, App
556	11.6	35.2	36	3	US-08-923-854-1	Sequence 1, Appl	629	11.6	35.2	41	1	US-08-409-442A-278	Sequence 278, App
557	11.6	35.2	36	5	PCT-US91-09133-1	Sequence 1, Appl	c 630	11.6	35.2	41	1	US-08-317-432A-44	Sequence 44, Appl
558	11.6	35.2	36	5	PCT-US91-09133-11	Sequence 11, Appl	631	11.6	35.2	41	1	US-08-317-432A-44	Sequence 44, Appl
c 559	11.6	35.2	38	1	US-08-390-850-916	Sequence 916, App	632	11.6	35.2	41	2	US-08-469-609A-278	Sequence 278, App
c 560	11.6	35.2	38	1	US-08-390-850-917	Sequence 917, App	633	11.6	35.2	41	2	US-08-469-609A-278	Sequence 278, App
c 561	11.6	35.2	38	1	US-08-435-634-916	Sequence 916, App	634	11.6	35.2	41	3	US-09-143-190-278	Sequence 278, App
c 562	11.6	35.2	38	1	US-08-435-634-917	Sequence 917, App	635	11.6	35.2	41	3	US-09-502-344-278	Sequence 278, App
563	11.6	35.2	38	2	US-08-292-620A-2213	Sequence 2213, Ap	636	11.6	35.2	41	4	US-10-150-051-11	Sequence 11, Appl
564	11.6	35.2	38	2	US-08-292-620A-2304	Sequence 2304, Ap	637	11.6	35.2	42	1	US-07-931-473B-291	Sequence 291, App
565	11.6	35.2	38	2	US-08-292-620A-2341	Sequence 2341, Ap	638	11.6	35.2	42	1	US-07-714-131C-291	Sequence 291, App
c 566	11.6	35.2	38	2	US-08-292-620A-2381	Sequence 2381, Ap	639	11.6	35.2	42	1	US-08-412-110-291	Sequence 291, App
567	11.6	35.2	38	2	US-08-723-306-16	Sequence 16, Appl	640	11.6	35.2	42	1	US-08-409-442A-291	Sequence 291, App
c 568	11.6	35.2	38	2	US-08-537-811-34	Sequence 34, Appl	641	11.6	35.2	42	2	US-08-469-609A-291	Sequence 291, App
569	11.6	35.2	38	3	US-09-071-845-2213	Sequence 2213, Ap	c 642	11.6	35.2	42	2	US-08-675-566-115	Sequence 115, App
570	11.6	35.2	38	3	US-09-071-845-2304	Sequence 2304, Ap	643	11.6	35.2	42	3	US-09-143-190-291	Sequence 291, App
571	11.6	35.2	38	3	US-09-071-845-2341	Sequence 2341, Ap	644	11.6	35.2	42	3	US-09-502-344-291	Sequence 291, App
c 572	11.6	35.2	38	3	US-09-071-845-2381	Sequence 2381, Ap	c 645	11.6	35.2	43	3	US-09-526-416-12	Sequence 12, Appl
573	11.6	35.2	38	4	US-09-474-432B-1268	Sequence 1268, Ap	646	11.6	35.2	43	4	US-08-227-476-10	Sequence 10, Appl
574	11.6	35.2	38	4	US-09-474-432B-1368	Sequence 1368, Ap	647	11.6	35.2	44	1	US-08-236-311-13	Sequence 13, Appl
575	11.6	35.2	38	4	US-09-474-432B-1404	Sequence 1404, Ap	c 648	11.6	35.2	44	3	US-08-457-918-13	Sequence 13, Appl
576	11.6	35.2	38	4	US-09-371-772B-7327	Sequence 7327, Ap	649	11.6	35.2	44	4	US-09-355-434-6	Sequence 6, Appl
c 577	11.6	35.2	38	4	US-09-371-772B-7592	Sequence 7592, Ap	c 650	11.6	35.2	44	4	US-10-157-408-13	Sequence 13, Appl
c 578	11.6	35.2	38	4	US-09-371-772B-8069	Sequence 8069, Ap	c 651	11.6	35.2	45	1	US-08-349-696-16	Sequence 16, Appl
c 579	11.6	35.2	38	4	US-09-371-772B-8659	Sequence 8659, Ap	c 652	11.6	35.2	45	1	US-08-233-009-16	Sequence 16, Appl
c 580	11.6	35.2	38	4	US-09-371-772B-8813	Sequence 8813, Ap	c 653	11.6	35.2	45	1	US-08-560-231-16	Sequence 16, Appl
c 581	11.6	35.2	38	4	US-09-371-772B-9040	Sequence 9040, Ap	c 654	11.6	35.2	45	3	US-09-080-704A-16	Sequence 29, Appl
c 582	11.6	35.2	38	4	US-09-371-772B-9083	Sequence 9083, Ap	c 655	11.6	35.2	45	4	US-09-759-112A-29	Sequence 29, Appl
c 583	11.6	35.2	38	4	US-09-371-772B-9129	Sequence 9129, Ap	656	11.6	35.2	46	1	US-08-105-483-454	Sequence 454, App
584	11.6	35.2	38	4	US-09-371-772B-9382	Sequence 9382, Ap	657	11.6	35.2	46	1	US-08-709-209-454	Sequence 454, App
585	11.6	35.2	38	4	US-09-371-772B-9580	Sequence 9580, Ap	658	11.6	35.2	46	1	US-08-303-275-166	Sequence 166, App
c 586	11.6	35.2	38	4	US-09-371-772B-9982	Sequence 9982, Ap	659	11.6	35.2	46	1	US-08-458-101-454	Sequence 454, App
c 587	11.6	35.2	38	4	US-09-371-772B-10245	Sequence 10245, A	660	11.6	35.2	47	1	US-08-171-389-168	Sequence 168, App
c 588	11.6	35.2	38	4	US-09-371-772B-10514	Sequence 10514, A	661	11.6	35.2	47	1	US-08-123-936-168	Sequence 168, App
589	11.6	35.2	38	4	US-09-371-772B-10518	Sequence 10518, A	662	11.6	35.2	47	2	US-08-475-228A-168	Sequence 168, App
c 590	11.6	35.2	38	4	US-09-371-772B-10579	Sequence 10579, A	663	11.6	35.2	47	3	US-08-482-080A-168	Sequence 168, App
c 591	11.6	35.2	38	4	US-09-371-772B-10684	Sequence 10684, A	664	11.6	35.2	47	3	US-09-354-947-168	Sequence 168, App
592	11.6	35.2	38	4	US-09-371-772B-10713	Sequence 10713, A	c 665	11.6	35.2	47	4	US-09-671-317-842	Sequence 642, App
593	11.6	35.2	38	4	US-09-371-772B-11645	Sequence 11645, A	c 666	11.6	35.2	47	4	US-09-671-317-827	Sequence 927, App
c 594	11.6	35.2	38	4	US-09-371-772B-11820	Sequence 11820, A	667	11.6	35.2	47	4	US-09-422-978-378	Sequence 378, App
595	11.6	35.2	38	4	US-09-371-772B-11941	Sequence 11941, A	668	11.6	35.2	47	4	US-09-422-978-739	Sequence 739, App
596	11.6	35.2	38	4	US-09-371-772B-11978	Sequence 11978, A	c 669	11.6	35.2	47	4	US-09-422-978-978	Sequence 978, App
597	11.6	35.2	38	4	US-09-371-772B-13529	Sequence 13529, A	c 670	11.6	35.2	47	4	US-09-422-978-1425	Sequence 1425, Ap
598	11.6	35.2	38	4	US-09-371-772B-13612	Sequence 13612, A	671	11.6	35.2	47	4	US-09-422-978-1911	Sequence 1911, Ap
c 599	11.6	35.2	38	4	US-09-371-772B-13803	Sequence 13803, A	c 672	11.6	35.2	47	4	US-09-422-978-2519	Sequence 2519, Ap
c 600	11.6	35.2	38	4	US-09-371-772B-13975	Sequence 13975, A	673	11.6	35.2	47	4	US-09-422-978-3569	Sequence 3569, Ap
601	11.6	35.2	38	4	US-09-476-387-1267	Sequence 1267, Ap	674	11.6	35.2	47	5	PCT-US93-12388-168	Sequence 168, App
602	11.6	35.2	38	4	US-09-476-387-1367	Sequence 1367, Ap	675	11.6	35.2	48	3	US-08-789-333F-72	Sequence 72, Appl
603	11.6	35.2	38	4	US-09-476-387-1403	Sequence 1403, Ap	676	11.6	35.2	48	4	US-09-136-801-28	Sequence 28, Appl
c 604	11.6	35.2	38	5	PCT-US96-10041-16	Sequence 16, Appl	677	11.6	35.2	48	4	US-08-787-738B-72	Sequence 72, Appl
c 605	11.6	35.2	39	1	US-08-418-859-38	Sequence 38, Appl	678	11.6	35.2	48	4	US-09-202-088A-28	Sequence 28, Appl
c 606	11.6	35.2	39	2	US-08-643-181-38	Sequence 38, Appl	679	11.6	35.2	48	4	US-09-916-940-72	Sequence 72, Appl
607	11.6	35.2	39	2	US-08-723-306-12	Sequence 12, Appl	c 680	11.6	35.2	49	1	US-08-105-483-453	Sequence 453, App
608	11.6	35.2	39	5	PCT-US96-10041-12	Sequence 12, Appl	c 681	11.6	35.2	49	1	US-08-371-986-18	Sequence 18, Appl
609	11.6	35.2	39	6	5256648-32	Patent No. 5256648	c 682	11.6	35.2	49	1	US-08-709-209-453	Sequence 453, App
610	11.6	35.2	40	1	US-07-931-473B-277	Sequence 277, App	c 683	11.6	35.2	49	1	US-08-303-275-165	Sequence 165, App
611	11.6	35.2	40	1	US-07-931-473B-279	Sequence 279, App	c 684	11.6	35.2	49	1	US-08-458-101-453	Sequence 453, App

C 685	11.6	35.2	49	3	US-09-023-2288-63	Sequence 63, Appl	758	11.4	34.5	33	2	US-08-600-783-9	Sequence 9, Appl
C 686	11.6	35.2	49	3	US-09-163-025B-63	Sequence 63, Appl	759	11.4	34.5	33	2	US-08-985-124A-7	Sequence 7, Appl
C 687	11.6	35.2	49	3	US-09-391-104-3	Sequence 3, Appl	760	11.4	34.5	33	2	US-08-985-320A-7	Sequence 7, Appl
C 688	11.6	35.2	49	3	US-10-037-282-63	Sequence 63, Appl	761	11.4	34.5	33	3	US-08-984-732A-7	Sequence 7, Appl
C 689	11.6	35.2	50	1	US-08-236-311-20	Sequence 20, Appl	762	11.4	34.5	33	3	US-09-195-578-19	Sequence 19, Appl
C 690	11.6	35.2	50	1	US-08-171-389-433	Sequence 433, Appl	763	11.4	34.5	33	3	US-09-170-951-19	Sequence 19, Appl
C 691	11.6	35.2	50	1	US-08-171-389-477	Sequence 477, Appl	764	11.4	34.5	33	3	US-08-164-482-19	Sequence 42, Appl
C 692	11.6	35.2	50	1	US-08-123-936-433	Sequence 433, Appl	765	11.4	34.5	33	3	US-08-463-160B-42	Sequence 14, Appl
C 693	11.6	35.2	50	1	US-08-123-936-477	Sequence 477, Appl	766	11.4	34.5	33	3	US-09-332-769-14	Sequence 14, Appl
C 694	11.6	35.2	50	2	US-08-475-228A-433	Sequence 433, Appl	767	11.4	34.5	33	3	US-09-456-153-14	Sequence 14, Appl
C 695	11.6	35.2	50	2	US-08-475-228A-477	Sequence 477, Appl	768	11.4	34.5	33	3	US-09-187-180-19	Sequence 19, Appl
C 696	11.6	35.2	50	3	US-08-482-080A-433	Sequence 433, Appl	769	11.4	34.5	33	3	US-09-455-627-14	Sequence 14, Appl
C 697	11.6	35.2	50	3	US-08-482-080A-477	Sequence 477, Appl	770	11.4	34.5	33	3	US-09-426-533-14	Sequence 14, Appl
C 698	11.6	35.2	50	3	US-08-457-918-20	Sequence 20, Appl	771	11.4	34.5	33	3	US-09-609-205-15	Sequence 15, Appl
C 699	11.6	35.2	50	3	US-09-354-947-433	Sequence 433, Appl	772	11.4	34.5	33	3	US-09-516-945-14	Sequence 15, Appl
C 700	11.6	35.2	50	3	US-09-354-947-477	Sequence 477, Appl	773	11.4	34.5	33	3	US-09-757-218-15	Sequence 15, Appl
C 701	11.6	35.2	50	4	US-10-157-408-20	Sequence 20, Appl	774	11.4	34.5	33	3	US-09-516-757-14	Sequence 14, Appl
C 702	11.6	35.2	50	4	US-09-900-425B-32	Sequence 32, Appl	775	11.4	34.5	33	3	US-09-342-577-15	Sequence 15, Appl
C 703	11.6	35.2	50	5	PCT-US93-12388-433	Sequence 433, Appl	776	11.4	34.5	33	3	US-09-516-756-14	Sequence 14, Appl
C 704	11.6	35.2	50	5	PCT-US93-12388-477	Sequence 477, Appl	777	11.4	34.5	33	3	US-09-828-061A-15	Sequence 15, Appl
C 705	11.4	34.5	19	1	US-07-936-421-12	Sequence 12, Appl	778	11.4	34.5	33	3	US-09-463-917-14	Sequence 14, Appl
C 706	11.4	34.5	20	2	US-09-679-299A-21	Sequence 21, Appl	779	11.4	34.5	33	4	US-09-347-673-15	Sequence 15, Appl
C 707	11.4	34.5	20	2	US-08-697-404-8	Sequence 8, Appl	780	11.4	34.5	33	4	US-09-757-213-15	Sequence 15, Appl
C 708	11.4	34.5	21	3	US-08-545-196B-45	Sequence 45, Appl	781	11.4	34.5	33	4	US-09-656-653-14	Sequence 14, Appl
C 709	11.4	34.5	21	3	US-07-974-409C-352	Sequence 352, Appl	782	11.4	34.5	33	4	US-09-757-251-15	Sequence 15, Appl
C 710	11.4	34.5	21	4	US-08-469-260A-138	Sequence 138, Appl	783	11.4	34.5	33	4	US-09-828-259A-15	Sequence 15, Appl
C 711	11.4	34.5	21	4	US-08-469-260A-148	Sequence 148, Appl	784	11.4	34.5	33	4	US-09-719-878-15	Sequence 15, Appl
C 712	11.4	34.5	21	4	US-08-488-446-138	Sequence 138, Appl	785	11.4	34.5	33	4	US-09-828-325A-15	Sequence 15, Appl
C 713	11.4	34.5	21	4	US-08-488-446-148	Sequence 148, Appl	786	11.4	34.5	33	4	US-09-756-248-14	Sequence 14, Appl
C 714	11.4	34.5	21	4	US-08-467-344A-138	Sequence 138, Appl	787	11.4	34.5	33	4	US-09-269-576G-10	Sequence 10, Appl
C 715	11.4	34.5	21	4	US-08-467-344A-148	Sequence 148, Appl	788	11.4	34.5	33	4	US-08-446-729-6	Sequence 6, Appl
C 716	11.4	34.5	21	4	US-08-424-550B-138	Sequence 138, Appl	789	11.4	34.5	34	1	US-08-455-968E-30	Sequence 30, Appl
C 717	11.4	34.5	21	4	US-08-424-550B-148	Sequence 148, Appl	790	11.4	34.5	35	2	US-09-181-183-21	Sequence 21, Appl
C 718	11.4	34.5	21	4	US-09-657-472-879	Sequence 879, Appl	791	11.4	34.5	35	3	US-09-852-793-384	Sequence 384, Appl
C 719	11.4	34.5	21	4	US-09-657-472-2154	Sequence 2154, Appl	792	11.4	34.5	35	3	US-09-280-040-21	Sequence 21, Appl
C 720	11.4	34.5	21	4	US-08-538-875-34	Sequence 34, Appl	793	11.4	34.5	35	3	US-09-277-700-21	Sequence 21, Appl
C 721	11.4	34.5	24	1	US-08-697-404-7	Sequence 7, Appl	794	11.4	34.5	35	3	US-09-849-928-384	Sequence 384, Appl
C 722	11.4	34.5	25	1	US-08-591-989-67	Sequence 67, Appl	795	11.4	34.5	35	4	US-09-874-585D-21	Sequence 21, Appl
C 723	11.4	34.5	25	2	US-08-743-637B-44	Sequence 44, Appl	796	11.4	34.5	35	4	US-09-042-460-20	Sequence 20, Appl
C 724	11.4	34.5	25	3	US-08-526-840B-44	Sequence 44, Appl	797	11.4	34.5	35	4	PCT-US96-09455A-384	Sequence 384, Appl
C 725	11.4	34.5	25	3	US-08-946-914-53	Sequence 53, Appl	798	11.4	34.5	35	5	US-09-199-637A-187	Sequence 187, Appl
C 726	11.4	34.5	25	3	US-08-946-914-53	Sequence 53, Appl	799	11.4	34.5	36	3	US-09-313-221A-103	Sequence 103, Appl
C 727	11.4	34.5	25	3	US-09-656-450-53	Sequence 53, Appl	800	11.4	34.5	36	4	US-09-589-483-2	Sequence 2, Appl
C 728	11.4	34.5	25	4	US-09-656-450-60	Sequence 60, Appl	801	11.4	34.5	36	4	US-08-086-428B-104	Sequence 104, Appl
C 729	11.4	34.5	25	4	US-09-829-855-156	Sequence 156, Appl	802	11.4	34.5	36	4	US-08-086-428B-106	Sequence 106, Appl
C 730	11.4	34.5	25	4	US-09-866-108A-14605	Sequence 14605, A	803	11.4	34.5	37	3	US-08-086-428B-108	Sequence 108, Appl
C 731	11.4	34.5	25	4	US-09-866-108A-14606	Sequence 14606, A	804	11.4	34.5	37	3	US-08-468-570-106	Sequence 106, Appl
C 732	11.4	34.5	25	4	US-09-866-108A-14607	Sequence 14607, A	805	11.4	34.5	37	3	US-08-468-570-108	Sequence 108, Appl
C 733	11.4	34.5	25	4	US-09-866-108A-14608	Sequence 14608, A	806	11.4	34.5	37	3	US-08-468-570-110	Sequence 110, Appl
C 734	11.4	34.5	25	4	US-09-866-108A-14609	Sequence 14609, A	807	11.4	34.5	37	3	US-09-431-349C-33	Sequence 33, Appl
C 735	11.4	34.5	25	4	US-09-253-396A-97	Sequence 97, Appl	808	11.4	34.5	37	3	US-09-225-670-33	Sequence 33, Appl
C 736	11.4	34.5	27	3	US-08-117-364A-3	Sequence 3, Appl	809	11.4	34.5	37	3	US-09-431-349C-33	Sequence 33, Appl
C 737	11.4	34.5	28	1	US-08-647-584-21	Sequence 21, Appl	810	11.4	34.5	38	4	US-09-746-359A-48	Sequence 48, Appl
C 738	11.4	34.5	28	1	US-08-457-733-3	Sequence 3, Appl	811	11.4	34.5	38	4	US-08-675-566-105	Sequence 105, Appl
C 739	11.4	34.5	28	2	US-08-457-733-3	Sequence 3, Appl	812	11.4	34.5	39	4	US-09-267-311-13	Sequence 13, Appl
C 740	11.4	34.5	28	3	US-09-523-849-37	Sequence 37, Appl	813	11.4	34.5	39	4	US-08-086-428B-104	Sequence 104, Appl
C 741	11.4	34.5	29	4	US-09-304-232-251	Sequence 251, Appl	814	11.4	34.5	40	1	US-08-086-428B-106	Sequence 106, Appl
C 742	11.4	34.5	29	4	US-09-304-232-504	Sequence 504, Appl	815	11.4	34.5	40	1	US-08-086-428B-108	Sequence 108, Appl
C 743	11.4	34.5	29	4	US-08-859-998-430	Sequence 430, Appl	816	11.4	34.5	40	1	US-08-468-570-106	Sequence 106, Appl
C 744	11.4	34.5	30	2	US-08-696-932A-40	Sequence 40, Appl	817	11.4	34.5	40	2	US-08-468-570-108	Sequence 108, Appl
C 745	11.4	34.5	30	3	US-08-859-998-430	Sequence 430, Appl	818	11.4	34.5	40	2	US-08-290-665A-208	Sequence 208, Appl
C 746	11.4	34.5	30	3	US-09-225-928-430	Sequence 430, Appl	819	11.4	34.5	40	2	US-08-290-665A-210	Sequence 210, Appl
C 747	11.4	34.5	30	3	US-09-225-928-430	Sequence 430, Appl	820	11.4	34.5	40	2	US-08-290-665A-212	Sequence 212, Appl
C 748	11.4	34.5	30	4	US-09-706-649-5	Sequence 5, Appl	821	11.4	34.5	40	2	US-09-164-714-19	Sequence 19, Appl
C 749	11.4	34.5	32	1	US-08-484-686B-26	Sequence 26, Appl	822	11.4	34.5	40	4	US-09-060-299-185	Sequence 185, Appl
C 750	11.4	34.5	32	1	US-08-484-686B-26	Sequence 26, Appl	823	11.4	34.5	40	4	US-09-402-923A-185	Sequence 185, Appl
C 751	11.4	34.5	32	5	PCT-US91-02568-27	Sequence 27, Appl	824	11.4	34.5	40	4	US-08-466-601A-104	Sequence 104, Appl
C 752	11.4	34.5	32	5	PCT-US91-02568-29	Sequence 29, Appl	825	11.4	34.5	40	4	US-08-466-601A-106	Sequence 106, Appl
C 753	11.4	34.5	32	5	PCT-US91-02568-42	Sequence 42, Appl	826	11.4	34.5	40	4	US-08-466-601A-108	Sequence 108, Appl
C 754	11.4	34.5	33	1	US-08-538-875-70	Sequence 70, Appl	827	11.4	34.5	40	4	PCT-US95-10398-208	Sequence 208, Appl
C 755	11.4	34.5	33	1	US-08-484-686B-42	Sequence 42, Appl	828	11.4	34.5	40	5	PCT-US95-10398-210	Sequence 210, Appl
C 756	11.4	34.5	33	1	US-08-985-337A-7	Sequence 7, Appl	829	11.4	34.5	40			
C 757	11.4	34.5	33	2	US-08-600-783-8	Sequence 8, Appl	830	11.4	34.5	40			

C 831	11.4	34.5	40	5	PCT-US95-10398-212	Sequence 212, App	C 904	11.2	33.9	21	4	US-09-657-472-2072	Sequence 2072, Ap
C 832	11.4	34.5	41	2	US-08-428-257A-57	Sequence 57, Appl	C 905	11.2	33.9	22	3	US-09-280-409-7	Sequence 7, Appl
C 833	11.4	34.5	41	4	US-08-913-370-10	Sequence 10, Appl	C 906	11.2	33.9	22	4	US-09-792-024-378	Sequence 378, App
C 834	11.4	34.5	41	4	US-09-938-077-3	Sequence 3, Appl	C 907	11.2	33.9	23	3	US-08-068-754-2	Sequence 2, Appl
C 835	11.4	34.5	43	2	US-08-714-070A-9	Sequence 9, Appl	C 908	11.2	33.9	23	3	US-09-325-926-2	Sequence 2, Appl
C 836	11.4	34.5	43	3	US-08-604-986-13	Sequence 13, Appl	C 909	11.2	33.9	24	3	US-09-035-619-3	Sequence 3, Appl
C 837	11.4	34.5	45	1	US-08-250-859-8	Sequence 8, Appl	C 910	11.2	33.9	24	3	US-09-514-006-3	Sequence 3, Appl
C 838	11.4	34.5	45	1	US-08-334-499-1	Sequence 1, Appl	C 911	11.2	33.9	24	3	US-09-423-744A-2	Sequence 2, Appl
C 839	11.4	34.5	45	1	US-08-490-803-8	Sequence 8, Appl	C 912	11.2	33.9	24	3	US-09-798-743-9	Sequence 9, Appl
C 840	11.4	34.5	45	2	US-08-464-073-35	Sequence 35, Appl	C 913	11.2	33.9	25	1	US-08-448-204-26	Sequence 26, Appl
C 841	11.4	34.5	45	2	US-08-457-254-20	Sequence 20, Appl	C 914	11.2	33.9	25	4	US-09-142-138-2	Sequence 2, Appl
C 842	11.4	34.5	45	2	US-08-484-257-8	Sequence 8, Appl	C 915	11.2	33.9	25	4	US-09-538-709-350	Sequence 350, App
C 843	11.4	34.5	45	5	PCT-US94-08806-8	Sequence 8, Appl	C 916	11.2	33.9	25	4	US-09-398-858-10	Sequence 10, Appl
C 844	11.4	34.5	45	5	PCT-US95-01775-8	Sequence 8, Appl	C 917	11.2	33.9	25	4	US-09-866-108A-4845	Sequence 4845, Ap
C 845	11.4	34.5	45	5	PCT-US95-16626-20	Sequence 20, Appl	C 918	11.2	33.9	25	4	US-09-866-108A-11254	Sequence 11254, A
C 846	11.4	34.5	46	1	US-08-403-762A-14	Sequence 14, Appl	C 919	11.2	33.9	25	4	US-09-866-108A-11255	Sequence 11255, A
C 847	11.4	34.5	46	3	US-09-164-023-8	Sequence 8, Appl	C 920	11.2	33.9	25	4	US-09-866-108A-11256	Sequence 11256, A
C 848	11.4	34.5	46	3	US-08-869-276-10	Sequence 10, Appl	C 921	11.2	33.9	25	4	US-09-866-108A-11257	Sequence 11257, A
C 849	11.4	34.5	46	3	US-09-635-344-10	Sequence 10, Appl	C 922	11.2	33.9	25	4	US-09-866-108A-11258	Sequence 11258, A
C 850	11.4	34.5	46	3	US-09-398-629-10	Sequence 10, Appl	C 923	11.2	33.9	25	4	US-09-866-108A-11259	Sequence 11259, A
C 851	11.4	34.5	46	4	US-09-799-160-10	Sequence 10, Appl	C 924	11.2	33.9	25	4	US-09-866-108A-11260	Sequence 11260, A
C 852	11.4	34.5	47	4	US-09-641-638-663	Sequence 663, App	C 925	11.2	33.9	25	4	US-09-866-108A-11261	Sequence 11261, A
C 853	11.4	34.5	47	4	US-09-641-638-1141	Sequence 1141, Ap	C 926	11.2	33.9	25	4	US-09-866-108A-11262	Sequence 11262, A
C 854	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 927	11.2	33.9	25	4	US-09-866-108A-11263	Sequence 11263, A
C 855	11.4	34.5	47	4	US-09-422-978-986	Sequence 986, App	C 928	11.2	33.9	25	4	US-09-866-108A-15115	Sequence 15115, A
C 856	11.4	34.5	47	4	US-09-422-978-3328	Sequence 3328, Ap	C 929	11.2	33.9	26	2	US-08-766-439-48	Sequence 48, Appl
C 857	11.4	34.5	47	4	US-10-170-097-663	Sequence 663, App	C 930	11.2	33.9	26	4	US-09-395-017B-34	Sequence 34, Appl
C 858	11.4	34.5	47	4	US-10-170-097-1141	Sequence 1141, Ap	C 931	11.2	33.9	27	1	US-07-986-963-6	Sequence 6, Appl
C 859	11.4	34.5	48	2	US-08-896-410-26	Sequence 26, Appl	C 932	11.2	33.9	27	1	US-08-707-793A-11	Sequence 11, Appl
C 860	11.4	34.5	48	2	US-08-697-404-2	Sequence 2, Appl	C 933	11.2	33.9	27	1	US-08-707-792A-11	Sequence 11, Appl
C 861	11.4	34.5	49	2	US-08-464-073-23	Sequence 23, Appl	C 934	11.2	33.9	27	2	US-08-244-122-12	Sequence 12, Appl
C 862	11.4	34.5	49	2	US-08-428-252-23	Sequence 23, Appl	C 935	11.2	33.9	27	2	US-08-447-430A-21	Sequence 21, Appl
C 863	11.4	34.5	49	3	US-08-416-516A-23	Sequence 23, Appl	C 936	11.2	33.9	27	2	US-08-447-430A-22	Sequence 22, Appl
C 864	11.4	34.5	49	4	US-09-968-255-18	Sequence 18, Appl	C 937	11.2	33.9	27	3	US-08-985-162-844	Sequence 844, App
C 865	11.4	34.5	50	1	US-07-994-469A-37	Sequence 37, Appl	C 938	11.2	33.9	27	3	US-08-584-040-6733	Sequence 6733, Ap
C 866	11.4	34.5	50	1	US-08-688-649-19	Sequence 19, Appl	C 939	11.2	33.9	27	4	US-09-706-197-6	Sequence 6, Appl
C 867	11.4	34.5	50	2	US-08-464-073-36	Sequence 36, Appl	C 940	11.2	33.9	27	4	US-09-553-690-43	Sequence 43, Appl
C 868	11.4	34.5	50	3	US-08-377-503-3	Sequence 3, Appl	C 941	11.2	33.9	27	4	US-09-179-162A-2	Sequence 2, Appl
C 869	11.4	34.5	50	3	US-08-178-019-3	Sequence 3, Appl	C 942	11.2	33.9	27	4	US-09-342-673-21	Sequence 21, Appl
C 870	11.4	34.5	50	4	US-08-956-171E-5177	Sequence 5177, Ap	C 943	11.2	33.9	27	4	US-09-342-673-22	Sequence 22, Appl
C 871	11.4	34.5	50	4	US-08-781-986A-5177	Sequence 5177, Ap	C 944	11.2	33.9	27	4	US-09-401-063-844	Sequence 844, App
C 872	11.2	33.9	16	1	US-08-469-802B-9	Sequence 9, Appl	C 945	11.2	33.9	27	4	US-09-950-459-2	Sequence 2, Appl
C 873	11.2	33.9	16	2	US-08-267-803B-27	Sequence 27, Appl	C 946	11.2	33.9	28	1	US-08-462-894-22	Sequence 22, Appl
C 874	11.2	33.9	17	1	US-08-373-124A-1335	Sequence 1335, Ap	C 947	11.2	33.9	28	1	US-08-206-185-22	Sequence 22, Appl
C 875	11.2	33.9	17	1	US-08-435-628-1335	Sequence 1335, Ap	C 948	11.2	33.9	28	1	US-09-183-846A-17	Sequence 17, Appl
C 876	11.2	33.9	17	2	US-08-404-531B-17	Sequence 17, Appl	C 949	11.2	33.9	28	3	US-09-267-177-6	Sequence 6, Appl
C 877	11.2	33.9	17	3	US-08-476-900A-17	Sequence 17, Appl	C 950	11.2	33.9	28	4	US-08-961-578C-17	Sequence 17, Appl
C 878	11.2	33.9	17	3	US-08-488-546A-17	Sequence 17, Appl	C 951	11.2	33.9	28	4	US-08-887-497A-72	Sequence 72, Appl
C 879	11.2	33.9	17	4	US-09-866-108A-6362	Sequence 6362, Ap	C 952	11.2	33.9	28	4	US-08-670-216-17	Sequence 17, Appl
C 880	11.2	33.9	17	4	US-09-866-108A-6363	Sequence 6363, Ap	C 953	11.2	33.9	29	4	US-08-734-443-3	Sequence 3, Appl
C 881	11.2	33.9	18	1	US-08-120-780-2	Sequence 2, Appl	C 954	11.2	33.9	30	2	US-08-829-876-20	Sequence 20, Appl
C 882	11.2	33.9	18	3	US-08-624-290B-2	Sequence 2, Appl	C 955	11.2	33.9	30	2	US-08-743-637B-101	Sequence 101, App
C 883	11.2	33.9	19	3	US-08-851-843A-95	Sequence 95, Appl	C 956	11.2	33.9	30	3	US-08-526-840B-101	Sequence 101, App
C 884	11.2	33.9	19	3	US-08-974-549A-387	Sequence 387, App	C 957	11.2	33.9	30	3	US-08-234-874A-20	Sequence 20, Appl
C 885	11.2	33.9	19	3	US-08-854-050-95	Sequence 95, Appl	C 958	11.2	33.9	30	4	US-09-684-385-40	Sequence 40, Appl
C 886	11.2	33.9	19	3	US-08-430-323-95	Sequence 95, Appl	C 959	11.2	33.9	30	4	US-09-234-873A-20	Sequence 20, Appl
C 887	11.2	33.9	19	4	US-08-912-951-154	Sequence 154, App	C 960	11.2	33.9	31	6	5466668-47	Patent No. 5466668
C 888	11.2	33.9	19	4	US-09-402-181B-387	Sequence 387, App	C 961	11.2	33.9	32	1	US-08-612-895A-58	Sequence 58, Appl
C 889	11.2	33.9	19	4	US-09-721-456-387	Sequence 387, App	C 962	11.2	33.9	32	3	US-09-093-233-58	Sequence 58, Appl
C 890	11.2	33.9	19	4	US-09-696-791-3881	Sequence 3881, Ap	C 963	11.2	33.9	32	3	US-09-303-084-39	Sequence 39, Appl
C 891	11.2	33.9	20	1	US-08-531-556-53	Sequence 53, Appl	C 964	11.2	33.9	32	3	US-09-459-553-58	Sequence 58, Appl
C 892	11.2	33.9	20	1	US-08-472-416-53	Sequence 53, Appl	C 965	11.2	33.9	32	3	US-09-086-503-39	Sequence 39, Appl
C 893	11.2	33.9	20	3	US-09-428-584-12	Sequence 12, Appl	C 966	11.2	33.9	32	4	US-09-882-246-58	Sequence 58, Appl
C 894	11.2	33.9	20	3	US-09-290-640-28	Sequence 28, Appl	C 967	11.2	33.9	32	5	PCT-US94-10562A-58	Sequence 58, Appl
C 895	11.2	33.9	20	3	US-09-657-042A-33	Sequence 33, Appl	C 968	11.2	33.9	34	1	US-08-591-989-65	Sequence 65, Appl
C 896	11.2	33.9	20	3	US-09-183-636-3	Sequence 3, Appl	C 969	11.2	33.9	34	3	US-08-123-764-7	Sequence 7, Appl
C 897	11.2	33.9	20	4	US-09-422-978-5364	Sequence 5364, Ap	C 970	11.2	33.9	34	3	US-08-815-190A-7	Sequence 7, Appl
C 898	11.2	33.9	20	4	US-09-665-615B-28	Sequence 28, Appl	C 971	11.2	33.9	34	3	US-09-645-629-30	Sequence 30, Appl
C 899	11.2	33.9	21	1	US-08-290-937B-7	Sequence 7, Appl	C 972	11.2	33.9	35	1	US-08-233-030-9	Sequence 9, Appl
C 900	11.2	33.9	21	4	US-09-553-231-3	Sequence 3, Appl	C 973	11.2	33.9	35	1	US-08-361-337-17	Sequence 17, Appl
C 901	11.2	33.9	21	4	US-09-585-174-30	Sequence 30, Appl	C 974	11.2	33.9	36	1	US-07-988-194A-27	Sequence 27, Appl
C 902	11.2	33.9	21	4	US-09-192-854-202	Sequence 202, App	C 975	11.2	33.9	36	1	US-08-311-760A-146	Sequence 146, App
C 903	11.2	33.9	21	4	US-09-657-472-382	Sequence 382, App	C 976	11.2	33.9	36	1	US-08-319-492B-183	Sequence 183, App

Sequence 334, App
Sequence 637, App
Sequence 635, App
Sequence 29, Appl
Sequence 159, App
Sequence 176, App
Sequence 210, App
Sequence 399, App
Sequence 860, App
Sequence 304, App
Sequence 898, App
Sequence 29, Appl
Sequence 1131, App
Sequence 1442, App
Sequence 29, Appl
Sequence 481, App
Sequence 1028, App
Sequence 1460, App
Sequence 1555, App
Sequence 1593, App
Sequence 2005, App
Sequence 2006, App
Sequence 146, App
Sequence 1131, App

ALIGNMENTS

RESULT 1
US-09-438-954-8
; Sequence 8, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer KXD
US-09-438-954-8

Query Match 46.7%; Score 15.4; DB 4; Length 30;
Best Local Similarity 76.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 8 GACTGGCAGCGCTCTGGTGATACC 32
DB 2 GACTGGCAGCGTTTGTGTGATACC 26
RESULT 2
US-09-233-493-28/c
; Sequence 28, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; SOFTWARE: Patent In Release #1.0, Version #1.30
; NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-493-28
Query Match 46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAGCGCTCTGGTGATA 30
DB 32 ATGAGTGGCAGCGCGCGGCGTAATA 8
RESULT 3
US-09-005-476-28/c
; Sequence 28, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476

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; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-005-476-28

Query Match 46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 4
US-09-233-492-28/c
; Sequence 28, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-09-233-492-28

Query Match 46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 5
US-09-296-280-28/c
; Sequence 28, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
; US-09-296-280-28

Query Match 46.7%; Score 15.4; DB 3; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 6
US-09-498-074-28/c
; Sequence 28, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-28

Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGTCTCGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 7
PCT-US96-10082A-28/c
; Sequence 28, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-498-074-28

Query Match 46.7%; Score 15.4; DB 5; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGTCTCGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 8
PCT-US96-10082A-28/c
; Sequence 28, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; PCT-US96-10082A-28

Query Match 46.7%; Score 15.4; DB 5; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGTCTCGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 9
US-08-323-192D-23
; Sequence 23, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
```



```
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-323-192D-23
Query Match          46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 10
US-08-323-192D-25
; Sequence 25, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
```

```
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-323-192D-25
Query Match          46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 11
US-08-470-887A-22
; Sequence 22, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-22
Query Match          46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGGCGGGCGTAATA 31

RESULT 12
US-08-470-887A-24
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us-10-087-631b-5.max.rni

Wed Nov 24 08:46:06 2004

```

; Sequence 24, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-24

Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGCGGCGTAATA 31

RESULT 13
US-08-316-439A-20
; Sequence 20, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A

; Sequence 24, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-470-887A-24

Query Match 46.7%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGCGGCGTAATA 31

RESULT 14
US-08-316-439A-22
; Sequence 22, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A

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; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 22:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-22
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Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 6 ATGAGTGCACAGCGCTCTGGTGATA 30
|||
Db 7 ATGAGTGCACAGCGCGGCGTAATA 31
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```
RESULT 15
US-08-252-508B-22
; Sequence 22, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 30,742
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-252-508B-22

Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGCACAGCGCTCTGGTGATA 30
|||
Db 7 ATGAGTGCACAGCGCGGCGTAATA 31

RESULT 16
US-08-252-508B-24
; Sequence 24, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 7682-034
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-252-508B-24
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```
Query Match 46.7%; Score 15.4; DB 2; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-09-106-377-24

Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGGCGGTAATA 31

RESULT 19
5166057-35
; Patent No. 5166057
; APPLICANT: PALESE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; EXPRESSION-SYSTEMS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/527,237
; FILING DATE: 22-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,053
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 399,728
; FILING DATE: 28-AUG-1989
; SEQ ID NO: 35:
; LENGTH: 34
5166057-35

Query Match 46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   |||||
Db 7 ATGAGTGGCAGGCGGGCGGTAATA 31

RESULT 20
US-08-323-192D-24/c

```

; Sequence 24, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 7682-035
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-323-192D-24

Query Match 46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 21
US-08-323-192D-26/c
; Sequence 26, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 7682-035
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-323-192D-26

Query Match 46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 22
US-08-470-887A-23/c
; Sequence 23, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; REFERENCE/DOCKET NUMBER: 7682-035
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-470-887A-23

Query Match 46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 23

US-08-470-887A-25/c
; Sequence 25, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-470-887A-25

Query Match 46.7%; Score 15.4; DB 1; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 24

US-08-316-439A-23/c
; Sequence 23, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GORDWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/440,053
; FILING DATE: No. 5840520ember 21, 1989
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-23

Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 25

US-08-252-508B-23/c
; Sequence 23, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

```
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/252.508B
; APPLICATION NUMBER: US/08/252.508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-252-508B-23

Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 26
US-08-252-508B-25/c
; Sequence 25, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252.508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-252-508B-25

Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 27
US-09-106-377-23/c
; Sequence 23, Application US/09106377
; Patent No. 6001834
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-106-377-23

Query Match 46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGCGCGGGCGGTAATA 8

RESULT 28
US-09-106-377-25/c
; Sequence 25, Application US/09106377
```

Patent No. 6001634
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-106-377-25
Query Match 46.7%; Score 15.4; DB 3; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTATA 30
Db 32 ATGAGTGGCAGCGGGCGGCGTAATA 8
RESULT 29
5166057-37/c
; Patent No. 5166057
; APPLICANT: PALESE, PETER; PARVIN, JEFFREY D.; KRISTAL, MARK
; TITLE OF INVENTION: RECOMBIANT NEGATIVE STRAND RNA VIRUS
; EXPRESSION-SYSTEMS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/527,237
; FILING DATE: 22-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,053
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 399,728
; FILING DATE: 28-AUG-1989
; SEQ ID NO: 37:
; LENGTH: 38
5166057-37
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTATA 30
Db 32 ATGAGTGGCAGCGGGCGGCGTAATA 8
RESULT 30
US-09-223-139-1/c
; Sequence 1, Application US/09223139
; Patent No. 6441158
; GENERAL INFORMATION:
; APPLICANT: Dynan, William S.
; APPLICANT: Yoo, Sunghan
; TITLE OF INVENTION: Oligomers that Bind to KU Protein
; FILE REFERENCE: MCG 102
; CURRENT APPLICATION NUMBER: US/09/223,139
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: 60/070,278
; EARLIER FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: (1)..(40)
; OTHER INFORMATION: oligomer SC6
US-09-223-139-1
Query Match 46.7%; Score 15.4; DB 4; Length 40;
Best Local Similarity 76.0%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCACATGAGTGGCAAGCGCTCTGGT 26
Db 37 CAAGACCAGTGGCAAGCGGTATGGT 13
RESULT 31
US-09-485-737B-8/c
; Sequence 8, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS-015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
US-09-485-737B-8
Query Match 44.2%; Score 14.6; DB 3; Length 40;

Best Local Similarity 69.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ACATGAGTGGCAAGCGCTCTGTGTATACC 32
| | | | | | | | | | | | | | | | | | | | | |
Db 37 AGATCAGCTGCAAGCGGCTTATACC 9
| | | | | | | | | | | | | | | | | | | | | |

RESULT 32
US-09-340-798A-39
; Sequence 39, Application US/09340798A
; Patent No. 6534312
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.
; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,798A
; FILING DATE: 28-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19729Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-340-798A-39

Query Match 44.2%; Score 14.6; DB 4; Length 40;
Best Local Similarity 69.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGCGCTCTGTGTAT 29
| | | | | | | | | | | | | | | | | | | | | |
Db 8 GCTAAATGGTGGCAAGTGGCCCGGCAT 36
| | | | | | | | | | | | | | | | | | | | | |

RESULT 33
US-08-053-451B-149
; Sequence 149, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.

Query Match 44.2%; Score 14.6; DB 3; Length 48;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CATGAGTGGCAAGCGCTCTGTGTATACG 33
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CATCAGCAGCCTGGAGTCTGACGATACAG 45
| | | | | | | | | | | | | | | | | | | | | |

RESULT 34
US-08-789-333F-66
; Sequence 66, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DJBRMSDS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-789-333F-66

Query Match 44.2%; Score 14.6; DB 3; Length 48;

; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-053-451B-149

Query Match 44.2%; Score 14.6; DB 2; Length 45;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CATGAGTGGCAAGCGCTCTGTGTATACG 33
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CATCAGCAGCCTGGAGTCTGACGATACAG 45
| | | | | | | | | | | | | | | | | | | | | |

RESULT 34
US-08-789-333F-66
; Sequence 66, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DJBRMSDS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-789-333F-66

Query Match 44.2%; Score 14.6; DB 3; Length 48;

```

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-916-940-66

Query Match          44.2%; Score 14.6; DB 4; Length 48;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0;

QY      1  GCACATGAGTGCACAGGCGCTCTGGTGAT 29
      |||  |||  |||  |||  |||  |||  |||  |||
Db      5  GCAAGAGAAAGGCGACGGCGCTCTGATGCT 33

RESULT 37
US-08-053-451B-148
; Sequence 148, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THERE
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THERE
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; US-08-053-451B-148

Query Match 44.2%; Score 14.6; DB 2; Length 50;
Best Local Similarity 69.0%; Pred.No.1.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CATCAGTGGCAAGCGCTCTGGTGATACCG 33
   ||| ||| ||| ||| ||| ||| |||
DB 22 CATCAGCAGCGCTGGAGTCTGACGATACAG 50

RESULT 38
US-09-275-850-283/c
; Sequence 283, Application US/09275850A
; Patent No. 6261774
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Shtatland, Timur

```

APPLICANT: Javornik, Brenda
TITLE OF INVENTION: Truncation SELEX Method
FILE REFERENCE: NEX 79
CURRENT APPLICATION NUMBER: US/09/275,850A
CURRENT FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 351
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 283
LENGTH: 50
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: modified base
LOCATION: (1)..(50)
OTHER INFORMATION: All pyrimidines are 2'-F; N at positions 7, 25,
OTHER INFORMATION: and 32 are A, C, G or U.

US-09-275-850-283

Query Match 44.2%; Score 14.6; DB 3; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCGAAGGCGTCTGGTGATACCG 33
|||||
DB 47 GCGGAGTCTCTGGGNATACCG 26
|||||

RESULT 39

US-08-872-855-13/c
Sequence 13, Application US/08872855
Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"

US-08-872-855-13

Query Match 43.6%; Score 14.4; DB 3; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCAAGGCGTCTGG 25
|||||
DB 19 GTGGCAAGGCGTCTGG 4
|||||
RESULT 40
US-09-422-978-2994
Sequence 2994, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
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EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2994
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21492-310 : polymorphic base C or T
US-09-422-978-2994

Query Match 43.6%; Score 14.4; DB 4; Length 47;
Best Local Similarity 69.2%; Pred. No. 1.7e+03;
Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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DB 8 TGAATGCCAAGGCTGCYCTTGATCCC 33
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Search completed: November 23, 2004, 22:26:30
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93	13.8	41.8	21	18	US-10-667-271-1470	Sequence 1470, App	c 166	13.2	40.0	35	17	US-10-164-290A-7	Sequence 7, Appl
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100	13.8	41.8	36	9	US-09-504-231A-2496	Sequence 2496, App	c 173	13.2	40.0	38	10	US-09-792-818-1492	Sequence 1492, App
101	13.8	41.8	38	10	US-09-780-533A-4243	Sequence 4243, App	c 174	13.2	40.0	38	10	US-09-745-237A-1894	Sequence 1894, App
102	13.8	41.8	39	16	US-10-434-469-38	Sequence 38, Appl	c 175	13.2	40.0	38	15	US-10-156-306-893	Sequence 893, App
103	13.8	41.8	39	16	US-10-434-469-39	Sequence 39, Appl	c 176	13.2	40.0	38	15	US-10-156-306-1010	Sequence 1010, App
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107	13.8	41.8	45	11	US-09-883-375-8	Sequence 8, Appl	c 180	13.2	40.0	39	14	US-10-147-284-7	Sequence 7, Appl
108	13.8	41.8	50	10	US-09-389-782-26	Sequence 26, Appl	c 181	13.2	40.0	41	16	US-10-035-833A-1234	Sequence 1234, App
109	13.8	41.8	50	16	US-10-131-827-5876	Sequence 5876, App	c 182	13.2	40.0	41	16	US-10-035-833A-2960	Sequence 2960, App
110	13.6	41.2	20	9	US-09-885-188-13	Sequence 13, Appl	c 183	13.2	40.0	41	16	US-10-035-833A-5123	Sequence 5123, App
111	13.6	41.2	20	9	US-09-885-189-13	Sequence 13, Appl	c 184	13.2	40.0	42	16	US-10-353-678-36	Sequence 36, Appl
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124	13.6	41.2	44	10	US-09-942-891-4	Sequence 4, Appl	c 197	13	39.4	22	8	US-08-964-716-23	Sequence 23, Appl
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131	13.4	40.6	27	15	US-10-005-956-1282	Sequence 1282, App	c 204	13	39.4	30	15	US-10-283-881-58	Sequence 58, Appl
132	13.4	40.6	27	17	US-10-689-200-23	Sequence 23, Appl	c 205	13	39.4	30	15	US-09-907-111-278	Sequence 278, App
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136	13.4	40.6	33	17	US-10-383-135-32	Sequence 32, Appl	c 209	13	39.4	38	9	US-10-418-226-7	Sequence 7, Appl
137	13.4	40.6	34	9	US-09-874-475-9	Sequence 9, Appl	c 210	13	39.4	38	15	US-10-283-881-73	Sequence 73, Appl
138	13.4	40.6	34	17	US-10-164-290A-9	Sequence 9, Appl	c 211	13	39.4	40	15	US-10-283-881-74	Sequence 74, Appl
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148	13.4	40.6	41	16	US-10-035-833A-7042	Sequence 7042, App	c 221	13	39.4	47	15	US-10-367-438-36	Sequence 36, Appl
149	13.4	40.6	50	16	US-10-131-827-5247	Sequence 5247, App	c 222	13	39.4	47	15	US-10-402-365-27	Sequence 27, Appl
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151	13.2	40.0	20	15	US-10-092-208-21	Sequence 21, Appl	c 224	13	39.4	50	16	US-10-300-236-28	Sequence 28, Appl
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153	13.2	40.0	21	17	US-10-627-253A-142	Sequence 142, App	c 226	12.8	38.8	25	9	US-09-974-051-34	Sequence 34, Appl
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C 236	12.8	38.8	25	15	US-10-098-263B-57398	Sequence 57398, A	309	12.6	38.2	38	15	US-10-230-006-1006	Sequence 1006, App
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C 246	12.8	38.8	30	15	US-10-154-515-6	Sequence 6, Appli	319	12.6	38.2	39	15	US-10-331-907-217	Sequence 217, App
C 247	12.8	38.8	30	15	US-10-299-180-6	Sequence 6, Appli	320	12.6	38.2	40	15	US-10-062-809-73	Sequence 73, Appl
C 248	12.8	38.8	31	9	US-09-747-538-23	Sequence 23, Appl	321	12.6	38.2	40	17	US-10-611-527-17	Sequence 17, Appl
C 249	12.8	38.8	31	10	US-09-825-805-1520	Sequence 1520, Ap	322	12.6	38.2	41	16	US-10-035-833A-477	Sequence 477, App
C 250	12.8	38.8	34	10	US-09-852-370-67	Sequence 67, Appl	323	12.6	38.2	41	16	US-10-035-833A-720	Sequence 720, App
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C 252	12.8	38.8	35	16	US-10-422-366-23	Sequence 23, Appl	325	12.6	38.2	41	16	US-10-035-833A-3434	Sequence 3434, Ap
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C 254	12.8	38.8	36	9	US-09-274-553D-1668	Sequence 1668, Ap	327	12.6	38.2	41	16	US-10-035-833A-6659	Sequence 6659, Ap
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C 256	12.8	38.8	38	9	US-09-864-785-1123	Sequence 1123, Ap	329	12.6	38.2	42	10	US-09-155-106-42	Sequence 42, Appli
C 257	12.8	38.8	38	10	US-09-776-474-1643	Sequence 1643, Ap	330	12.6	38.2	45	10	US-09-771-287-45	Sequence 45, Appl
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C 259	12.8	38.8	38	16	US-10-138-674-13855	Sequence 13855, A	332	12.6	38.2	45	15	US-10-006-343-45	Sequence 45, Appl
C 260	12.8	38.8	38	16	US-10-138-674-14906	Sequence 14906, A	333	12.6	38.2	47	15	US-10-367-438-36	Sequence 36, Appl
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C 263	12.8	38.8	38	17	US-10-287-949A-14906	Sequence 14906, A	336	12.6	38.2	50	10	US-09-993-346-494	Sequence 494, App
C 264	12.8	38.8	38	17	US-10-679-620-45	Sequence 45, Appl	337	12.6	38.2	50	16	US-10-131-827-2269	Sequence 2269, Ap
C 265	12.8	38.8	39	15	US-10-314-861-14	Sequence 14, Appl	338	12.6	38.2	50	16	US-10-131-827-3168	Sequence 3168, Ap
C 266	12.8	38.8	41	9	US-09-825-561A-56	Sequence 56, Appl	339	12.6	38.2	50	16	US-10-131-827-4099	Sequence 4099, Ap
C 267	12.8	38.8	41	14	US-10-109-812-35	Sequence 35, Appl	340	12.6	38.2	50	16	US-10-131-827-4900	Sequence 4900, Ap
C 268	12.8	38.8	45	16	US-10-474-832-28	Sequence 28, Appl	341	12.6	38.2	50	16	US-10-131-827-8054	Sequence 8054, Ap
C 269	12.8	38.8	48	9	US-09-822-698A-56	Sequence 56, Appl	342	12.4	37.6	18	15	US-10-440-998-12	Sequence 12, Appl
C 270	12.8	38.8	49	10	US-09-990-586-42	Sequence 42, Appl	343	12.4	37.6	22	15	US-10-204-884-105	Sequence 105, App
C 271	12.8	38.8	49	15	US-10-310-113-38	Sequence 38, Appl	344	12.4	37.6	22	16	US-10-001-052-4	Sequence 4, Appli
C 272	12.8	38.8	49	15	US-10-230-880-42	Sequence 42, Appl	345	12.4	37.6	23	16	US-10-280-183A-417	Sequence 417, App
C 273	12.8	38.8	50	8	US-08-781-986A-2367	Sequence 2367, Ap	346	12.4	37.6	25	10	US-09-847-102A-18	Sequence 18, Appl
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C 282	12.6	38.2	24	10	US-09-940-185-798	Sequence 798, App	355	12.4	37.6	25	15	US-10-098-263B-54102	Sequence 54102, A
C 283	12.6	38.2	25	10	US-09-940-185-4763	Sequence 4763, Ap	356	12.4	37.6	25	15	US-10-098-263B-88521	Sequence 88521, A
C 284	12.6	38.2	25	15	US-10-098-263B-16177	Sequence 16177, A	357	12.4	37.6	25	15	US-10-098-263B-101439	Sequence 101439, A
C 285	12.6	38.2	25	15	US-10-098-263B-99145	Sequence 99145, A	358	12.4	37.6	25	15	US-10-098-263B-113339	Sequence 113339, A
C 286	12.6	38.2	28	17	US-10-312-197-9	Sequence 9, Appli	359	12.4	37.6	25	17	US-10-308-503-204	Sequence 204, App
C 287	12.6	38.2	28	17	US-10-312-197-9	Sequence 9, Appli	360	12.4	37.6	25	17	US-10-775-169-3968	Sequence 3968, Ap
C 288	12.6	38.2	30	17	US-10-220-481-251	Sequence 251, App	361	12.4	37.6	29	9	US-09-952-663-10	Sequence 10, Appl
C 289	12.6	38.2	32	15	US-10-322-656-47	Sequence 47, Appl	362	12.4	37.6	29	15	US-10-171-452A-4	Sequence 4, Appli
C 290	12.6	38.2	36	9	US-09-504-231A-1784	Sequence 1784, Ap	363	12.4	37.6	29	15	US-10-336-638-91	Sequence 91, Appl
C 291	12.6	38.2	36	9	US-09-504-231A-1784	Sequence 1784, Ap	364	12.4	37.6	29	15	US-10-353-708-4	Sequence 4, Appli
C 292	12.6	38.2	36	9	US-09-504-231A-2750	Sequence 2750, Ap	365	12.4	37.6	29	17	US-10-731-984-38	Sequence 38, Appl
C 293	12.6	38.2	36	9	US-09-274-553D-1784	Sequence 1784, Ap	366	12.4	37.6	30	14	US-10-423-170-10	Sequence 10, Appl
C 294	12.6	38.2	36	9	US-09-274-553D-2750	Sequence 2750, Ap	367	12.4	37.6	31	15	US-10-100-294A-66	Sequence 66, Appl
C 295	12.6	38.2	36	9	US-09-966-955A-50	Sequence 50, Appl	368	12.4	37.6	31	15	US-10-085-388-1	Sequence 1, Appli
C 296	12.6	38.2	37	9	US-09-504-231A-3167	Sequence 3167, Ap	369	12.4	37.6	32	9	US-09-813-781-79	Sequence 79, Appl
C 297	12.6	38.2	38	9	US-09-864-785-825	Sequence 825, App	370	12.4	37.6	32	10	US-09-747-377-467	Sequence 467, App
C 298	12.6	38.2	38	9	US-09-864-785-1314	Sequence 1314, Ap	371	12.4	37.6	32	14	US-10-105-613-467	Sequence 467, App
C 299	12.6	38.2	38	10	US-09-730-289B-2863	Sequence 2863, Ap	372	12.4	37.6	33	15	US-10-289-498-10	Sequence 10, Appl
C 300	12.6	38.2	38	10	US-09-780-533A-3865	Sequence 3865, Ap	373	12.4	37.6	33	15	US-10-289-527-10	Sequence 10, Appl
C 301	12.6	38.2	38	10	US-09-877-478-2776	Sequence 2776, Ap	374	12.4	37.6	33	17	US-10-383-135-33	Sequence 33, Appl
C 302	12.6	38.2	38	10	US-09-877-478-3470	Sequence 3470, Ap	375	12.4	37.6	36	15	US-10-424-233-69	Sequence 69, Appl
C 303	12.6	38.2	38	10	US-09-848-754A-4719	Sequence 4719, Ap	376	12.4	37.6	36	15	US-10-423-399-54	Sequence 54, Appl
C 304	12.6	38.2	38	10	US-09-848-754A-4930	Sequence 4930, Ap	377	12.4	37.6	37	10	US-09-848-754A-6147	Sequence 6147, Ap

378	12.4	37.6	37	10	US-09-848-754A-6152	Sequence 6152, Ap	c 451	12.2	37.0	36	9	US-09-504-231A-1865	Sequence 1865, Ap
379	12.4	37.6	37	10	US-09-848-754A-6272	Sequence 6272, Ap	452	12.2	37.0	36	9	US-09-504-231A-1897	Sequence 1897, Ap
380	12.4	37.6	37	10	US-09-848-754A-6427	Sequence 6427, Ap	c 453	12.2	37.0	36	9	US-09-274-5530-1865	Sequence 1865, Ap
381	12.4	37.6	39	15	US-10-378-168-85	Sequence 85, Appl	c 454	12.2	37.0	36	9	US-09-274-5530-1897	Sequence 1897, Ap
382	12.4	37.6	39	16	US-10-252-155-775	Sequence 775, Appl	c 455	12.2	37.0	36	14	US-10-056-41A-653	Sequence 653, Appl
383	12.4	37.6	41	16	US-10-035-833A-2713	Sequence 2713, Ap	c 456	12.2	37.0	36	15	US-10-440-850-1676	Sequence 1676, Ap
384	12.4	37.6	41	16	US-10-035-833A-6140	Sequence 6140, Ap	c 457	12.2	37.0	36	16	US-10-420-194-602	Sequence 602, Appl
385	12.4	37.6	43	15	US-10-032-585-1869	Sequence 1869, Ap	c 458	12.2	37.0	38	10	US-09-825-805-1324	Sequence 1324, Ap
386	12.4	37.6	43	16	US-10-001-052-18	Sequence 18, Appl	c 459	12.2	37.0	38	10	US-09-780-533A-2883	Sequence 2883, Ap
387	12.4	37.6	45	11	US-09-883-375-7	Sequence 7, Appl	c 460	12.2	37.0	38	10	US-09-327-046-2208	Sequence 2208, Ap
388	12.4	37.6	45	11	US-10-193-764-14	Sequence 14, Appl	c 461	12.2	37.0	38	10	US-09-927-046-2959	Sequence 2959, Ap
389	12.4	37.6	46	14	US-10-125-789A-2	Sequence 2, Appl	c 462	12.2	37.0	38	10	US-09-877-478-2804	Sequence 2804, Ap
390	12.4	37.6	46	15	US-10-199-820-157	Sequence 157, Appl	c 463	12.2	37.0	38	10	US-09-877-478-2974	Sequence 2974, Ap
391	12.4	37.6	50	15	US-10-422-934-61	Sequence 61, Appl	c 464	12.2	37.0	38	10	US-09-848-754A-4142	Sequence 4142, Ap
392	12.4	37.6	50	16	US-10-131-827-1219	Sequence 1219, Ap	c 465	12.2	37.0	38	10	US-09-848-754A-4249	Sequence 4249, Ap
393	12.4	37.6	50	16	US-10-131-827-2375	Sequence 2375, Ap	c 466	12.2	37.0	38	10	US-09-848-754A-4630	Sequence 4630, Ap
394	12.2	37.0	17	10	US-09-877-478-2405	Sequence 2405, Ap	c 467	12.2	37.0	38	10	US-09-848-754A-4630	Sequence 4630, Ap
395	12.2	37.0	17	10	US-09-930-423-1556	Sequence 1556, Ap	c 468	12.2	37.0	38	10	US-09-848-754A-5233	Sequence 5233, Ap
396	12.2	37.0	17	10	US-09-745-237A-1556	Sequence 1556, Ap	c 469	12.2	37.0	38	10	US-09-848-754A-5233	Sequence 5233, Ap
397	12.2	37.0	17	16	US-10-342-902-2405	Sequence 2405, Ap	c 470	12.2	37.0	38	10	US-09-848-754A-5552	Sequence 5552, Ap
398	12.2	37.0	17	17	US-10-669-841-2208	Sequence 2208, Ap	c 471	12.2	37.0	38	10	US-09-930-423-1877	Sequence 1877, Ap
399	12.2	37.0	18	15	US-10-440-998-19	Sequence 19, Appl	c 472	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
400	12.2	37.0	20	13	US-10-044-671-10	Sequence 10, Appl	c 473	12.2	37.0	38	10	US-09-930-423-2330	Sequence 2330, Ap
401	12.2	37.0	20	15	US-10-174-465-25	Sequence 25, Appl	c 474	12.2	37.0	38	10	US-09-927-395A-1134	Sequence 1134, Ap
402	12.2	37.0	20	15	US-10-174-465-58	Sequence 58, Appl	c 475	12.2	37.0	38	10	US-09-745-237A-1877	Sequence 1877, Ap
403	12.2	37.0	20	15	US-10-348-431-25	Sequence 25, Appl	c 476	12.2	37.0	38	10	US-09-745-237A-2325	Sequence 2325, Ap
404	12.2	37.0	20	15	US-10-348-431-58	Sequence 58, Appl	c 477	12.2	37.0	38	10	US-09-745-237A-2330	Sequence 2330, Ap
405	12.2	37.0	20	16	US-10-236-392-72	Sequence 72, Appl	c 478	12.2	37.0	38	15	US-10-156-306-2056	Sequence 2056, Ap
406	12.2	37.0	20	17	US-10-303-633-72	Sequence 72, Appl	c 479	12.2	37.0	38	15	US-10-230-006-984	Sequence 984, Appl
407	12.2	37.0	20	17	US-10-416-530-11	Sequence 11, Appl	c 480	12.2	37.0	38	15	US-10-430-882-1134	Sequence 1134, Ap
408	12.2	37.0	20	17	US-10-317-248-22	Sequence 22, Appl	c 481	12.2	37.0	38	15	US-10-191-540-95	Sequence 95, Appl
409	12.2	37.0	20	17	US-10-317-248-98	Sequence 98, Appl	c 482	12.2	37.0	38	16	US-10-453-483-74	Sequence 74, Appl
410	12.2	37.0	22	15	US-10-296-995-97	Sequence 97, Appl	c 483	12.2	37.0	38	16	US-10-342-902-2804	Sequence 2804, Ap
411	12.2	37.0	24	10	US-09-992-665-333	Sequence 333, Appl	c 484	12.2	37.0	38	16	US-10-342-902-2974	Sequence 2974, Ap
412	12.2	37.0	24	10	US-09-940-188-2764	Sequence 2764, Ap	c 485	12.2	37.0	38	16	US-10-342-902-2974	Sequence 2974, Ap
413	12.2	37.0	25	9	US-09-866-108-4846	Sequence 4846, Ap	c 486	12.2	37.0	38	16	US-10-138-674-11470	Sequence 11470, A
414	12.2	37.0	25	9	US-09-866-108-15114	Sequence 15114, A	c 487	12.2	37.0	38	16	US-10-138-674-11470	Sequence 11470, A
415	12.2	37.0	25	15	US-10-098-263B-12001	Sequence 12001, A	c 488	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
416	12.2	37.0	25	15	US-10-098-263B-23699	Sequence 23699, A	c 489	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
417	12.2	37.0	25	15	US-10-098-263B-24966	Sequence 24966, A	c 490	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
418	12.2	37.0	25	15	US-10-098-263B-29509	Sequence 29509, A	c 491	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
419	12.2	37.0	25	15	US-10-098-263B-31484	Sequence 31484, A	c 492	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
420	12.2	37.0	25	15	US-10-098-263B-35724	Sequence 35724, A	c 493	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
421	12.2	37.0	25	15	US-10-098-263B-35954	Sequence 35954, A	c 494	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
422	12.2	37.0	25	15	US-10-098-263B-49008	Sequence 49008, A	c 495	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
423	12.2	37.0	25	15	US-10-098-263B-97709	Sequence 97709, A	c 496	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
424	12.2	37.0	25	15	US-10-098-263B-99425	Sequence 99425, A	c 497	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
425	12.2	37.0	25	15	US-10-098-263B-100962	Sequence 100962, A	c 498	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
426	12.2	37.0	25	15	US-10-098-263B-108332	Sequence 108332, A	c 499	12.2	37.0	38	16	US-10-138-674-12309	Sequence 12309, A
427	12.2	37.0	25	15	US-10-098-263B-119973	Sequence 119973, A	c 500	12.2	37.0	39	17	US-10-344-607-5	Sequence 5, Appl
428	12.2	37.0	25	15	US-10-321-163-41	Sequence 41, Appl	c 501	12.2	37.0	40	9	US-09-245-802-98	Sequence 98, Appl
429	12.2	37.0	25	15	US-10-413-661-41	Sequence 41, Appl	c 502	12.2	37.0	40	16	US-10-651-558-13	Sequence 13, Appl
430	12.2	37.0	25	15	US-10-084-839-3305	Sequence 3305, Ap	c 503	12.2	37.0	41	14	US-10-043-573-165	Sequence 165, Appl
431	12.2	37.0	25	17	US-10-723-361-4846	Sequence 4846, Ap	c 504	12.2	37.0	41	15	US-10-316-194-115	Sequence 115, Appl
432	12.2	37.0	25	17	US-10-723-361-15114	Sequence 15114, A	c 505	12.2	37.0	41	16	US-10-453-827-40	Sequence 40, Appl
433	12.2	37.0	25	17	US-10-789-129-41	Sequence 41, Appl	c 506	12.2	37.0	41	16	US-10-035-833A-42	Sequence 42, Appl
434	12.2	37.0	25	17	US-10-789-251-41	Sequence 41, Appl	c 507	12.2	37.0	41	16	US-10-035-833A-138	Sequence 138, Appl
435	12.2	37.0	25	17	US-10-789-968-41	Sequence 41, Appl	c 508	12.2	37.0	41	16	US-10-035-833A-1920	Sequence 1920, Ap
436	12.2	37.0	25	17	US-10-748-484-41	Sequence 41, Appl	c 509	12.2	37.0	41	16	US-10-035-833A-2209	Sequence 2209, Ap
437	12.2	37.0	26	10	US-09-907-111-220	Sequence 220, Appl	c 510	12.2	37.0	41	16	US-10-035-833A-3247	Sequence 3247, Ap
438	12.2	37.0	27	15	US-10-290-579-19	Sequence 19, Appl	c 511	12.2	37.0	41	16	US-10-035-833A-3919	Sequence 3919, Ap
439	12.2	37.0	28	9	US-10-328-675A-21	Sequence 21, Appl	c 512	12.2	37.0	41	16	US-10-035-833A-4515	Sequence 4515, Ap
440	12.2	37.0	29	16	US-09-733-042-32	Sequence 32, Appl	c 513	12.2	37.0	41	16	US-10-035-833A-5477	Sequence 5477, Ap
441	12.2	37.0	30	8	US-08-837-459-16	Sequence 2, Appl	c 514	12.2	37.0	41	16	US-10-085-853-8	Sequence 8, Appl
442	12.2	37.0	30	15	US-10-150-058-16	Sequence 16, Appl	c 515	12.2	37.0	43	13	US-10-443-466A-48	Sequence 48, Appl
443	12.2	37.0	31	9	US-09-801-274-1768	Sequence 1768, Ap	c 516	12.2	37.0	45	16	US-10-443-466A-81	Sequence 81, Appl
444	12.2	37.0	31	9	US-09-747-538-23	Sequence 23, Appl	c 517	12.2	37.0	45	16	US-10-443-466A-89	Sequence 89, Appl
445	12.2	37.0	31	9	US-09-782-504-2	Sequence 2, Appl	c 518	12.2	37.0	45	16	US-10-338-552-62	Sequence 62, Appl
446	12.2	37.0	33	16	US-10-336-672-2	Sequence 2, Appl	c 519	12.2	37.0	45	17	US-10-338-672-62	Sequence 62, Appl
447	12.2	37.0	33	16	US-10-459-729-1	Sequence 1, Appl	c 520	12.2	37.0	46	15	US-10-191-540-94	Sequence 94, Appl
448	12.2	37.0	33	16	US-10-459-729-1	Sequence 1, Appl	c 521	12.2	37.0	46	15	US-10-453-483-73	Sequence 73, Appl
449	12.2	37.0	33	9	US-09-987-456-139	Sequence 139, Appl	c 522	12.2	37.0	46	16	US-10-349-143-1500	Sequence 1500, Ap
450	12.2	37.0	35	10	US-09-921-819-47	Sequence 47, Appl	c 523	12.2	37.0	47	16		

524	12.2	37.0	47	16	US-10-349-143-2025	Sequence 2025, Ap	597	12.	36.4	38	10	US-09-780-533A-4033	Sequence 4033, Ap
525	12.2	37.0	47	16	US-10-349-143-2249	Sequence 2249, Ap	598	12	36.4	38	10	US-09-780-533A-4116	Sequence 4116, Ap
c 526	12.2	37.0	50	15	US-10-218-567-89	Sequence 89, Appl	599	12	36.4	38	10	US-09-780-533A-4186	Sequence 4186, Ap
527	12.2	37.0	50	15	US-10-322-360-91	Sequence 91, Appl	600	12	36.4	38	10	US-09-927-046-2416	Sequence 2416, Ap
528	12.2	37.0	50	16	US-10-131-827-2960	Sequence 2960, Ap	601	12	36.4	38	10	US-09-927-046-3146	Sequence 3146, Ap
c 529	12.2	37.0	50	16	US-10-131-827-4355	Sequence 4355, Ap	602	12	36.4	38	10	US-09-927-046-3360	Sequence 3360, Ap
c 530	12	36.4	20	16	US-10-187-659A-69	Sequence 69, Appl	603	12	36.4	38	10	US-09-877-478-2770	Sequence 2770, Ap
c 531	12	36.4	20	16	US-10-187-659A-126	Sequence 126, Appl	604	12	36.4	38	10	US-09-877-478-3210	Sequence 3210, Ap
c 532	12	36.4	22	9	US-09-803-687-1	Sequence 1, Appl	605	12	36.4	38	10	US-09-877-478-3408	Sequence 3408, Ap
c 533	12	36.4	23	14	US-10-146-574-10	Sequence 10, Appl	606	12	36.4	38	10	US-09-877-478-3446	Sequence 3446, Ap
c 534	12	36.4	24	15	US-10-117-109-21	Sequence 21, Appl	607	12	36.4	38	10	US-09-877-478-3481	Sequence 3481, Ap
c 535	12	36.4	24	15	US-10-117-109-22	Sequence 22, Appl	608	12	36.4	38	10	US-09-877-478-3611	Sequence 3611, Ap
c 536	12	36.4	24	15	US-10-117-109-23	Sequence 23, Appl	609	12	36.4	38	10	US-09-877-478-3657	Sequence 3657, Ap
c 537	12	36.4	24	15	US-10-117-109-24	Sequence 24, Appl	610	12	36.4	38	10	US-09-877-478-3761	Sequence 3761, Ap
c 538	12	36.4	24	15	US-10-407-078-21	Sequence 21, Appl	611	12	36.4	38	10	US-09-877-478-4230	Sequence 4230, Ap
c 539	12	36.4	24	15	US-10-407-078-22	Sequence 22, Appl	612	12	36.4	38	10	US-09-877-478-4504	Sequence 4504, Ap
c 540	12	36.4	24	15	US-10-407-078-23	Sequence 23, Appl	613	12	36.4	38	10	US-09-848-754A-3897	Sequence 3897, Ap
c 541	12	36.4	24	15	US-10-407-078-24	Sequence 24, Appl	614	12	36.4	38	10	US-09-848-754A-4001	Sequence 4001, Ap
c 542	12	36.4	24	16	US-10-332-553-1	Sequence 1, Appl	615	12	36.4	38	10	US-09-848-754A-4623	Sequence 4623, Ap
c 543	12	36.4	25	15	US-10-098-263B-2237	Sequence 2237, Ap	616	12	36.4	38	10	US-09-848-754A-5057	Sequence 5057, Ap
c 544	12	36.4	25	15	US-10-098-263B-2238	Sequence 2238, Ap	617	12	36.4	38	10	US-09-848-754A-5081	Sequence 5081, Ap
545	12	36.4	25	15	US-10-098-263B-2270	Sequence 2270, Ap	618	12	36.4	38	10	US-09-848-754A-5798	Sequence 5798, Ap
c 546	12	36.4	25	15	US-10-098-263B-2565	Sequence 2565, Ap	619	12	36.4	38	10	US-09-776-474-1329	Sequence 1329, Ap
c 547	12	36.4	25	15	US-10-098-263B-3254	Sequence 3254, Ap	620	12	36.4	38	10	US-09-930-423-2214	Sequence 2214, Ap
c 548	12	36.4	25	15	US-10-098-263B-5534	Sequence 5534, Ap	621	12	36.4	38	10	US-09-930-423-2648	Sequence 2648, Ap
549	12	36.4	25	15	US-10-098-263B-14685	Sequence 14685, A	622	12	36.4	38	10	US-09-930-423-3152	Sequence 3152, Ap
c 550	12	36.4	25	15	US-10-098-263B-32209	Sequence 32209, A	623	12	36.4	38	10	US-09-780-164-1096	Sequence 1096, Ap
c 551	12	36.4	25	15	US-10-098-263B-35648	Sequence 35648, A	624	12	36.4	38	10	US-09-780-164-1156	Sequence 1156, Ap
c 552	12	36.4	25	15	US-10-098-263B-74471	Sequence 74471, A	625	12	36.4	38	10	US-09-827-395A-1104	Sequence 1104, Ap
c 553	12	36.4	25	15	US-10-098-263B-104126	Sequence 104126, A	626	12	36.4	38	10	US-09-827-395A-1239	Sequence 1239, Ap
c 554	12	36.4	25	15	US-10-098-263B-107584	Sequence 107584, A	627	12	36.4	38	10	US-09-827-395A-1275	Sequence 1275, Ap
c 555	12	36.4	25	15	US-10-098-263B-108927	Sequence 108927, A	628	12	36.4	38	10	US-09-827-395A-1370	Sequence 1370, Ap
c 556	12	36.4	25	15	US-10-098-263B-108928	Sequence 108928, A	629	12	36.4	38	10	US-09-792-818-1315	Sequence 1315, Ap
c 557	12	36.4	25	17	US-10-775-169-3476	Sequence 3476, Ap	630	12	36.4	38	10	US-09-792-818-1554	Sequence 1554, Ap
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563	12	36.4	30	10	US-09-907-111-173	Sequence 173, Appl	636	12	36.4	38	15	US-10-230-006-981	Sequence 981, App
564	12	36.4	30	10	US-09-844-861A-70	Sequence 70, Appl	637	12	36.4	38	15	US-10-230-006-1004	Sequence 1004, Ap
565	12	36.4	30	15	US-10-283-881-57	Sequence 57, Appl	638	12	36.4	38	15	US-10-230-006-1023	Sequence 1023, Ap
566	12	36.4	31	9	US-09-801-274-1668	Sequence 1668, Ap	639	12	36.4	38	15	US-10-230-006-1049	Sequence 1049, Ap
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c 568	12	36.4	31	16	US-10-198-447A-11	Sequence 11, Appl	641	12	36.4	38	15	US-10-430-882-1104	Sequence 1104, Ap
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c 570	12	36.4	33	14	US-10-139-683-27	Sequence 27, Appl	643	12	36.4	38	15	US-10-430-882-1275	Sequence 1275, Ap
c 571	12	36.4	33	15	US-10-143-618-27	Sequence 27, Appl	644	12	36.4	38	15	US-10-430-882-1370	Sequence 1370, Ap
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c 573	12	36.4	34	17	US-10-641-001-11	Sequence 11, Appl	646	12	36.4	38	16	US-10-342-902-3210	Sequence 3210, Ap
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576	12	36.4	37	15	US-10-156-306-6231	Sequence 6231, Ap	649	12	36.4	38	16	US-10-342-902-3481	Sequence 3481, Ap
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585	12	36.4	37	17	US-10-287-949A-20488	Sequence 20488, A	658	12	36.4	38	16	US-10-138-674-11258	Sequence 11258, A
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587	12	36.4	38	9	US-09-864-785-1023	Sequence 1023, Ap	660	12	36.4	38	16	US-10-138-674-12053	Sequence 12053, A
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671	12	36.4	38	17	US-10-287-949A-10512	Sequence 10512, A	744	12	36.4	50	17	US-10-702-676A-22	Sequence 22, Appl
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675	12	36.4	38	17	US-10-287-949A-12453	Sequence 12453, A	748	11.8	35.8	19	15	US-10-084-839-3306	Sequence 3306, Ap
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678	12	36.4	38	17	US-10-287-949A-14125	Sequence 14125, A	751	11.8	35.8	20	15	US-10-032-585-5638	Sequence 5638, Ap
679	12	36.4	38	17	US-10-287-949A-14313	Sequence 14313, A	752	11.8	35.8	20	16	US-10-630-399-45	Sequence 45, Appl
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684	12	36.4	38	17	US-10-712-672-3478	Sequence 3478, Ap	757	11.8	35.8	24	10	US-09-940-185-324	Sequence 324, Ap
685	12	36.4	38	17	US-10-712-672-3648	Sequence 3648, Ap	758	11.8	35.8	24	10	US-09-940-185-324	Sequence 49, Appl
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699	12	36.4	39	14	US-10-075-846-80	Sequence 80, Appl	772	11.8	35.8	25	15	US-10-098-263B-40169	Sequence 40169, A
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701	12	36.4	41	9	US-09-823-829-45	Sequence 45, Appl	774	11.8	35.8	25	15	US-10-098-263B-49679	Sequence 49679, A
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706	12	36.4	41	15	US-10-035-833A-2984	Sequence 2984, Ap	779	11.8	35.8	25	15	US-10-098-263B-83728	Sequence 83728, A
707	12	36.4	41	18	US-10-843-720-69	Sequence 69, Appl	780	11.8	35.8	25	15	US-10-098-263B-101436	Sequence 101436, A
708	12	36.4	42	15	US-10-852-289-69	Sequence 69, Appl	781	11.8	35.8	25	15	US-10-098-263B-110744	Sequence 110744, A
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716	12	36.4	47	8	US-10-251-085B-52	Sequence 52, Appl	789	11.8	35.8	26	9	US-09-733-741A-5	Sequence 5, Appl
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718	12	36.4	48	16	US-10-251-085B-60	Sequence 60, Appl	791	11.8	35.8	26	15	US-10-317-444-59	Sequence 59, Appl
719	12	36.4	48	16	US-10-251-085B-60	Sequence 60, Appl	792	11.8	35.8	26	15	US-10-317-444-60	Sequence 60, Appl
720	12	36.4	48	17	US-10-737-252-52	Sequence 52, Appl	793	11.8	35.8	26	17	US-10-738-455-8	Sequence 8, Appl
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722	12	36.4	48	17	US-10-737-252-60	Sequence 60, Appl	795	11.8	35.8	27	16	US-10-204-889-3	Sequence 3, Appl
723	12	36.4	49	10	US-09-801-485-5	Sequence 5, Appl	796	11.8	35.8	27	16	US-10-829-430-3	Sequence 3, Appl
724	12	36.4	49	13	US-10-006-009-7	Sequence 7, Appl	797	11.8	35.8	28	16	US-10-401-520-126	Sequence 126, Appl
725	12	36.4	49	13	US-10-006-009-18	Sequence 18, Appl	798	11.8	35.8	31	9	US-09-801-274-593	Sequence 593, Appl
726	12	36.4	49	15	US-10-310-677-160	Sequence 160, Appl	799	11.8	35.8	31	9	US-09-801-274-845	Sequence 845, Appl
727	12	36.4	49	17	US-10-471-136-10	Sequence 10, Appl	800	11.8	35.8	31	9	US-09-801-274-1699	Sequence 1699, Ap
728	12	36.4	50	10	US-09-993-346-478	Sequence 478, Appl	801	11.8	35.8	31	18	US-10-474-239-4	Sequence 4, Appl
729	12	36.4	50	13	US-10-006-009-22	Sequence 22, Appl	802	11.8	35.8	33	14	US-10-318-142-16	Sequence 431, Appl
730	12	36.4	50	15	US-10-144-679-34	Sequence 34, Appl	803	11.8	35.8	35	9	US-09-765-272-431	Sequence 22, Appl
731	12	36.4	50	15	US-10-144-679-34	Sequence 34, Appl	804	11.8	35.8	35	9	US-09-747-538-22	Sequence 16, Appl
732	12	36.4	50	16	US-10-131-827-1384	Sequence 1384, Ap	805	11.8	35.8	35	9	US-09-757-207-16	Sequence 3849, Ap
733	12	36.4	50	16	US-10-131-827-2208	Sequence 2208, Ap	806	11.8	35.8	35	15	US-10-276-709-2	Sequence 2, Appl
734	12	36.4	50	16	US-10-131-827-4257	Sequence 4257, Ap	807	11.8	35.8	35	15	US-10-360-101-32	Sequence 32, Appl
735	12	36.4	50	16	US-10-131-827-5603	Sequence 5603, Ap	808	11.8	35.8	35	16	US-10-360-101-32	Sequence 2281, Ap
736	12	36.4	50	16	US-10-131-827-5603	Sequence 5603, Ap	809	11.8	35.8	36	9	US-09-504-231A-2281	Sequence 2281, Ap
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738	12	36.4	50	16	US-10-131-827-7160	Sequence 7160, Ap	811	11.8	35.8	36	14	US-10-056-414-640	Sequence 1, Appl
739	12	36.4	50	16	US-10-131-827-7454	Sequence 7454, Ap	812	11.8	35.8	36	15	US-10-331-446-1	Sequence 1, Appl
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741	12	36.4	50	16	US-10-131-827-7645	Sequence 7645, Ap	814	11.8	35.8	36	15	US-10-129-422-10	Sequence 10, Appl
742	12	36.4	50	16	US-10-144-094-22	Sequence 22, Appl	815	11.8	35.8	36	15		

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C 817	11.8	35.8	37	9	US-09-860-996-3	Sequence 3, Appl	C 890	11.8	35.8	47	16	US-10-349-143-1709	Sequence 1709, Ap
C 818	11.8	35.8	37	9	US-09-864-785-2001	Sequence 2001, Ap	C 891	11.8	35.8	47	16	US-10-349-143-3761	Sequence 3761, Ap
C 819	11.8	35.8	37	9	US-09-864-785-3850	Sequence 3850, Ap	C 892	11.8	35.8	48	10	US-09-893-512-6	Sequence 6, Appl
C 820	11.8	35.8	37	10	US-09-927-046-3744	Sequence 3744, Ap	C 893	11.8	35.8	49	10	US-09-405-032-96	Sequence 96, Appl
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C 822	11.8	35.8	37	10	US-09-848-754A-6451	Sequence 6451, Ap	C 895	11.8	35.8	50	16	US-10-131-827-1793	Sequence 1793, Ap
C 823	11.8	35.8	37	10	US-09-827-395A-1579	Sequence 1579, Ap	C 896	11.8	35.8	50	16	US-10-131-827-2438	Sequence 2438, Ap
C 824	11.8	35.8	37	10	US-09-827-395A-1809	Sequence 1809, Ap	C 897	11.8	35.8	50	16	US-10-131-827-6152	Sequence 6152, Ap
C 825	11.8	35.8	37	15	US-10-156-306-2516	Sequence 2516, Ap	C 898	11.8	35.8	50	16	US-10-035-833A-7114	Sequence 7114, Ap
C 826	11.8	35.8	37	15	US-10-430-882-1579	Sequence 1579, Ap	C 899	11.8	35.8	50	16	US-10-343-319-47	Sequence 47, Appl
C 827	11.8	35.8	37	15	US-10-430-882-1809	Sequence 1809, Ap	C 900	11.8	35.8	50	16	US-10-343-319-64	Sequence 64, Appl
C 828	11.8	35.8	37	16	US-10-138-674-18481	Sequence 18481, A	C 901	11.8	35.8	50	16	US-10-343-319-65	Sequence 65, Appl
C 829	11.8	35.8	37	16	US-10-138-674-18682	Sequence 18682, A	C 902	11.8	35.8	50	16	US-10-343-319-67	Sequence 67, Appl
C 830	11.8	35.8	37	16	US-10-138-674-20240	Sequence 20240, A	C 903	11.8	35.8	50	16	US-10-343-319-68	Sequence 68, Appl
C 831	11.8	35.8	37	16	US-10-138-674-20261	Sequence 20261, A	C 904	11.6	35.2	17	9	US-09-865-018-20	Sequence 20, Appl
C 832	11.8	35.8	37	16	US-10-138-674-20545	Sequence 20545, A	C 905	11.6	35.2	18	9	US-09-865-018-21	Sequence 21, Appl
C 833	11.8	35.8	37	16	US-10-138-674-20575	Sequence 20575, A	C 906	11.6	35.2	20	15	US-10-027-983-72	Sequence 72, Appl
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APPLICANT:	Kevin P. Baker
APPLICANT:	Luc A. Botstre
APPLICANT:	Dave Desnoyers
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APPLICANT:	Margaret Ann Rol
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APPLICANT:	Daniel Tumas
APPLICANT:	Colin K. Watanabe
APPLICANT:	P. Mickey Willia
APPLICANT:	William I. Wood
APPLICANT:	Zemin Zang
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FILE OF INVENTION: ACIDS	
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; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
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; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
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Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGAGTGCAAGGCGTCTGCT 26
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Db 43 GCCACAGTTGGCAGAGATGTTGCT 18

RESULT 5

US-10-066-273-61/c
; Sequence 61, Application US/10066273
; Publication No. US20030032062A1

GENERAL INFORMATION:

; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas P. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C2
; CURRENT APPLICATION NUMBER: US/10/066.273
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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Query Match          49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCACATGAGTGGCAAGCGGTGTGCT 26
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Db 43 GCCACAGTGTGGCAAGATGTGTGCT 18

RESULT 6
US-10-066-494-61/c
; Sequence 61, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kjavlin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tunas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C9
; CURRENT APPLICATION NUMBER: US/10/066,494
; CURRENT FILING DATE: 2002-02-01
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Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGCACAGGGCTCTGGT 26
Db 43 GCCACATGAGTGCACAGGGCTCTGGT 18

RESULT 7
US-10-066-269-61/c
; Sequence 61, Application US/10066269
; Publication No. US20030040014A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
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; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C4
; CURRENT APPLICATION NUMBER: US/10/066,269
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: 60/079294

Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;

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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. NO. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGCGTCTGCT 26
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Db 43 GCCACAGTTGTGGCAGATGCTGCT 18

RESULT 8
US-10-066-211-61/c
; Sequence 61, Application US/10066211
; Publication No. US20030044844A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleon Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C8
; CURRENT APPLICATION NUMBER: US/10/066,211
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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Query Match          49.7%; Score 16.4; DB 14; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 43 GCCACAGTTGTGGCAAGATGTGTGT 18
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RESULT 9

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US-10-066-193-61/c
; Sequence 61, Application US/10066193
; Publication No. US20030044902A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
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; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C3
; CURRENT APPLICATION NUMBER: US/10/066.193
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/099601
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; PRIOR APPLICATION NUMBER: 60/099812
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RESULTS TO
US-10-226-739-61/c
; Sequence 61, Application US/10226739
; Publication No. US20030104558A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi
; APPLICANT: Baker
; APPLICANT: Botstein
; APPLICANT: Desnoyers
; APPLICANT: Eaton
; APPLICANT: Ferrara
; APPLICANT: Fong
; APPLICANT: Gao
; APPLICANT: Gerber, Gerritsen

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; APPLICANT: Goddard
 ; APPLICANT: Godowski
 ; APPLICANT: Gurney
 ; APPLICANT: Kljavin
 ; APPLICANT: Mather
 ; APPLICANT: Napier
 ; APPLICANT: Pan
 ; APPLICANT: Paoni
 ; APPLICANT: Roy
 ; APPLICANT: Stewart
 ; APPLICANT: Tamas
 ; APPLICANT: Watanabe
 ; APPLICANT: Williams
 ; APPLICANT: Wood
 ; APPLICANT: Zang

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3130R1C10

; CURRENT FILING DATE: 2002-08-23
 ; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 10/002,796
 ; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: PCT/US99/20111
 ; PRIOR FILING DATE: 1999-09-01

; PRIOR APPLICATION NUMBER: US 09/403,297
 ; PRIOR FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: US 60/106,032
 ; PRIOR FILING DATE: 1998-10-28

; NUMBER OF SEQ ID NOS: 151
 ; SEQ ID NO 61

; LENGTH: 43
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; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-226-739-61

Query Match 49.7%; Score 16.4; DB 15; Length 43;
 Best Local Similarity 76.9%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGGCAAGCGCTGCTGT 26
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 Db 43 GCCACAGTTGTGGCAAGATGTGCTGT 18

RESULT 11

US-10-066-198-61/c

; Sequence 61, Application US/10066198

; Publication No. US20030170721A1

; GENERAL INFORMATION:

; APPLICANT: Avi J. Ashkenazi

; APPLICANT: Kevin P. Baker

; APPLICANT: David A. Botstein

; APPLICANT: Luc Desnoyers

; APPLICANT: Dan L. Eaton

; APPLICANT: Napoleone Ferrara

; APPLICANT: Sherman Fong

; APPLICANT: Wei-Qiang Gao

; APPLICANT: Hanspeter Gerber

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; APPLICANT: Audrey Goddard

; APPLICANT: Paul J. Godowski

; APPLICANT: Austin L. Gurney

; APPLICANT: Ivar J. Kljavin

; APPLICANT: Jennie P. Mather

; APPLICANT: Mary A. Napier

; APPLICANT: James Pan

; APPLICANT: Nicholas F. Paoni

; APPLICANT: Margaret Ann Roy

; APPLICANT: Timothy A. Stewart

; APPLICANT: Daniel Tamas
 ; APPLICANT: Colin K. Watanabe
 ; APPLICANT: P. Mickey Williams
 ; APPLICANT: William I. Wood
 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3130R1C6
 ; CURRENT FILING DATE: 2002-02-01
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; PRIOR FILING DATE: 1999-10-18
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; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/423844
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 09/522342
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 09/548815
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 09/664610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/665350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/767609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/808689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/866028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/870574
; PRIOR FILING DATE: 2001-05-30

;
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/886342
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: PCT/US98/14552
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/19093
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/25190
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
;
Query Match 49.7%; Score 16.4; DB 15; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCAAGCGCTCTGGT 26
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DB 43 GCCACAGTTGTGGCAAGATGTGGT 18

RESULT 12
US-10-066-203-61/c
; Sequence 61, Application US/10066203
; Publication No. US20030180796A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleon Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Geixtsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3130RLCS
CURRENT APPLICATION NUMBER: US/10/066,203
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/095998
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/097000
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/099601
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/145070
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1998-07-26
PRIOR APPLICATION NUMBER: 60/149396
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1998-12-07
PRIOR APPLICATION NUMBER: 08/918874
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 08/933821
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 08/960507
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 09/114844
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: 09/136801
PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: 09/136804
PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: 09/136828
PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: 09/158342
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/202088
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: 09/254311
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/254460
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/254465
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 09/284663
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 09/332928
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/332929
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/33075
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/33077
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403296
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/423844
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/808689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/870574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US98/18824

Query Match	DB 15;	Length 43;	DB 15;	Length 25;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;				
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY 1 GCCACATGATGGCGAAGCGCTCTGGT 26				
DB 43 GCCACATGTTGTGGCAAGATGTGTGGT 18				
RESULT 13				
US-10-098-263B-65283/c				
Sequence 65283, Application US/10098263B				
Publication No. US20030104410A1				
GENERAL INFORMATION:				
APPLICANT: Mittman, Michael				
TITLE OF INVENTION: Human Microarray				
FILE REFERENCE: 3118.1				
CURRENT APPLICATION NUMBER: US/10/098,263B				
CURRENT FILING DATE: 2003-01-08				
PRIOR APPLICATION NUMBER: 60/276,759				
PRIOR FILING DATE: 2001-03-16				
NUMBER OF SEQ ID NOS: 131066				
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1				
SEQ ID NO 65283				
LENGTH: 25				
TYPE: DNA				
ORGANISM: Homo sapien				
US-10-098-263B-65283				
Query Match 47.3%; Score 15.6; DB 15;				
Best Local Similarity 81.8%; Pred. No. 3.5e+03;				
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
QY 1 GCCACATGATGGCGAAGCGCTC 22				
DB 22 GCCACATGATGGCGCGGCAC 1				
RESULT 14				
US-10-667-271-1525				
Sequence 1525, Application US/10667271				
Publication No. US20040209831A1				
GENERAL INFORMATION:				
APPLICANT: Sirna Therapeutics				
APPLICANT: McSwiggen, James				
APPLICANT: Macejak, Dennis				
APPLICANT: Beigelman, Leonid				
APPLICANT: Morisseau, David				

OTHER INFORMATION: 2'-deoxy-2'-fluoro
 NAME/KEY: misc feature
 LOCATION: (18)..(19)
 OTHER INFORMATION: 2'-deoxy
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (20)..(21)
 OTHER INFORMATION: n stands for thymidine
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (21)..(21)
 OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
 US-10-667-271-1525

Query Match 46.7%; Score 15.4; DB 18; Length 21;
 Best Local Similarity 76.5%; Pred. No. 4.3e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCCAAGGCGTCTGGTGA 28
 Db 3 GCCAAGGCGUCUGGUGA 19

RESULT 15

US-10-667-271-1537/c

; Sequence 1537, Application US/10667271
 ; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBH02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; PRIOR FILING DATE: 2003-09-16

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1537

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: 2'-deoxy-2'-fluoro

; FEATURE:

; NAME/KEY: misc feature
 LOCATION: (3)..(3)
 OTHER INFORMATION: 2'-O-methyl
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4)..(5)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (6)..(8)
 OTHER INFORMATION: 2'-O-methyl
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (9)..(9)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (10)..(10)
 OTHER INFORMATION: 2'-O-methyl
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (11)..(14)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (15)..(16)
 OTHER INFORMATION: 2'-O-methyl
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (17)..(18)
 OTHER INFORMATION: 2'-deoxy-2'-fluoro
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (19)..(19)
 OTHER INFORMATION: 2'-O-methyl
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (20)..(20)
 OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (20)..(21)
 OTHER INFORMATION: n stands for thymidine
 US-10-667-271-1537

Query Match 46.7%; Score 15.4; DB 18; Length 21;
 Best Local Similarity 94.1%; Pred. No. 4.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCCAAGGCGTCTGGTGA 28
 Db 17 GCCAAGGCGTCTGGTGA 1

RESULT 16

US-10-667-271-1582

; Sequence 1582, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBH02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

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; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1582
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
; US-10-667-271-1582
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 76.5%; Pred. No. 4.3e+03;
; Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGGA 28
; Db 3 GCCAAGGCGCUCUGGUGA 19
;
; RESULT 17
; US-10-667-271-1594/c
; Sequence 1594, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 94.1%; Pred. No. 4.3e+03;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGGA 28
; Db 17 GCCAAGGCGCTGCTGGA 1
;
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1594
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; US-10-667-271-1594
;
; Query Match 46.7%; Score 15.4; DB 18; Length 21;
; Best Local Similarity 94.1%; Pred. No. 4.3e+03;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 12 GCCAAGGCGCTGCTGGA 28
; Db 17 GCCAAGGCGCTGCTGGA 1
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RESULT 18
US-10-098-263B-57900
; Sequence 57900, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 57900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-57900

Query Match          46.7%; Score 15.4; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CACATGACTGGCAAGCGCTCTGGTG 27
Db 1 CACATGAGGGTCAAGTCCTCCGAG 25

RESULT 19
US-10-233-996-8
; Sequence 8, Application US/10233996
; Publication No. US20030096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB-00503 AND LB-00506 SPECIFIC FOR HUMAN 4-1
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
; FILE REFERENCE: 4363-0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer KXD
US-10-233-996-8

Query Match          46.7%; Score 15.4; DB 14; Length 30;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 8 GAGTGGCAAGCGCTCTGGTGATACC 32
Db 2 GACTGCCCAGGTTTWTGTTGATACC 26

RESULT 20
US-09-855-797A-28/c
; Sequence 28, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
US-09-855-797A-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 21
US-09-907-900-28/c
; Sequence 28, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-907-900-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 22
US-09-907-719-28/c
; Sequence 28, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
US-09-907-719-28/c

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
```

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; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-855-797A-28

Query Match          46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
```

;; APPLICANT: Fox, Donna K.
;; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
;; FILE REFERENCE: 0942,2850004
;; CURRENT APPLICATION NUMBER: US/09/907,719
;; CURRENT FILING DATE: 2001-07-19
;; PRIOR APPLICATION NUMBER: US/09/177,387
;; PRIOR FILING DATE: 1998-10-23
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 28
;; LENGTH: 33
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; OTHER INFORMATION: oligonucleotide
US-09-907-719-28

Query Match 46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGCTGATA 30
|||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 23

US-09-432-085-28/c
; Sequence 28, Application US/09432085
; Publication No. US2003010010A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 33 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cDNA
US-09-432-085-28

Query Match 46.7%; Score 15.4; DB 10; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGCTGATA 30
|||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 24

US-09-985-448-28/c
; Sequence 28, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942,2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-985-448-28

Query Match 46.7%; Score 15.4; DB 10; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGCTGATA 30
|||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 25

US-10-058-292-28/c
; Sequence 28, Application US/10058292
; Publication No. US2003005452A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934


```
;
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-162-879-28
Query Match 46.7%; Score 15.4; DB 14; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 28
US-10-300-892-28/c
; Sequence 28, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-10-300-892-28

Query Match 46.7%; Score 15.4; DB 15; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 29
US-10-680-316-28/c
; Sequence 28, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28

;
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-10-680-316-28

Query Match 46.7%; Score 15.4; DB 16; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 30
US-10-815-730-28/c
; Sequence 28, Application US/10815730
; Publication No. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815,730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-10-815-730-28

Query Match 46.7%; Score 15.4; DB 17; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
   ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8

RESULT 31
US-10-820-133-28/c
; Sequence 28, Application US/10820133
; Publication No. US20040171157A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
```



```
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-820-133-28
Query Match          46.7%; Score 15.4; DB 17; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 32
US-10-796-868A-28/c
; Sequence 28, Application US/10796868A
; Publication No. US20040219673A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
; FILE REFERENCE: 0942-285000K
; CURRENT APPLICATION NUMBER: US/10/796,868A
; CURRENT FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 09/498,074
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/005,476
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 08/663,002
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/486,139
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA/RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CAT right PCR primer
US-10-796-868A-28

Query Match          46.7%; Score 15.4; DB 18; Length 33;
Best Local Similarity 76.0%; Pred. No. 4.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
    ||||| ||||| ||||| |||||
Db 32 ATGAGTGGCAGGGCGGGCGGTAATA 8

RESULT 33
US-10-430-984-1
; Sequence 1, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: Crew, Mark D
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
; FILE REFERENCE: 8793-53098
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 1
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; LENGTH: 44
; TYPE: DNA
; ORGANISM: human leukocyte antigen E
US-10-430-984-1

Query Match          46.7%; Score 15.4; DB 18; Length 44;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GCCACATGAGTGCAAGGCGTCTGGTGATACCG 33
    ||||| ||||| ||||| ||||| |||||
Db 11 GCGACATGGGTGGTGGCGGTCTCTGGTGGCG 43

RESULT 34
US-10-411-954-85/c
; Sequence 85, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 85
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-85

Query Match          46.1%; Score 15.2; DB 15; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 AGTGGCAAGGCGTCTGGTGA 28
    ||||| ||||| ||||| |||||
Db 37 AGTGGCAGGGGGCGCTGGTGA 18

RESULT 35
US-10-411-954-282/c
; Sequence 282, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 282
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-282

Query Match          46.1%; Score 15.2; DB 15; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 36
US-10-617-070-85/c
; Sequence 85, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-85

Query Match 46.1%; Score 15.2; DB 16; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 37
US-10-617-070-282/c
; Sequence 282, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 282
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-282

Query Match 46.1%; Score 15.2; DB 16; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 38
US-10-617-070-382/c
; Sequence 382, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 382
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-382

Query Match 46.1%; Score 15.2; DB 16; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGCTCTGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 39
US-10-191-540-87/c
; Sequence 87, Application US/10191540
; Publication No. US20030224494A1
; GENERAL INFORMATION:
; APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tsutomu Honma
; TITLE OF INVENTION: Polyhydroxyalkanoate-containing structure and manufacturing method
; FILE REFERENCE: CF016534
; CURRENT APPLICATION NUMBER: US/10/191,540
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: JP P2001-210052
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: JP P2002-172978
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for PCR multiplication
US-10-191-540-87

```
Query Match      45.5%; Score 15; DB 15; Length 38;
Best Local Similarity 67.7%; Pred. No. 6.8e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
Db 38 CAACGTGACCAGCACCGCGTTTATTGATACC 8

RESULT 40
US-10-453-483-66/c
; Sequence 86, Application US/10453483
; Publication No. US20040005638A1
; GENERAL INFORMATION:
; APPLICANT: Tetsuya Yano
; APPLICANT: Tutomu Honma
; APPLICANT: Tsuyoshi No. US20040005638A1oto
; APPLICANT: Shinya Kozaki
; TITLE OF INVENTION: Immunoassay, reagent for immunoassay, and production method of th
; FILE REFERENCE: CF017318
; CURRENT APPLICATION NUMBER: US/10/453,483
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: JP P2002-173027
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; PRIOR APPLICATION NUMBER: JP P2003-127099
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; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: complementary to 65
US-10-453-483-66

Query Match      45.5%; Score 15; DB 16; Length 38;
Best Local Similarity 67.7%; Pred. No. 6.8e+03;
Matches 21; Conservative 0; Mismatches -10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
Db 38 CAACGTGACCAGCACCGCGTTTATTGATACC 8

Search completed: November 24, 2004, 03:42:34
Job time : 163.842 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1582.15 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-5

Perfect score: 33

Sequence: 1 gccacatgagtcgaaggcgtctggtataccg 33

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gssi.*

9: gb_gssi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	15.6	47.3	50	1	AU103444
3	15.6	47.3	50	1	AU103445
4	15	45.5	25	8	AZ582580
5	15	45.5	50	1	AU103463
6	14.6	44.2	36	8	AZ481987
7	14.4	43.6	34	8	AZ329468
8	14.4	43.6	34	8	AZ480659
9	14.4	43.6	38	8	AZ818206
10	14.2	43.0	50	1	AU103440
11	14.2	43.0	50	1	AU103448
12	14	42.4	36	8	AZ783989
13	14	42.4	47	8	T51935
14	14	42.4	47	8	AZ490009
15	14	42.4	49	4	BG489537
16	13.8	41.8	45	2	BF578678
17	13.8	41.8	43	8	AZ664916
18	13.8	41.8	50	1	AZ206278
19	13.8	41.8	50	9	EX289625
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22	13.4	40.6	44	8	AZ990977
23	13.4	40.6	46	8	BH853635
24	13.4	40.6	50	1	AU103740

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100	12	36.4	36	8	AZ663045	1M0542P19	173	11.6	35.2	41	8	AZ449036	1M0247P02
101	12	36.4	36	8	BH902764	SALK_0990	174	11.6	35.2	42	4	BI665361	603288893
102	12	36.4	37	1	A1721492	IC28d01.x	175	11.6	35.2	42	4	BM400471	5009-0-73
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104	12	36.4	40	8	AZ952424	2M0217B17	c 177	11.6	35.2	43	1	AA534781	nf1e01.s
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106	12	36.4	44	8	AQ073165	EP(X)0371	179	11.6	35.2	44	9	TA294F02P	T. brucei
107	12	36.4	45	6	CB074815	EST00060	180	11.6	35.2	44	9	AG221236	Lotus cor
108	12	36.4	47	8	AZ815240	2M0083C19	181	11.6	35.2	46	2	BE884491	601510781
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113	12	36.4	50	1	AU105488	AU105488	186	11.6	35.2	50	1	AU103627	AU103627
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117	12	36.4	50	9	BE589868	Arabiidops	c 190	11.6	35.2	50	1	AU106866	AU106866
118	11.8	35.8	23	8	AZ447157	1M0243G22	191	11.6	35.2	50	1	AU106914	AU106914
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122	11.8	35.8	33	8	BZ770290	SALK 1432	195	11.6	35.2	50	1	AU106920	AU106920
123	11.8	35.8	34	1	A1047833	ud64C05.x	196	11.6	35.2	50	1	AU106922	AU106922
124	11.8	35.8	34	1	A1132558	ue33b11.x	c 197	11.6	35.2	50	1	AU107349	AU107349
125	11.8	35.8	36	8	AZ583007	1M0376N11	198	11.6	35.2	50	2	AW248122	2819697.5
126	11.8	35.8	37	1	AA423390	ve39c02.r	c 199	11.6	35.2	50	8	AF087243	AF087243
127	11.8	35.8	38	1	AI182596	AI182596	200	11.6	35.2	50	8	AZ921706	1006031E1
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129	11.8	35.8	38	1	AI255816	ui89e11.x	c 202	11.6	35.2	50	9	TA179D03P	TA179D03P
130	11.8	35.8	38	1	AI256061	ui94f01.x	203	11.4	34.5	22	8	AZ588797	1M0397D21
131	11.8	35.8	38	1	AI256061	ui94f01.x	204	11.4	34.5	28	8	AZ410454	1M0182K16
132	11.8	35.8	38	1	AI786184	uj52c08.x	205	11.4	34.5	29	8	AZ658502	1M0535M12
133	11.8	35.8	38	1	AI875207	1J30h03.x	206	11.4	34.5	32	4	AZ799831	2M0057G03
134	11.8	35.8	38	1	AA619263	vo50g04.r	207	11.4	34.5	34	5	EX557840	EX557840
135	11.8	35.8	39	1	AI256185	ui96a06.x	208	11.4	34.5	35	6	CA585970	CA585970
136	11.8	35.8	39	9	DME545087	Drosophila	209	11.4	34.5	35	6	BG914491	602813233
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142	11.8	35.8	41	8	AZ580746	1M0369111	c 215	11.4	34.5	40	1	AI084761	Oz79h04.x
143	11.8	35.8	42	8	AQ939867	hmbxgs13	216	11.4	34.5	41	9	BX289962	Arabiidops
144	11.8	35.8	42	8	AZ586799	1M0394F04	217	11.4	34.5	41	9	CNS07ERI	Anopheles
145	11.8	35.8	42	8	BH800878	1008028B0	218	11.4	34.5	43	8	AZ512618	1M0358P17
146	11.8	35.8	44	8	BZ377472	SALK 0828	c 219	11.4	34.5	43	8	BH644282	1008043D0
147	11.8	35.8	44	9	AG198602	Pan trogl	220	11.4	34.5	44	8	BH905069	SALK 1055
148	11.8	35.8	46	7	R66026	Yp12f04.r1	221	11.4	34.5	44	8	AZ639684	1M0501L13
149	11.8	35.8	46	9	TA314C05P	T. brucei	c 222	11.4	34.5	45	8	AZ412102	1M0185J24
150	11.8	35.8	47	8	BG777442	602664745	c 223	11.4	34.5	45	9	CG806284	1118067G1
151	11.8	35.8	47	8	AZ832536	2M0113E05	c 224	11.4	34.5	46	1	AA834374	of67e02.s
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154	11.8	35.8	49	8	AZ658888	1M0335J21	227	11.4	34.5	46	9	BX125933	BX125933
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156	11.8	35.8	50	1	AU102540	AU102540	c 229	11.4	34.5	49	8	AZ830102	2M0109E11
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158	11.8	35.8	50	1	AU105075	AU105075	231	11.4	34.5	49	9	CG723151	T. brucei
159	11.8	35.8	50	1	AU105083	AU105083	232	11.4	34.5	50	1	AU103895	AU103895
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162	11.8	35.8	50	4	BG721131	602892987	235	11.4	34.5	50	1	AU105170	AU105170
163	11.8	35.8	50	7	CN936328	000304AVB	236	11.4	34.5	50	1	AU105174	AU105174
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165	11.6	35.2	30	8	AZ666375	1M0548C20	238	11.4	34.5	50	1	AU105176	AU105176
166	11.6	35.2	33	2	BE539711	601059362	239	11.4	34.5	50	1	AU105644	AU105644
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169	11.6	35.2	40	1	AI499289	tc09c08.x	242	11.4	34.5	50	1	AU105651	AU105651
170	11.6	35.2	40	4	BM3944053	50072-2-1	243	11.4	34.5	50	1	AU105651	AU105651

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245	11.4	34.5	50	1	AUI05654	AUI05654	AUI05654	318	11.2	33.9	50	1	AUI03789	AUI03789
246	11.4	34.5	50	1	AUI06240	AUI06240	AUI06240	319	11.2	33.9	50	1	AUI03799	AUI03799
247	11.4	34.5	50	1	AUI06872	AUI06872	AUI06872	320	11.2	33.9	50	1	AUI03805	AUI03805
248	11.4	34.5	50	1	AUI08081	AUI08081	AUI08081	321	11.2	33.9	50	1	AUI03868	AUI03868
249	11.4	34.5	50	1	AUI08081	AUI08081	AUI08081	322	11.2	33.9	50	1	AUI04730	AUI04730
250	11.4	34.5	50	2	AUI08536	AUI08536	AUI08536	323	11.2	33.9	50	1	AUI05060	AUI05060
251	11.4	34.5	19	8	B2425239	B2425239	B2425239	324	11.2	33.9	50	1	AUI05482	AUI05482
252	11.2	33.9	21	8	A2862876	A2862876	A2862876	325	11.2	33.9	50	1	AUI05483	AUI05483
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254	11.2	33.9	25	1	A1594892	A1594892	A1594892	327	11.2	33.9	50	1	AUI06295	AUI06295
255	11.2	33.9	26	8	A2389492	A2389492	A2389492	328	11.2	33.9	50	1	AUI06296	AUI06296
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259	11.2	33.9	29	1	AJ807265	AJ807265	AJ807265	332	11.2	33.9	50	1	AUI07300	AUI07300
260	11.2	33.9	31	1	AJ619417	AJ619417	AJ619417	333	11.2	33.9	50	1	AUI07302	AUI07302
261	11.2	33.9	31	9	EX535270	EX535270	EX535270	334	11.2	33.9	50	1	AUI07308	AUI07308
262	11.2	33.9	33	8	A2805273	A2805273	A2805273	335	11.2	33.9	50	1	AUI07309	AUI07309
263	11.2	33.9	34	9	TA244E09Q	TA244E09Q	TA244E09Q	336	11.2	33.9	50	1	AUI07311	AUI07311
264	11.2	33.9	35	4	BI769066	BI769066	BI769066	337	11.2	33.9	50	1	AUI07313	AUI07313
265	11.2	33.9	35	4	BI906671	BI906671	BI906671	338	11.2	33.9	50	1	AUI07315	AUI07315
266	11.2	33.9	36	1	AJ652672	AJ652672	AJ652672	339	11.2	33.9	50	1	AUI07316	AUI07316
267	11.2	33.9	36	8	A2581836	A2581836	A2581836	340	11.2	33.9	50	1	AUI07317	AUI07317
268	11.2	33.9	37	4	BI766183	BI766183	BI766183	341	11.2	33.9	50	1	AUI07318	AUI07318
269	11.2	33.9	37	8	A20236	A20236	A20236	342	11.2	33.9	50	1	AUI07319	AUI07319
270	11.2	33.9	37	8	A2782753	A2782753	A2782753	343	11.2	33.9	50	1	AUI07321	AUI07321
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272	11.2	33.9	38	8	A2499479	A2499479	A2499479	345	11.2	33.9	50	1	AUI07330	AUI07330
273	11.2	33.9	39	8	B8874819	B8874819	B8874819	346	11.2	33.9	50	1	AUI07332	AUI07332
274	11.2	33.9	39	4	BI818665	BI818665	BI818665	347	11.2	33.9	50	1	AUI07741	AUI07741
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276	11.2	33.9	39	8	A2601737	A2601737	A2601737	349	11.2	33.9	50	8	AZ666374	1M0548C19
277	11.2	33.9	39	9	CG730671	CG730671	CG730671	350	11.2	33.9	50	8	AZ603049	2M0063A17
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285	11.2	33.9	40	8	BZ383943	BZ383943	BZ383943	358	11.2	33.9	27	8	AZ978415	2M0254D15
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294	11.2	33.9	44	8	AZ322603	AZ322603	AZ322603	367	11.2	33.9	34	9	TA102C06P	AL462338 T. brucei
295	11.2	33.9	44	8	BZ354782	BZ354782	BZ354782	368	11.2	33.9	35	7	R84783	Yt66C02.r1
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302	11.2	33.9	46	8	A2992697	A2992697	A2992697	375	11.2	33.9	37	2	BE548155	AV851317
303	11.2	33.9	46	9	CG804094	CG804094	CG804094	376	11.2	33.9	37	6	CF063618	QC70b01.x
304	11.2	33.9	46	9	CG805368	CG805368	CG805368	377	11.2	33.9	37	8	CF063618	QC70b01.x
305	11.2	33.9	47	4	BI916743	BI916743	BI916743	378	11.2	33.9	38	8	AZ447531	1M0244C15
306	11.2	33.9	47	7	CK446591	CK446591	CK446591	379	11.2	33.9	38	8	BH130009	G-6f16.f
307	11.2	33.9	47	9	CG804917	CG804917	CG804917	380	11.2	33.9	38	8	BH791568	BH791568
308	11.2	33.9	48	1	AG201231	AG201231	AG201231	381	11.2	33.9	38	8	BH791568	BH791568
309	11.2	33.9	49	1	AI766723	AI766723	AI766723	382	11.2	33.9	39	8	BZ54203	BZ54203
310	11.2	33.9	49	1	AA569919	AA569919	AA569919	383	11.2	33.9	40	8	AA162748	AA162748
311	11.2	33.9	49	4	BI523939	BI523939	BI523939	384	11.2	33.9	40	8	AZ595949	AZ595949
312	11.2	33.9	49	9	CL256784	CL256784	CL256784	385	11.2	33.9	41	1	AJ656445	AJ656445
313	11.2	33.9	50	1	AUI02247	AUI02247	AUI02247	386	11.2	33.9	41	7	CO788347	CO788347
314	11.2	33.9	50	1	AUI02389	AUI02389	AUI02389	387	11.2	33.9	41	8	AZ848135	AZ848135
315	11.2	33.9	50	1	AUI02759	AUI02759	AUI02759	388	11.2	33.9	42	6	CF307497	CF307497
316	11.2	33.9	50	1	AUI02868	AUI02868	AUI02868	389	11.2	33.9	42	8	AZ467316	AZ467316

C 390	11	33.3	42	9	CL640531	CL640531 G076C11 G	C 463	10.8	32.7	37	9	AG216758	AG216758 Drosophil
C 391	11	33.3	43	1	AG256343	AG256343 zr79h08.s	C 464	10.8	32.7	37	9	AG217821	AG217821 Drosophil
C 392	11	33.3	43	7	D67714	D67714 CELX076H3.F	C 465	10.8	32.7	37	9	AG217899	AG217899 Drosophil
C 393	11	33.3	44	8	AZ940577	AZ940577 2M0200E06	C 466	10.8	32.7	38	8	AZ811077	AZ811077 2M0077K02
C 394	11	33.3	44	8	AG193375	AG193375 Pan trogl	C 467	10.8	32.7	38	9	CL436882	CL436882 FST4020-N
C 395	11	33.3	44	8	AZ453471	AZ453471 1M0254F17	C 468	10.8	32.7	39	4	BG968413	BG968413 602835A16
C 396	11	33.3	45	9	DME545484	AJ545484 Drosophil	C 469	10.8	32.7	39	8	AZ804350	AZ804350 2M0065M24
C 397	11	33.3	45	9	TA329607Q	AL492426 T. brucei	C 470	10.8	32.7	39	8	CC796635	CC796635 SALK 1362
C 398	11	33.3	46	1	AI006377	AI006377 ua71c10.r	C 471	10.8	32.7	40	1	AI189771	AI189771 qd33508.x
C 399	11	33.3	46	1	AI023393	AI023393 aw70a11.s	C 472	10.8	32.7	40	2	BE902785	BE902785 601676114
C 400	11	33.3	46	1	AJ789455	AJ789455 AW789455	C 473	10.8	32.7	40	8	AZ806050	AZ806050 2M0067B22
C 401	11	33.3	46	7	D19556	D19556 MUSGS00956	C 474	10.8	32.7	40	9	AJ592673	AJ592673 Arabidops
C 402	11	33.3	46	8	AZ666500	AZ666500 1M0548K12	C 475	10.8	32.7	40	9	TA339H05P	TA339H05P T. brucei
C 403	11	33.3	46	9	CL307788	CL307788 02S0135-1	C 476	10.8	32.7	41	5	BP069327	BP069327 BP069327
C 404	11	33.3	46	9	CL347041	CL347041 PST4371-N	C 477	10.8	32.7	41	9	CG773749	CG773749 1123014D0
C 405	11	33.3	47	7	R55441	R55441 YJ79d08.r1	C 478	10.8	32.7	42	6	CA587667	CA587667 LBEL4P25P
C 406	11	33.3	47	8	AZ488215	AZ488215 1M0318D20	C 479	10.8	32.7	42	8	AQ024965	AQ024965 EP(2)0822
C 407	11	33.3	47	8	BZ662640	BZ662640 SALK 0261	C 480	10.8	32.7	42	8	AZ452625	AZ452625 1M0252O02
C 408	11	33.3	47	9	BX658228	BX658228 Arabidops	C 481	10.8	32.7	42	8	BH804014	BH804014 100809780
C 409	11	33.3	48	1	AU012741	AU012741 AU012741	C 482	10.8	32.7	43	1	AA663711	AA663711 ae71a03.s
C 410	11	33.3	48	1	AA429295	AA429295 zw07a04.r	C 483	10.8	32.7	43	1	AJ364636	AJ364636 qw39e05.x
C 411	11	33.3	48	2	BF032107	BF032107 601559702	C 484	10.8	32.7	43	1	AA075270	AA075270 zm84d05.s
C 412	11	33.3	48	8	AZ930229	AZ930229 1M0515B06	C 485	10.8	32.7	43	1	AI687911	AI687911 tp80h05.x
C 413	11	33.3	48	9	BX661183	BX661183 Arabidops	C 486	10.8	32.7	43	4	BJ065096	BJ065096 BJ065096
C 414	11	33.3	49	6	CA965896	CA965896 CcLX05a20	C 487	10.8	32.7	43	8	BH895175	BH895175 3526_1_33
C 415	11	33.3	49	8	AZ836991	AZ836991 2M0132P04	C 488	10.8	32.7	43	8	BZ584220	BZ584220 3590_1_55
C 416	11	33.3	50	1	AU102449	AU102449 AU102449	C 489	10.8	32.7	44	2	BE967336	BE967336 601649333
C 417	11	33.3	50	1	AU102450	AU102450 AU102450	C 490	10.8	32.7	44	4	BG779515	BG779515 602666932
C 418	11	33.3	50	1	AU103692	AU103692 AU103692	C 491	10.8	32.7	44	8	AZ428590	AZ428590 1M0212H09
C 419	11	33.3	50	1	AU103793	AU103793 AU103793	C 492	10.8	32.7	44	8	AZ451728	AZ451728 1M0251D14
C 420	11	33.3	50	1	AU103820	AU103820 AU103820	C 493	10.8	32.7	44	8	AZ474015	AZ474015 1M0290A13
C 421	11	33.3	50	1	AU104378	AU104378 AU104378	C 494	10.8	32.7	44	8	BH611429	BH611429 SALK 0309
C 422	11	33.3	50	1	AU104857	AU104857 AU104857	C 495	10.8	32.7	45	8	AZ413281	AZ413281 1M0197M16
C 423	11	33.3	50	1	AU104860	AU104860 AU104860	C 496	10.8	32.7	46	1	AA001102	AA001102 zh82e02.r
C 424	11	33.3	50	1	AU104861	AU104861 AU104861	C 497	10.8	32.7	46	1	AI744320	AI744320 tr029d05.x
C 425	11	33.3	50	1	AU104968	AU104968 AU104968	C 498	10.8	32.7	46	8	BZ289563	BZ289563 SALK 0229
C 426	11	33.3	50	1	AU104969	AU104969 AU104969	C 499	10.8	32.7	46	9	CG778195	CG778195 112302600
C 427	11	33.3	50	1	AU105087	AU105087 AU105087	C 500	10.8	32.7	47	4	BG484978	BG484978 602503986
C 428	11	33.3	50	1	AU105484	AU105484 AU105484	C 501	10.8	32.7	47	8	AZ369672	AZ369672 1M0120E21
C 429	11	33.3	50	1	AU105491	AU105491 AU105491	C 502	10.8	32.7	47	9	CR327908	CR327908 Medicago
C 430	11	33.3	50	1	AU105493	AU105493 AU105493	C 503	10.8	32.7	47	9	DR4D108	DR4D108 Danio rer
C 431	11	33.3	50	1	AU106599	AU106599 AU106599	C 504	10.8	32.7	48	1	AV950291	AV950291 AV950291
C 432	11	33.3	50	1	AU107088	AU107088 AU107088	C 505	10.8	32.7	48	8	BH614033	BH614033 SALK 0353
C 433	11	33.3	50	1	AU107637	AU107637 AU107637	C 506	10.8	32.7	48	8	BZ663678	BZ663678 SALK 0272
C 434	11	33.3	50	2	AW630853	AW630853 hh88e07.y	C 507	10.8	32.7	48	8	BZ762629	BZ762629 SALK 1059
C 435	11	33.3	50	5	BUE62220	BUE62220 cl83a07.z	C 508	10.8	32.7	48	9	AL946210	AL946210 Arabidops
C 436	11	33.3	50	8	AZ627991	AZ627991 1M0476A10	C 509	10.8	32.7	49	1	AA927087	AA927087 oi58a06.s
C 437	11	33.3	50	8	AZ638664	AZ638664 1M0498L07	C 510	10.8	32.7	49	7	N51399	N51399 yz16h06.s1
C 438	11	33.3	50	8	BZ662269	BZ662269 SALK 0257	C 511	10.8	32.7	49	8	AZ514447	AZ514447 1M0361M14
C 439	10.8	32.7	22	7	CO784859	CO784859 BL281D.E1	C 512	10.8	32.7	49	8	AZ821504	AZ821504 2M0094K14
C 440	10.8	32.7	23	9	TA78E03P	AL461956 T. brucei	C 513	10.8	32.7	49	8	BH889223	BH889223 3526_1_32
C 441	10.8	32.7	24	8	AZ451051	AZ451051 1M0250D12	C 514	10.8	32.7	49	8	BH903159	BH903159 SALK 1021
C 442	10.8	32.7	27	8	AZ951944	AZ951944 2M0216O04	C 515	10.8	32.7	50	1	AI066783	AI066783 ov17b03.x
C 443	10.8	32.7	27	8	AZ966603	AZ966603 2M037J12	C 516	10.8	32.7	50	1	AU102283	AU102283 AU102283
C 444	10.8	32.7	27	8	BH910341	BH910341 SALK 0590	C 517	10.8	32.7	50	1	AU102387	AU102387 AU102387
C 445	10.8	32.7	29	8	AZ345823	AZ345823 1M0080M09	C 518	10.8	32.7	50	1	AU103057	AU103057 AU103057
C 446	10.8	32.7	29	8	AZ829296	AZ829296 2M0106E22	C 519	10.8	32.7	50	1	AU103582	AU103582 AU103582
C 447	10.8	32.7	30	8	AZ810546	AZ810546 2M0076F10	C 520	10.8	32.7	50	1	AU103659	AU103659 AU103659
C 448	10.8	32.7	31	4	B1154913	B1154913 602902712	C 521	10.8	32.7	50	1	AU103734	AU103734 AU103734
C 449	10.8	32.7	31	7	U44252	U44252 ENU44252.As	C 522	10.8	32.7	50	1	AU103738	AU103738 AU103738
C 450	10.8	32.7	33	4	BM401378	BM401378 5009-0-9	C 523	10.8	32.7	50	1	AU103741	AU103741 AU103741
C 451	10.8	32.7	33	8	AZ304883	AZ304883 1M0005L23	C 524	10.8	32.7	50	1	AU103743	AU103743 AU103743
C 452	10.8	32.7	34	2	BE748594	BE748594 601571567	C 525	10.8	32.7	50	1	AU103747	AU103747 AU103747
C 453	10.8	32.7	34	8	AZ419323	AZ419323 1M0195H17	C 526	10.8	32.7	50	1	AU103754	AU103754 AU103754
C 454	10.8	32.7	35	9	AG204326	AG204326 Pan trogl	C 527	10.8	32.7	50	1	AU103760	AU103760 AU103760
C 455	10.8	32.7	36	8	AZ427281	AZ427281 1M0209H10	C 528	10.8	32.7	50	1	AU103769	AU103769 AU103769
C 456	10.8	32.7	37	1	AA961266	AA961266 on96a05.s	C 529	10.8	32.7	50	1	AU103776	AU103776 AU103776
C 457	10.8	32.7	37	9	AJ599517	AJ599517 Arabidops	C 530	10.8	32.7	50	1	AU103771	AU103771 AU103771
C 458	10.8	32.7	37	9	AG215935	AG215935 Drosophil	C 531	10.8	32.7	50	1	AU103787	AU103787 AU103787
C 459	10.8	32.7	37	9	AG216163	AG216163 Drosophil	C 532	10.8	32.7	50	1	AU103792	AU103792 AU103792
C 460	10.8	32.7	37	9	AG216196	AG216196 Drosophil	C 533	10.8	32.7	50	1	AU103797	AU103797 AU103797
C 461	10.8	32.7	37	9	AG216210	AG216210 Drosophil	C 534	10.8	32.7	50	1	AU103800	AU103800 AU103800
C 462	10.8	32.7	37	9	AG216512	AG216512 Drosophil	C 535	10.8	32.7	50	1	AU103801	AU103801 AU103801

C	828	10.4	31.5	50	1	AUI03955
		10.4	31.5	50	1	AUI03962
C	829	10.4	31.5	50	1	AUI03962
		10.4	31.5	50	1	AUI04742
C	830	10.4	31.5	50	1	AUI04742
		10.4	31.5	50	1	AUI04973
C	831	10.4	31.5	50	1	AUI04973
		10.4	31.5	50	1	AUI05057
C	832	10.4	31.5	50	1	AUI05057
		10.4	31.5	50	1	AUI05073
C	833	10.4	31.5	50	1	AUI05073
		10.4	31.5	50	1	AUI0586
C	834	10.4	31.5	50	1	AUI0586
		10.4	31.5	50	1	AUI06618
C	835	10.4	31.5	50	1	AUI06618
		10.4	31.5	50	1	AUI06769
C	836	10.4	31.5	50	1	AUI06769
		10.4	31.5	50	1	AUI06822
C	837	10.4	31.5	50	1	AUI06822
		10.4	31.5	50	1	AUI06970
C	838	10.4	31.5	50	1	AUI06970
		10.4	31.5	50	1	AUI07138
C	839	10.4	31.5	50	1	AUI07138
		10.4	31.5	50	1	AUI07354
C	840	10.4	31.5	50	1	AUI07354
		10.4	31.5	50	1	AUI07355
C	841	10.4	31.5	50	1	AUI07355
		10.4	31.5	50	1	AUI07356
C	842	10.4	31.5	50	1	AUI07356
		10.4	31.5	50	1	AUI07358
C	843	10.4	31.5	50	1	AUI07358
		10.4	31.5	50	1	AUI07359
C	844	10.4	31.5	50	1	AUI07359
		10.4	31.5	50	1	AUI07361
C	845	10.4	31.5	50	1	AUI07361
		10.4	31.5	50	1	AUI07365
C	846	10.4	31.5	50	1	AUI07365
		10.4	31.5	50	1	AUI07366
C	847	10.4	31.5	50	1	AUI07366
		10.4	31.5	50	1	AUI07369
C	848	10.4	31.5	50	1	AUI07369
		10.4	31.5	50	1	AUI07370
C	849	10.4	31.5	50	1	AUI07370
		10.4	31.5	50	1	AUI07371
C	850	10.4	31.5	50	1	AUI07371
		10.4	31.5	50	1	AUI07372
C	851	10.4	31.5	50	1	AUI07372
		10.4	31.5	50	1	AUI07373
C	852	10.4	31.5	50	1	AUI07373
		10.4	31.5	50	1	AUI07375
C	853	10.4	31.5	50	1	AUI07375
		10.4	31.5	50	1	AUI07376
C	854	10.4	31.5	50	1	AUI07376
		10.4	31.5	50	1	AUI07377
C	855	10.4	31.5	50	1	AUI07377
		10.4	31.5	50	1	AUI07378
C	856	10.4	31.5	50	1	AUI07378
		10.4	31.5	50	2	B8976895
C	857	10.4	31.5	50	2	B8976895
		10.4	31.5	50	5	BP132714
C	858	10.4	31.5	50	5	BP132714
		10.4	31.5	50	6	C00960
C	859	10.4	31.5	50	6	C00960
		10.4	31.5	50	7	CF543112
C	860	10.4	31.5	50	7	CF543112
		10.4	31.5	50	8	A7879909
C	861	10.4	31.5	50	8	A7879909
		10.4	31.5	50	9	CC033445
C	862	10.4	31.5	50	9	CC033445
		10.4	31.5	50	9	EX192560
C	863	10.4	31.5	50	9	EX192560
		10.4	31.5	50	9	CR082324
C	864	10.4	31.5	50	9	CR082324
		10.4	31.5	50	9	CL313251
C	865	10.4	31.5	50	9	CL313251
		10.4	31.5	50	9	AG242574
C	866	10.4	31.5	50	9	AG242574
		10.4	31.5	50	9	AZ366535
C	867	10.2	30.9	20	8	AZ366535
		10.2	30.9	20	8	CD533377
C	868	10.2	30.9	21	6	CD533377
		10.2	30.9	22	8	AZ623338
C	869	10.2	30.9	22	8	AZ623338
		10.2	30.9	23	1	AJ791120
C	870	10.2	30.9	24	1	AJ791120
		10.2	30.9	24	7	L32034
C	871	10.2	30.9	27	1	L32034
		10.2	30.9	27	8	AZ805942
C	872	10.2	30.9	24	8	AZ805942
		10.2	30.9	25	1	AU254095
C	873	10.2	30.9	25	1	AU254095
		10.2	30.9	25	8	AZ234338
C	874	10.2	30.9	25	8	AZ234338
		10.2	30.9	25	8	AZ764603
C	875	10.2	30.9	25	8	AZ764603
		10.2	30.9	25	9	TA2808P
C	876	10.2	30.9	27	9	TA2808P
		10.2	30.9	27	7	D19150
C	877	10.2	30.9	27	7	D19150
		10.2	30.9	27	8	AZ303969
C	878	10.2	30.9	27	8	AZ303969
		10.2	30.9	27	8	AZ367484
C	879	10.2	30.9	27	8	AZ367484
		10.2	30.9	27	8	BH907088
C	880	10.2	30.9	27	8	BH907088
		10.2	30.9	28	1	A8936125
C	881	10.2	30.9	28	1	A8936125
		10.2	30.9	28	1	AJ799189
C	882	10.2	30.9	28	1	AJ799189
		10.2	30.9	28	8	AZ412849
C	883	10.2	30.9	28	8	AZ412849
		10.2	30.9	28	8	AZ463714
C	884	10.2	30.9	28	8	AZ463714
		10.2	30.9	28	8	AZ840409
C	885	10.2	30.9	28	8	AZ840409
		10.2	30.9	29	8	AZ808606
C	886	10.2	30.9	29	8	AZ808606
		10.2	30.9	29	8	AZ871142
C	887	10.2	30.9	29	8	AZ871142
		10.2	30.9	29	8	BF209105
C	888	10.2	30.9	30	8	BF209105
		10.2	30.9	30	8	BG772537
C	889	10.2	30.9	30	8	BG772537
		10.2	30.9	30	8	AZ451718
C	890	10.2	30.9	30	8	AZ451718
		10.2	30.9	30	8	BH740820
C	891	10.2	30.9	30	8	BH740820
		10.2	30.9	31	1	A1140482
C	892	10.2	30.9	31	1	A1140482
		10.2	30.9	31	8	BG2844226
C	893	10.2	30.9	31	8	BG2844226
		10.2	30.9	31	8	AZ844531
C	894	10.2	30.9	31	8	AZ844531
		10.2	30.9	31	8	CL436258
C	895	10.2	30.9	32	9	CL436258
		10.2	30.9	32	8	BG545479
C	896	10.2	30.9	32	8	BG545479
		10.2	30.9	32	9	CR397869
C	897	10.2	30.9	32	9	CR397869
		10.2	30.9	32	9	CG721758
C	898	10.2	30.9	32	9	CG721758
		10.2	30.9	32	9	AG203845
C	899	10.2	30.9	33	9	AG203845
		10.2	30.9	33	4	BF656315
C	900	10.2	30.9	33	4	BF656315

C 901	10.2	30.9	33	8	BH790108	SALK_0544
C 902	10.2	30.9	34	1	A1381014	tg20e10.x
C 903	10.2	30.9	34	4	B1553461	603193222
C 904	10.2	30.9	34	8	A2421063	1M0199009
C 905	10.2	30.9	34	8	A25856275	2M0160F12
C 906	10.2	30.9	34	8	B2358990	SALK_1336
C 907	10.2	30.9	34	8	B2665782	KG10552-S
C 908	10.2	30.9	35	2	B5542178	601066507
C 909	10.2	30.9	35	8	AZ428773	1M0212123
C 910	10.2	30.9	35	8	BH814760	SALK_0669
C 911	10.2	30.9	36	1	AV680090	AV680090
C 912	10.2	30.9	36	5	BX621489	BX621489
C 913	10.2	30.9	36	7	H71797	YS05909.s1
C 914	10.2	30.9	36	7	R85295	Yq24608.s1
C 915	10.2	30.9	36	8	A2613697	1M0442K08
C 916	10.2	30.9	36	8	A2797263	2M0053G23
C 917	10.2	30.9	36	8	A2834877	2M0117L15
C 918	10.2	30.9	36	8	A2983835	2M0265E10
C 919	10.2	30.9	37	9	CG719378	1119057D.s
C 920	10.2	30.9	37	8	A2312666	1M0028L14
C 921	10.2	30.9	37	8	A2800309	2M0058F15
C 922	10.2	30.9	37	8	A2800309	2M0058F15
C 923	10.2	30.9	37	8	A2809839	2M0074G05
C 924	10.2	30.9	37	8	A2835900	2M0130D21
C 925	10.2	30.9	37	8	A2960486	2M0228L01
C 926	10.2	30.9	37	8	BH791796	SALK_0613
C 927	10.2	30.9	38	1	AA035969	mi70h01.r
C 928	10.2	30.9	38	4	BJ034631	BJ034631
C 929	10.2	30.9	38	7	H30464	Y058402.r1
C 930	10.2	30.9	38	8	A2975236	2M0250B17
C 931	10.2	30.9	38	8	BH848869	BH848869
C 932	10.2	30.9	38	9	CG718161	1119051H0
C 933	10.2	30.9	38	9	AG217395	Drosophila
C 934	10.2	30.9	39	8	A2307710	1M0009L01
C 935	10.2	30.9	39	8	A2416776	1M0192J07
C 936	10.2	30.9	39	8	A2659033	1M0536109
C 937	10.2	30.9	39	9	TA100F02Q	
C 938	10.2	30.9	39	9	AG188570	Pan trogl
C 939	10.2	30.9	40	1	AI1098410	uc05e09.r
C 940	10.2	30.9	40	1	AA456867	aa38b02.r
C 941	10.2	30.9	40	8	A2439838	1M0230H07
C 942	10.2	30.9	40	8	A2454771	1M0256C22
C 943	10.2	30.9	40	8	A2786213	2M0031F04
C 944	10.2	30.9	40	9	CR405146	Arabidops
C 945	10.2	30.9	40	9	TA14B10Q	Arabidops
C 946	10.2	30.9	40	9	CL266024	03S3081-1
C 947	10.2	30.9	40	9	AG260533	Lotus cor
C 948	10.2	30.9	41	4	BJ046937	BJ046937
C 949	10.2	30.9	41	6	CB305228	3'EST-NF1
C 950	10.2	30.9	41	7	D74277	CELK079AXF
C 951	10.2	30.9	41	8	A2758979	1M0551D18
C 952	10.2	30.9	41	9	TA90D03Q	
C 953	10.2	30.9	41	9	CL25893	EY04451-5
C 954	10.2	30.9	42	4	BG252356	602365945
C 955	10.2	30.9	42	8	A2499983	1M0338P02
C 956	10.2	30.9	42	8	A2579550	1M0376K02
C 957	10.2	30.9	42	8	B2288809	SALK_0221
C 958	10.2	30.9	42	9	AL947757	Arabidops
C 959	10.2	30.9	42	9	CR360039	Arabidops
C 960	10.2	30.9	42	9	TA92F10Q	
C 961	10.2	30.9	43	1	A1492250	tf59a03.x
C 962	10.2	30.9	43	1	AJ660103	AJ660103
C 963	10.2	30.9	43	1	AAJ660103	AJ660103
C 964	10.2	30.9	43	1	AA522067	V108h09.r
C 965	10.2	30.9	43	4	BG250039	602362124
C 966	10.2	30.9	43	4	BG259962	602371733
C 967	10.2	30.9	43	4	B1094800	EST-CD34N
C 968	10.2	30.9	43	4	B1453108	EST-CD34N
C 969	10.2	30.9	43	7	H09843	Ym01d05.r1
C 970	10.2	30.9	43	7	H14006	EST00032 Ch
C 971	10.2	30.9	43	8	A2789239	2M0036A23
C 972	10.2	30.9	43	8	BH792796	SALK_0650
C 973	10.2	30.9	43	8	BH813587	SALK_0644
C 974	10.2	30.9	43	9	CL520645	DA17F12 F

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c 974 10.2 30.9 44 8 A2347569 1M0083P11
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978 10.2 30.9 44 8 B2358244 SALK_1321
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983 10.2 30.9 45 5 BX621624 BX621624
984 10.2 30.9 45 8 A2451564 1M0251801
985 10.2 30.9 45 8 A2453471 1M0254F17
986 10.2 30.9 45 8 BH810080 SALK_0406
987 10.2 30.9 45 8 BZ764481 SALK_1249
988 10.2 30.9 45 9 BX894755 Arabidops
989 10.2 30.9 45 9 TA388A10Q AL498176 T. brucei
990 10.2 30.9 45 9 CL439197 PST8831-N
991 10.2 30.9 46 1 AA983189 am18b12.s
992 10.2 30.9 46 1 AA980407 aa52b05.r
993 10.2 30.9 46 1 AA137422 wq58d12.r
994 10.2 30.9 46 1 AJ673709 R72707 YJ95a01.r1
995 10.2 30.9 46 4 B1646968 603278737
996 10.2 30.9 46 7 W89968 mf64g11.r1
997 10.2 30.9 46 7 W89968
998 10.2 30.9 46 8 A2628883 1M0481A22
999 10.2 30.9 46 8 A2665608 1M0547G11
1000 10.2 30.9 46 8 BH895155 3526_1_33

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ALIGNMENTS

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RESULT 1
AA615310 50 bp mRNA linear EST 07-OCT-1997
LOCUS V001h08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1040223 5', mRNA sequence.
ACCESSION AA615310.1 GI:2502538
VERSION V001h08.r1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 50)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gaisel,S., Kucaba,F., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:580247
Seq primer: -28m13 rev1 ET from Amersham.
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clones="IMAGE:1040223"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"

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FEATURES

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source
1..50
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clones="IMAGE:1040223"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"

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/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCAGG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

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ORIGIN
Query Match 48.5%; Score 16; DB 1; Length 50;
Best Local Similarity 79.2%; Pred. No. 4.le+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 GCCACATGAGTGCACAGGCGTCTG 24
Db 24 GCCACATGAGTGCACAGGCGTCTG 47

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RESULT 2
AUI03444/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03444 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03841, mRNA sequence.
ACCESSION AUI03444
VERSION AUI03444.1 GI:13552965
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

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Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 8 GAGTGGCAAGGCGTCTGGTGAT 29
Db 39 GAGTGGCAAGGCGGATGGTGT 18

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RESULT 3
AUI03445/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445

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Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 8 GAGTGGCAAGGCGTCTGGTGAT 29
Db 39 GAGTGGCAAGGCGGATGGTGT 18

```

```

RESULT 3
AUI03445/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI03445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP03842, mRNA sequence.
ACCESSION AUI03445

```

```

VERSION AU103445.1 GI:13552966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03842"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 47.3%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 GAGTGGCAAGCGCTCTGGTGAT 29
Db 34 GAGTGGCAAGCGCGGATGGTGGT 13

RESULT 4
AZ582580/c
LOCUS 25 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0376N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0376N05 F, genomic survey sequence.
ACCESSION AZ582580
VERSION AZ582580.1 GI:11701604
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: N column: 05
Seq primer: CGTTGTAACACGACGCCAGT

FEATURES
source Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0376N05"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 45.5%; Score 15; DB 8; Length 25;
Best Local Similarity 78.3%; Pred No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGGCAAGCGCTCTG 24
Db 23 CCCCATGAGCGCCAGCGCGCAG 1

RESULT 5
AU103463/c
LOCUS 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103463 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP15715, mRNA sequence.
ACCESSION AU103463
VERSION AU103463.1 GI:13552984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source Location/Qualifiers

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Wed Nov 24 08:46:07 2004

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP15715"
/clone_lib="Sugano Homo sapiens cDNA library"

source

ORIGIN

Query Match 45.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 GAGTGGCAAGGCGTCTGGTGATA 30
|||||||
Db 49 GAGTGGCAAGGCGGATGGTCTTA 27

RESULT 6

AZ481987/c 36 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0306M08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0306M08 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

REFERENCE

AUTHORS
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: M column: 08
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.

FEATURES

source

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/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

ORIGIN

Query Match 44.2%; Score 14.6; DB 8; Length 36;
Best Local Similarity 69.0%; Pred. No. 1.6e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 4 ACATGAGTGGCAAGGCGTCTGGTGATACC 32
|||||||
Db 34 AAAAGATGAATAGTGTGTGTGACACC 6

RESULT 7

AZ329468 34 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0053B14R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0053B14 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

REFERENCE

AUTHORS
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: B column: 14
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.

FEATURES

source

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/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 43.6%; Score 14.4; DB 8; Length 34;
 Best Local Similarity 75.0%; Pred. No. 2e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGACTGCGACAGCGCTCTGGTGAT 29
 ||||| ||||| || ||||| |||||
 DB 7 ATGACTGGCTGAGCACCTGGTGAT 30

RESULT 8
 AZ480659/c
 LOCUS
 DEFINITION IM0302B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0302B24 F, genomic survey sequence.

ACCESSION AZ480659
 VERSION AZ480659.1 GI:10641724

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 34)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0302 row: B column: 24

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 34.

Location/Qualifiers

FEATURES

source

1..34

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0302B24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

ORIGIN

Query Match 43.6%; Score 14.4; DB 8; Length 34;
 Best Local Similarity 65.6%; Pred. No. 2e+05;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCAAGCGCTCTGGTGATACC 32
 ||||| ||||| ||||| ||||| |||||
 DB 32 GTCTCATTTATCTCTAGTGCTGTGATGATACC 1

RESULT 9
 AZ818206/c
 LOCUS
 DEFINITION 2M0088P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0088P05 F, genomic survey sequence.

ACCESSION AZ818206

VERSION AZ818206.1 GI:12988114

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 38)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: P column: 05

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 38.

Location/Qualifiers

FEATURES

source

1..38

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0088P05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.4%; Score 14; DB 8; Length 47;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCACATGTCGGCAAGCGTCTGGTGATAC 31
|||||
Db 17 CCACATGTGTGAATGTGGTGACATAC 46

RESULT 15

LOCUS BG489537 49 bp mRNA linear EST 27-MAR-2001
DEFINITION 602517943F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4636427 5', mRNA sequence.

ACCESSION BG489537
VERSION BG489537.1 GI:13451047
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 49)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCMI395 row: f column: 12
High quality sequence stop: 49.
Location/Qualifiers

FEATURES

source

1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4636427"
/lab_host="DH10B (phage-resistant)"
/lab_host="NIH_MGC_18"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match 42.4%; Score 14; DB 4; Length 49;
Best Local Similarity 77.3%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GGCAAGCGCTCTGGTGATACCG 33
|||||
Db 1 GGCTAACCGCTCTGGTGATCTCG 22

RESULT 16

LOCUS BF578678 45 bp mRNA linear EST 12-DEC-2000
DEFINITION 602093151F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4207477 5', mRNA sequence.

ACCESSION BF578678
VERSION BF578678.1 GI:11652299
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 45)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM9770 row: e column: 14
High quality sequence stop: 45.
Location/Qualifiers

FEATURES

source

1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4207477"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 41.8%; Score 13.8; DB 2; Length 45;
Best Local Similarity 88.2%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GAGTGGCAAGCGCTCTG 24
|||||
Db 26 GGGTGGCAAGCGCGCTG 42

RESULT 17

LOCUS AZ664916 49 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0545N04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0545N04 R, genomic survey sequence.

ACCESSION AZ664916
VERSION AZ664916.1 GI:11802062
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

TITLE Weisshaar, B.
JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
MEDLINE flanking sequence tag-based reverse genetics
PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)
REFERENCE 23117147
AUTHORS 14756321
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weisshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
JOURNAL mutagenized Arabidopsis thaliana lines
PUBMED Biotechniques 35 (6), 1164-1168 (2003)
REFERENCE 14682050
 4 (bases 1 to 50)
AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At4g24760.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
 source
 1..50
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-428G07-018097"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /notes="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."
ORIGIN
 Query Match 41.8%; Score 13.8; DB 9; Length 50;
 Best Local Similarity 72.0%; Pred. No. 3.6e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 5 CATGACTGGCAAGGCGCTCTGGTGAT 29
 ||||| ||||| ||||| ||||| |||||
 Db 21 CATGAGCAGACGACGCGGTGGTGAT 45
 ||||| ||||| ||||| ||||| |||||
RESULT 20
 AU105625/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU105625 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HS107037, mRNA sequence.
ACCESSION AU105625
VERSION AU105625.1 GI:13555146
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072

PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
FEATURES Location/Qualifiers
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS107037"
 /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
 Query Match 41.2%; Score 13.6; DB 1; Length 50;
 Best Local Similarity 67.9%; Pred. No. 4.4e+05;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 GCCACATGAGTGGCAAGCGCTCTGGTGA 28
 ||||| ||||| ||||| ||||| |||||
 Db 33 GCAAAATGAGCGCAGAGAGTCAAGTCA 6
 ||||| ||||| ||||| ||||| |||||
RESULT 21
 AU19869 28 bp mRNA linear EST 30-MAR-1999
LOCUS tg52f07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2112421 3' similar to TR:Q15424 Q15424 SCAFFOLD ATTACHMENT
 FACTOR ; contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION AU19869
VERSION AU19869.1 GI:4265800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 28)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2382 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
FEATURES Location/Qualifiers
 source
 1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2112421"
 /lab_host="DH10B"
 /clone_lib="Soares NFL T_GBC_S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NbHL19, testis NHT, and B-cell
 NCI CGAP GCBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."


```

VERSION AU103740.1 GI:13553261
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai.T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S., Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HEP02423"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 40.6%; Score 13.4; DB 1; Length 50;
Best Local Similarity 73.9%; Pred. No. 5.4e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 5 CATGAGTGGCAGCGCTCTGGTG 27
Db 1 CATGCTGGATGATGCTCTCTG 23
RESULT 25
CR411978 50 bp mRNA linear EST 13-JUN-2004
LOCUS CR411978 XGC-tailbud Xenopus tropicalis cDNA clone TTbA063h15 5',
DEFINITION mRNA sequence.
ACCESSION CR411978.1 GI:48680225
VERSION CR411978
KEYWORDS Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
REFERENCE 1 (bases 1 to 50)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTbA063h15.p1kSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
FEATURES
source
Location/Qualifiers
1..50
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTbA063h15"
/dev_stage="tailbud (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCSI07; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCSI07 with
EcoRI at the 5' end and NotI at the 3' end."
ORIGIN
Query Match 40.6%; Score 13.4; DB 7; Length 50;
Best Local Similarity 73.9%; Pred. No. 5.4e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCCACATGAGTGGCAAGGGCTCT 23
Db 4 GCGAGGTGAGTGACATGGCGGCT 26
RESULT 26
AI123900/c
LOCUS AI123900 34 bp mRNA linear EST 03-SEP-1998
DEFINITION qa78g98.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:1692926 3' similar to TR:Q14976 Q14976 PHOSPHOPROTEIN. ;,
mRNA sequence.
ACCESSION AI123900
VERSION AI123900.1 GI:3539666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 34)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
Location/Qualifiers
1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1692926"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TTTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was sized selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
ORIGIN
Query Match 40.0%; Score 13.2; DB 1; Length 34;
Best Local Similarity 69.2%; Pred. No. 6.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 CACATGATGGCAAGCGCTCTGGTGA 28

```



```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
/db_xref="taxon:3702"
/clone="SALK_102169.22.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 49;
Best Local Similarity 83.3%; Pred. No. 6.5e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAGGCGCTCTGGT 26
DB 33 AGTGTCAAGCGCTCTTGT 16

RESULT 33
AUI02469 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI02469 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS01129, mRNA sequence.
ACCESSION AUI02469
VERSION AUI02469.1 GI:13551989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,I., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01129"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CCACATGAGTGGCAGGCGTCTGGT 27
DB 22 CCACATGATACAGAGCGCGTGGT 47

RESULT 34
AUI02478 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI02478 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION AUI02478 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
/db_xref="taxon:3702"
/clone="SALK_102169.22.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 49;
Best Local Similarity 83.3%; Pred. No. 6.5e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAGGCGCTCTGGT 26
DB 33 AGTGTCAAGCGCTCTTGT 16

RESULT 33
AUI02469 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI02469 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS01129, mRNA sequence.
ACCESSION AUI02469
VERSION AUI02469.1 GI:13551989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,I., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01129"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CCACATGAGTGGCAGGCGTCTGGT 27
DB 22 CCACATGATACAGAGCGCGTGGT 47

RESULT 34
AUI02478 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI02478 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION AUI02478 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

```

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CAS08717, mRNA sequence.
ACCESSION AU102478
VERSION AU102478.1 GI:13551998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Hata,H., Ota,T., Isogai,T., Tanaka,T., Tanaka,T., Morishita,S., Okubo,K., Suzuki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES             Location/Qualifiers
     source            1..50
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="KAT10979"
     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      8 GAGTGGCAAGCGCTCGTGATACCG 33
      ||| ||||| ||| ||||| |||
DB      34 GAGCGCAATCGGGCGGTGACGCG 9

RESULT 36
AZ611718
LOCUS AZ611718
DEFINITION IM0438B18F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUGC1M0438B18 F, genomic survey sequence.
ACCESSION AZ611718
VERSION AZ611718.1 GI:11733908
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: B column: 18
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES             Location/Qualifiers
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     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC1M0438B18"
     /sex="Male"
     /lab_host="F. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUC1M library"
     /note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

CAS08717, mRNA sequence.
ACCESSION AU102478
VERSION AU102478.1 GI:13551998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Hata,H., Ota,T., Isogai,T., Tanaka,T., Tanaka,T., Morishita,S., Okubo,K., Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES             Location/Qualifiers
     source            1..50
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="CAS08717"
     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      2 CCACATGATGCGCAAGCGCTCGTG 27
      ||||| ||| ||| ||| |||
DB      22 CCACATGATACAGAGCGCGTGTG 47

RESULT 35
AU107036/c
LOCUS AU107036
DEFINITION AU107036 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT10979, mRNA sequence.
ACCESSION AU107036
VERSION AU107036.1 GI:13556557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

```

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.4%; Score 13; DB 8; Length 23;
Best Local Similarity 76.2%; Pred. No. 7.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 GCAAGCGTCTGCTGATACCG 33
|||||
DB 2 GCNAGGGTTTGGTCTAGCG 22
|||||

RESULT 37
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LOCUS AZ828724 28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0105224R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105224 R, genomic survey sequence.

ACCESSION AZ828724.1 GI:12998632
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddumgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: E column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

FEATURES

High quality sequence stop: 28.
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.4%; Score 13; DB 8; Length 28;
Best Local Similarity 76.2%; Pred. No. 7.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CATGAGTGGCAAGCGCTCTGG 25
|||||
DB 27 CAGGAGGGGCAAGGGTAGGG 7
|||||

RESULT 38
H79914

LOCUS H79914 44 bp mRNA linear EST 09-NOV-1995
DEFINITION yul0f04.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:233407 5', similar to gb:X69532_rnal INTER-ALPHA-TRYPsin
INHIBITOR COMPLEX COMPONENT III (HUMAN);, mRNA sequence.

ACCESSION H79914.1 GI:1058003
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 44)

REFERENCE

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

97044478
8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2600

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2600 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .44
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3786584"
/db_xref="taxon:9606"
/clone="IMAGE:233407"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen lNFLS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac 1; Site_2: Eco RI;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 468.195 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-6

Perfect score: 26
Sequence: 1 gcgaagcgctagccatgcggtta 26

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hhg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	26	100.0	26	6	AR054575 Sequence
2	26	100.0	26	6	AR094137 Sequence
3	26	100.0	26	6	BD181367 A method
4	26	100.0	26	6	AX147021 Sequence
5	26	100.0	26	6	AX523947 Sequence
6	26	100.0	26	6	AX524845 Sequence
7	26	100.0	30	6	AR428911 Sequence
8	26	100.0	30	6	AR488114 Sequence
9	26	100.0	30	6	AX472307 Sequence
10	26	100.0	30	6	AX696019 Sequence
11	26	100.0	30	6	AX720383 Sequence
12	26	100.0	30	6	AX720387 Sequence
13	26	100.0	30	6	AX814298 Sequence
14	26	100.0	30	6	AX814301 Sequence
15	25	96.2	28	6	AR411537 Sequence
16	25	96.2	28	6	BD000263 Oligonucleotide
17	25	96.2	37	6	CQ830529 Sequence
18	24	92.3	24	6	A68287 Sequence 8
19	24	92.3	24	6	AR054578 Sequence

20	24	92.3	24	6	BD183046	BD183046 Nucleic acid
21	24	92.3	24	6	BD183877	BD183877 Method of
22	24	92.3	24	6	BD194954	BD194954 Method of
23	24	92.3	24	6	BD195155	BD195155 Ribonucleic
24	24	92.3	24	6	I22146	I22146 Sequence 5
25	24	92.3	24	6	I26949	I26949 Sequence 17
26	24	92.3	24	6	I40301	I40301 Sequence 9
27	24	92.3	24	6	I59678	I59678 Sequence 9
28	24	92.3	24	6	I68634	I68634 Sequence 7
29	24	92.3	24	6	AR211384	AR211384 Sequence
30	24	92.3	24	6	AX003941	AX003941 Sequence
31	24	92.3	24	6	AX021563	AX021563 Sequence
32	24	92.3	24	6	AX021622	AX021622 Sequence
33	24	92.3	24	6	AX147011	AX147011 Sequence
34	24	92.3	24	6	AX250664	AX250664 Sequence
35	24	92.3	24	6	AX428908	AX428908 Sequence
36	24	92.3	24	6	AX428981	AX428981 Sequence
37	24	92.3	24	6	BD138662	BD138662 Specific
38	24	92.3	26	6	I22147	I22147 Sequence 6
39	23	88.5	24	6	AX250672	AX250672 Sequence
40	22.8	87.7	50	6	AX397945	AX397945 Sequence
41	22.8	87.7	50	6	AX397956	AX397956 Sequence
42	22	84.6	36	6	BD171241	BD171241 Method of
43	21	80.8	21	6	AR131532	AR131532 Sequence
44	21	80.8	21	6	AR144109	AR144109 Sequence
45	21	80.8	21	6	BD175037	BD175037 Method of
46	21	80.8	21	6	AR199466	AR199466 Sequence
47	21	80.8	21	6	AR200937	AR200937 Sequence
48	21	80.8	21	6	AR488699	AR488699 Sequence
49	21	80.8	21	6	AR488923	AR488923 Sequence
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51	21	80.8	21	6	AX419688	AX419688 Sequence
52	21	80.8	21	6	AX710908	AX710908 Sequence
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54	21	80.8	21	6	BD001478	BD001478 Method an
55	21	80.8	21	6	BD084950	BD084950 Target and
56	21	80.8	21	6	BD102537	BD102537 Method fo
57	21	80.8	25	6	AX202932	AX202932 Sequence
58	20	76.9	20	6	AR167016	AR167016 Sequence
59	20	76.9	20	6	AR210671	AR210671 Sequence
60	20	76.9	20	6	AX803706	AX803706 Sequence
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62	20	76.9	20	6	BD095631	BD095631 Genotype
63	20	76.9	21	6	AR068468	AR068468 Sequence
64	20	76.9	21	6	AR105980	AR105980 Sequence
65	20	76.9	21	6	AR107975	AR107975 Sequence
66	20	76.9	37	6	E06353	E06353 Primer. 9/1
67	20	76.9	37	6	E06549	E06549 Primer. 9/1
68	20	76.9	40	6	E17187	E17187 Partial seq
69	20	76.9	46	6	E17191	E17191 Partial seq
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77	19	73.1	33	6	AR004390	AR004390 Sequence
78	19	73.1	33	6	AR064952	AR064952 Sequence
79	19	73.1	33	6	AR097182	AR097182 Sequence
80	19	73.1	33	6	AR130680	AR130680 Sequence
81	19	73.1	33	6	AR172029	AR172029 Sequence
82	19	73.1	33	6	BD189146	BD189146 HCV Genom
83	19	73.1	33	6	BD189293	BD189293 HCV Genom
84	19	73.1	33	6	BD189440	BD189440 HCV Genom
85	19	73.1	33	6	I82865	I82865 Sequence 44
86	18	69.2	21	6	AX802838	AX802838 Sequence
87	18	69.2	21	6	AR166993	AR166993 Sequence
88	18	69.2	21	6	AR210648	AR210648 Sequence
89	18	69.2	25	6	E09661	E09661 Primer for
90	18	69.2	25	6	I93329	I93329 Sequence 3
91	18	69.2	25	6	BD105581	BD105581 Process f
92	18	69.2	28	6	AR094966	AR094966 Sequence

93	18	69.2	28	6	AR094993	AR094993 Sequence	14	53.8	30	6	AR078329	AR078329 Sequence
94	18	69.2	41	6	AX802843	AX802843 Sequence	14	53.8	30	6	I34301	I34301 Sequence
95	17	65.4	18	6	AX397926	AX397926 Sequence	14	53.8	30	6	AR337308	AR337308 Sequence
96	17	65.4	20	6	AR106338	AR106338 Sequence	14	53.8	23	6	AR171739	AR171739 Sequence
97	17	65.4	20	6	AR106355	AR106355 Sequence	170	53.1	23	6	A36553	A36553 Sequence
98	17	65.4	20	6	E58846	E58846 Method for	171	53.1	27	6	I11507	I11507 Sequence
99	17	65.4	20	6	BD004846	BD004846 Method fo	172	53.1	27	6	I26933	I26933 Sequence
100	17	65.4	27	6	AD8434	AD8434 Sequence 18	173	53.1	27	6	I40097	I40097 Sequence
101	17	65.4	32	6	BD141962	BD141962 Gene dete	174	53.1	27	6	I50072	I50072 Sequence
102	16	61.5	16	6	AR234362	AR234362 Sequence	175	53.1	28	6	I12136	I12136 Sequence
103	16	61.5	26	6	A39031	A39031 Sequence 3	176	53.1	28	6	I41306	I41306 Sequence
104	16	61.5	26	6	AR063365	AR063365 Sequence	177	53.1	30	6	A38380	A38380 Sequence
105	16	61.5	26	6	AR123556	AR123556 Sequence	178	53.1	30	6	I74383	I74383 Sequence
106	16	61.5	26	6	BD178497	BD178497 Method of	179	53.1	36	6	I24862	I24862 Sequence
107	16	61.5	26	6	BD182890	BD182890 Detection	180	53.1	36	6	I40229	I40229 Sequence
108	16	61.5	26	6	AR267297	AR267297 Sequence	181	53.1	36	6	I72683	I72683 Sequence
109	16	61.5	26	6	AR305707	AR305707 Sequence	182	53.1	37	6	AX316122	AX316122 Sequence
110	16	61.5	26	6	AX023093	AX023093 Sequence	183	53.1	37	6	I12111	I12111 Sequence
111	16	61.5	26	6	AX398130	AX398130 Sequence	184	53.1	48	6	I41281	I41281 Sequence
112	16	61.5	26	6	AX417299	AX417299 Sequence	185	53.1	50	6	AX199516	AX199516 Sequence
113	16	61.5	26	6	AX717178	AX717178 Sequence	186	52.3	30	6	BD261533	BD261533 Assays fo
114	16	61.5	32	6	BD141964	BD141964 Gene dete	187	52.3	38	6	AX456890	AX456890 Sequence
115	16	61.5	37	6	AX686112	AX686112 Sequence	188	52.3	39	6	A71961	A71961 Sequence
116	16	61.5	40	6	E06352	E06352 Primer. 9/1	189	52.3	39	6	AR147149	AR147149 Sequence
117	16	61.5	40	6	E06548	E06548 Primer. 9/1	190	52.3	39	6	AR236310	AR236310 Sequence
118	15.8	60.8	38	6	AR287165	AR287165 Sequence	191	52.3	41	6	BD009837	BD009837 Avian pol
119	15.8	60.8	38	6	BD069830	BD069830 Transgeni	192	52.3	41	6	AX107440	AX107440 Sequence
120	15.8	60.8	48	6	I12113	I12113 Sequence 18	193	52.3	41	6	AX107451	AX107451 Sequence
121	15.8	60.8	48	6	I41283	I41283 Sequence	194	52.3	41	6	AX021614	AX021614 Sequence
122	15.6	60.0	50	6	AX021613	AX021613 Sequence	195	51.5	22	6	BD262493	BD262493 Informati
123	15.4	59.2	20	6	CQ759764	CQ759764 Enzymatic	196	51.5	26	6	BD013760	BD013760 Molecule
124	15	57.7	15	6	BD206412	BD206412 Enzymatic	197	51.5	29	6	AX766391	AX766391 Sequence
125	15	57.7	15	6	BD206413	BD206413 Enzymatic	198	51.5	29	6	AX766395	AX766395 Sequence
126	15	57.7	15	6	BD208261	BD208261 Enzymatic	199	51.5	29	6	AX766399	AX766399 Sequence
127	15	57.7	15	6	BD208262	BD208262 Enzymatic	200	51.5	29	6	AX754948	AX754948 Sequence
128	15	57.7	20	6	AR011616	AR011616 Sequence	201	51.5	38	6	AX033007	AX033007 Sequence
129	15	57.7	20	6	AR027775	AR027775 Sequence	202	51.5	44	6	AR022050	AR022050 Sequence
130	15	57.7	20	6	AR037561	AR037561 Sequence	203	50.8	33	6	I92840	I92840 Sequence
131	15	57.7	20	6	AR066317	AR066317 Sequence	204	50.8	33	6	AR350032	AR350032 Sequence
132	15	57.7	20	6	E04272	E04272 DNA encodin	205	50.8	36	6	AX600090	AX600090 Sequence
133	15	57.7	20	6	E07609	E07609 PCR primer	206	50.8	39	6	AR166973	AR166973 Sequence
134	15	57.7	20	6	E08280	E08280 PCR primer	207	50.8	40	6	AR178159	AR178159 Sequence
135	15	57.7	20	6	E09425	E09425 Synthetic n	208	50.8	40	6	BD016678	BD016678 Method fo
136	15	57.7	20	6	E10531	E10531 Y probe whi	209	50.8	44	6	AR094367	AR094367 Sequence
137	15	57.7	20	6	E16395	E16395 PCR primer	210	50.8	44	6	AR098581	AR098581 Sequence
138	15	57.7	20	6	E16395	E16395 PCR primer	211	50.8	47	6	BD105576	BD105576 Process f
139	15	57.7	20	6	I12602	I12602 Sequence 12	212	50.8	22	6	AX555047	AX555047 Sequence
140	15	57.7	20	6	I25195	I25195 Sequence 9	213	50.0	23	6	AX555066	AX555066 Sequence
141	15	57.7	20	6	AX250623	AX250623 Sequence	214	50.0	23	6	AR167897	AR167897 Sequence
142	15	57.7	20	6	BD012756	BD012756 Method fo	215	50.0	27	6	BD231848	BD231848 Method fo
143	15	57.7	24	6	AR406057	AR406057 Sequence	216	50.0	27	6	BD231970	BD231970 Modified
144	15	57.7	25	6	E06774	E06774 Primer to d	217	50.0	27	6	AX019768	AX019768 Sequence
145	15	57.7	25	6	E11710	E11710 PCR primer	218	50.0	27	6	AX019818	AX019818 Sequence
146	15	57.7	30	6	AX781256	AX781256 Sequence	219	50.0	28	6	AX036349	AX036349 Sequence
147	15	57.7	30	6	AX781266	AX781266 Sequence	220	50.0	30	6	A25936	A25936 Synthetic o
148	15	57.7	30	6	AX781280	AX781280 Sequence	221	50.0	31	6	BD175851	BD175851 Glutamina
149	15	57.7	39	6	AX537335	AX537335 Sequence	222	50.0	31	6	I24794	I24794 Sequence
150	15	57.7	39	6	AX537335	AX537335 Sequence	223	50.0	31	6	AR302480	AR302480 Sequence
151	14.6	56.2	27	6	AX024182	AX024182 Sequence	224	50.0	31	6	AR364105	AR364105 Sequence
152	14.6	56.2	28	6	AX829263	AX829263 Sequence	225	50.0	31	6	BD001952	BD001952 Transform
153	14.6	56.2	32	6	BD171299	BD171299 Seven-pas	226	50.0	31	6	BD266625	BD266625 Regulatio
154	14.4	55.4	24	6	I03568	I03568 Sequence 5	227	50.0	35	6	AX047306	AX047306 Sequence
155	14.4	54.6	28	6	AR381016	AR381016 Sequence	228	50.0	36	6	AX740373	AX740373 Sequence
156	14.2	54.6	28	6	BD137440	BD137440 Polymeras	229	50.0	40	6	CQ831801	CQ831801 Sequence
157	14.2	54.6	46	6	C0760665	C0760665 Sequence	230	50.0	40	6	AR258559	AR258559 Sequence
158	14.2	54.6	46	6	AR257024	AR257024 Sequence	231	50.0	42	6	I68791	I68791 Sequence
159	14	53.8	19	6	AX590323	AX590323 Sequence	232	50.0	42	6	AR253389	AR253389 Sequence
160	14	53.8	20	6	AR167017	AR167017 Sequence	233	50.0	42	6	AX696431	AX696431 Sequence
161	14	53.8	21	6	AX004407	AX004407 Sequence	234	50.0				
162	14	53.8	21	6	AX004407	AX004407 Sequence	235	50.0				
163	14	53.8	21	6	BD077113	BD077113 Hepatitis	236	50.0				
164	14	53.8	21	6	AR094965	AR094965 Sequence	237	50.0				
165	14	53.8	28	6	AR094992	AR094992 Sequence	238	50.0				

239	13	50.0	44	6	A25937	A25937 Synthetic o	c 312	12.4	47.7	41	6	AR109128	AR109128 Sequence
c 240	13	50.0	50	6	CQ005631	CQ005631 Sequence	c 313	12.4	47.7	41	6	AR200783	AR200783 Sequence
241	12.8	49.2	20	6	BD228435	BD228435 IL-17 hom	314	12.4	47.7	41	6	AR301117	AR301117 Sequence
242	12.8	49.2	20	6	AR359660	AR359660 Sequence	c 315	12.4	47.7	42	6	AR104423	AR104423 Sequence
c 243	12.8	49.2	30	6	AX455679	AX455679 Sequence	c 316	12.4	47.7	42	6	BD062183	BD062183 Bacterici
244	12.8	49.2	30	6	AX455680	AX455680 Sequence	c 317	12.4	47.7	42	6	AR437342	AR437342 Sequence
c 245	12.8	49.2	31	6	AX4249345	AX4249345 Sequence	c 318	12.4	47.7	45	6	AX367161	AX367161 Sequence
c 246	12.8	49.2	34	6	AR088320	AR088320 Sequence	319	12.4	47.7	47	6	AX378339	AX378339 Sequence
c 247	12.8	49.2	36	6	CQ803276	CQ803276 Sequence	320	12.4	47.7	48	6	AX052950	AX052950 Sequence
c 248	12.8	49.2	36	6	BD007242	BD007242 Novel flt	c 321	12.4	47.7	50	6	CQ003965	CQ003965 Sequence
c 249	12.8	49.2	36	6	BD022516	BD022516 Multi-fun	c 322	12.4	47.7	50	6	E08489	E08489 Primer. 9/1
c 250	12.8	49.2	37	6	AR019461	AR019461 Sequence	323	12.4	47.7	50	6	E08490	E08490 Primer. 9/1
c 251	12.8	49.2	37	6	AR156410	AR156410 Sequence	c 324	12.4	47.7	50	6	AR410253	AR410253 Sequence
c 252	12.8	49.2	38	6	BD263030	BD263030 Trans-Spe	c 325	12.4	47.7	50	6	AX523294	AX523294 Sequence
253	12.8	49.2	39	6	AX600083	AX600083 Sequence	c 326	12.4	47.7	50	12	SYN33M13L	SYN33M13L
254	12.6	48.5	24	6	AX289383	AX289383 Sequence	327	12.2	46.9	20	6	AR137500	AR137500 Sequence
255	12.6	48.5	29	6	AX683921	AX683921 Sequence	c 328	12.2	46.9	20	6	E29027	E29027 Novel colle
c 256	12.6	48.5	30	6	AR125701	AR125701 Sequence	329	12.2	46.9	20	6	E29029	E29029 Novel colle
c 257	12.6	48.5	30	6	I47113	I47113 Sequence 43	330	12.2	46.9	20	6	I31997	I31997 Sequence 8
c 258	12.6	48.5	30	6	AX611395	AX611395 Sequence	331	12.2	46.9	20	6	I32681	I32681 Sequence 8
259	12.6	48.5	37	6	AR028904	AR028904 Sequence	332	12.2	46.9	20	6	AX294016	AX294016 Sequence
260	12.6	48.5	37	6	AR070309	AR070309 Sequence	c 333	12.2	46.9	21	6	AX096296	AX096296 Sequence
261	12.6	48.5	37	6	E10378	E10378 Oligonucleo	334	12.2	46.9	24	6	AR350029	AR350029 Sequence
262	12.6	48.5	37	6	AR211464	AR211464 Sequence	c 335	12.2	46.9	25	6	BD235493	BD235493 Desaturas
263	12.6	48.5	38	6	AX498608	AX498608 Sequence	336	12.2	46.9	25	6	AX115408	AX115408 Sequence
264	12.6	48.5	38	6	AX537941	AX537941 Sequence	c 337	12.2	46.9	27	6	AR381020	AR381020 Sequence
c 265	12.6	48.5	41	6	BD217566	BD217566 Glucoamyl	c 338	12.2	46.9	27	6	BD137444	BD137444 Polymeras
c 266	12.6	48.5	41	6	AR198446	AR198446 Sequence	c 339	12.2	46.9	28	6	AX4168	AX4168 Sequence 11
267	12.6	48.5	49	6	E27256	E27256 4(R)-Hydrox	340	12.2	46.9	29	6	AX328144	AX328144 Sequence
c 268	12.4	47.7	14	6	AX021616	AX021616 Sequence	c 341	12.2	46.9	30	6	AR219302	AR219302 Sequence
c 269	12.4	47.7	20	6	AX297040	AX297040 Sequence	c 342	12.2	46.9	30	6	AX316118	AX316118 Sequence
270	12.4	47.7	24	6	A23024	A23024 oligonucleo	343	12.2	46.9	32	6	AX094808	AX094808 Sequence
c 271	12.4	47.7	24	6	I23842	I23842 Sequence 6	c 344	12.2	46.9	33	6	AR062181	AR062181 Sequence
c 272	12.4	47.7	24	6	AX292407	AX292407 Sequence	c 345	12.2	46.9	33	6	AR135159	AR135159 Sequence
c 273	12.4	47.7	25	6	A44199	A44199 Sequence 4	c 346	12.2	46.9	33	6	AX356198	AX356198 Sequence
c 274	12.4	47.7	25	6	AR020949	AR020949 Sequence	347	12.2	46.9	35	6	BD178794	BD178794 Gene pane
c 275	12.4	47.7	25	6	E15944	E15944 Primer. 7/1	348	12.2	46.9	35	6	CQ784048	CQ784048 Sequence
276	12.4	47.7	25	6	AX428019	AX428019 Sequence	c 349	12.2	46.9	35	6	AX716607	AX716607 Sequence
c 277	12.4	47.7	25	6	BD057994	BD057994 Nucleic a	350	12.2	46.9	35	6	AX750424	AX750424 Sequence
c 278	12.4	47.7	27	6	I14900	I14900 Sequence 29	351	12.2	46.9	35	6	AX837771	AX837771 Sequence
c 279	12.4	47.7	27	6	AX023915	AX023915 Sequence	352	12.2	46.9	35	6	BD127972	BD127972 Primer fo
c 280	12.4	47.7	27	6	AX537795	AX537795 Sequence	c 353	12.2	46.9	35	11	BX664502	BX664502 Arabidops
281	12.4	47.7	28	6	AR173071	AR173071 Sequence	354	12.2	46.9	36	6	BD179472	BD179472 Gene expr
c 282	12.4	47.7	28	6	AR173072	AR173072 Sequence	355	12.2	46.9	36	6	BD188811	BD188811 Gene exp
c 283	12.4	47.7	28	6	AR400791	AR400791 Sequence	356	12.2	46.9	36	6	CQ768249	CQ768249 Sequence
c 284	12.4	47.7	30	6	AR018082	AR018082 Sequence	357	12.2	46.9	36	6	AX551333	AX551333 Sequence
c 285	12.4	47.7	30	6	AR051922	AR051922 Sequence	358	12.2	46.9	36	6	AX552033	AX552033 Sequence
c 286	12.4	47.7	30	6	AR166532	AR166532 Sequence	c 359	12.2	46.9	37	6	AR473388	AR473388 Sequence
c 287	12.4	47.7	30	6	AR166533	AR166533 Sequence	c 360	12.2	46.9	37	6	BD138024	BD138024 Expressio
c 288	12.4	47.7	30	6	E03441	E03441 a primer to	c 361	12.2	46.9	38	6	CQ768250	CQ768250 Sequence
c 289	12.4	47.7	30	6	I14133	I14133 Sequence 7	c 362	12.2	46.9	38	6	AX349361	AX349361 Sequence
c 290	12.4	47.7	31	6	BD264523	BD264523 Compounds	c 363	12.2	46.9	38	6	AX551334	AX551334 Sequence
291	12.4	47.7	31	6	AR229334	AR229334 Sequence	c 364	12.2	46.9	38	6	AX552034	AX552034 Sequence
292	12.4	47.7	31	6	AR321952	AR321952 Sequence	c 365	12.2	46.9	39	6	CQ784049	CQ784049 Sequence
293	12.4	47.7	31	6	AX155961	AX155961 Sequence	c 366	12.2	46.9	39	6	AX716608	AX716608 Sequence
294	12.4	47.7	31	6	AX361811	AX361811 Sequence	c 367	12.2	46.9	39	6	AX750425	AX750425 Sequence
295	12.4	47.7	31	6	AX597830	AX597830 Sequence	c 368	12.2	46.9	39	6	AX754930	AX754930 Sequence
c 296	12.4	47.7	31	6	AX800166	AX800166 Sequence	c 369	12.2	46.9	39	6	AX837772	AX837772 Sequence
c 297	12.4	47.7	32	6	I58622	I58622 Sequence 8	c 370	12.2	46.9	39	6	BD127973	BD127973 Primer fo
c 298	12.4	47.7	32	6	I63520	I63520 Sequence 8	c 371	12.2	46.9	42	6	AX754928	AX754928 Sequence
c 299	12.4	47.7	33	6	AX2023	AX2023 oligonucleo	372	12.2	46.9	42	6	HSA224213	HSA224213 Homo sapi
300	12.4	47.7	33	6	AR171737	AR171737 Sequence	c 373	12.2	46.9	44	6	AR094370	AR094370 Sequence
301	12.4	47.7	33	6	CQ788404	CQ788404 Sequence	c 374	12.2	46.9	44	6	AR098584	AR098584 Sequence
302	12.4	47.7	33	6	CQ793255	CQ793255 Sequence	c 375	12.2	46.9	47	6	AR289956	AR289956 Sequence
303	12.4	47.7	33	6	CQ793624	CQ793624 Sequence	c 376	12.2	46.9	48	6	AR014580	AR014580 Sequence
c 304	12.4	47.7	33	6	I23841	I23841 Sequence 5	c 377	12.2	46.9	48	6	CQ775533	CQ775533 Sequence
c 305	12.4	47.7	34	6	AR301122	AR301122 Sequence	c 378	12.2	46.9	48	6	AR212171	AR212171 Sequence
306	12.4	47.7	35	6	A09905	A09905 Probe. 1/19	c 379	12.2	46.9	48	6	AR235382	AR235382 Sequence
c 307	12.4	47.7	38	6	AR075136	AR075136 Sequence	c 380	12.2	46.9	48	6	BD10372	BD10372 Chimeric
308	12.4	47.7	38	6	I40784	I40784 Sequence 11	c 381	12.2	46.9	48	6	BD135148	BD135148 Chitin-bi
c 309	12.4	47.7	39	6	CQ824334	CQ824334 Sequence	382	12.2	46.9	50	6	CQ003286	CQ003286 Sequence
c 310	12.4	47.7	40	6	CQ827143	CQ827143 Sequence	383	12.2	46.9	50	6	AR285631	AR285631 Sequence
c 311	12.4	47.7	40	6	E22422	E22422 Method for	384	12	46.2	16	6	AR397622	AR397622 Sequence

385	12	46.2	17	6	C0622720	Sequence	458	12	46.2	30	6	AX244134	Sequence
386	12	46.2	17	6	C0622721	Sequence	C 459	12	46.2	30	6	AX244135	Sequence
387	12	46.2	17	6	C0622722	Sequence	C 460	12	46.2	30	6	BD058042	Nucleic a
388	12	46.2	17	6	C0622723	Sequence	C 461	12	46.2	30	6	BD070090	Modified
389	12	46.2	17	6	C0622724	Sequence	C 462	12	46.2	33	6	AR106268	Sequence
390	12	46.2	17	6	C0622725	Sequence	C 463	12	46.2	33	6	AX958724	Sequence
391	12	46.2	17	6	AR463783	Sequence	C 464	12	46.2	33	6	BD008836	Sequence
392	12	46.2	17	6	AR463784	Sequence	C 465	12	46.2	34	6	AX467640	Sequence
393	12	46.2	17	6	AR463785	Sequence	C 466	12	46.2	35	6	AR050782	Sequence
394	12	46.2	17	6	AR463786	Sequence	C 467	12	46.2	35	6	E35050	Novel nucle
395	12	46.2	17	6	AR463787	Sequence	C 468	12	46.2	36	6	A20625	IN-Phase fu
396	12	46.2	17	6	AR463788	Sequence	C 469	12	46.2	36	6	E26546	DTST gene
397	12	46.2	18	6	I12114	Sequence 19	C 470	12	46.2	37	6	BD268930	Anti-vira
398	12	46.2	18	6	I12114	Sequence 19	C 471	12	46.2	37	6	AR302583	Sequence
399	12	46.2	18	6	AX059438	Sequence	C 472	12	46.2	37	6	AX019151	Sequence
400	12	46.2	20	6	A52657	Sequence 2	C 473	12	46.2	37	6	AX035482	Sequence
401	12	46.2	20	6	AR167015	Sequence	C 474	12	46.2	37	6	AX056855	Sequence
402	12	46.2	20	6	BD185858	A stabili	C 475	12	46.2	37	6	AX127699	Sequence
403	12	46.2	20	6	AR210670	Sequence	C 476	12	46.2	37	6	BD130487	Antiviral
404	12	46.2	21	6	AX959816	Sequence	C 477	12	46.2	38	6	A71965	Sequence 27
405	12	46.2	22	6	BD056594	Method to	C 478	12	46.2	38	6	AR147153	Sequence
406	12	46.2	22	6	I76916	Sequence 24	C 479	12	46.2	38	6	AR236314	Sequence
407	12	46.2	23	6	C0815557	Sequence	C 480	12	46.2	38	6	BD009841	Avian pol
408	12	46.2	23	6	AR400955	Sequence	C 481	12	46.2	39	6	AR111241	Sequence
409	12	46.2	23	6	AX074114	Sequence	C 482	12	46.2	39	6	BD086914	Nucleic a
410	12	46.2	24	6	A42939	Sequence 9	C 483	12	46.2	40	6	BD185268	Method fo
411	12	46.2	24	6	C0815555	Sequence	C 484	12	46.2	40	6	BD185271	Method fo
412	12	46.2	24	6	AR400953	Sequence	C 485	12	46.2	40	6	AX107452	Sequence
413	12	46.2	24	6	AX074112	Sequence	C 486	12	46.2	40	10	MARHV2	Woodchuck D
414	12	46.2	24	6	AX074113	Sequence	C 487	12	46.2	41	6	A98352	Sequence 26
415	12	46.2	25	6	AR82286	Sequence	C 488	12	46.2	41	6	C0841202	Sequence
416	12	46.2	25	6	AR120828	Sequence	C 489	12	46.2	41	6	AX107218	Sequence
417	12	46.2	25	6	C0627612	Sequence	C 490	12	46.2	41	6	AX107448	Sequence
418	12	46.2	25	6	C0627613	Sequence	C 491	12	46.2	41	6	AX515136	Sequence
419	12	46.2	25	6	C0627614	Sequence	C 492	12	46.2	41	6	AX521344	Sequence
420	12	46.2	25	6	C0627615	Sequence	C 493	12	46.2	42	6	AX107220	Sequence
421	12	46.2	25	6	C0627616	Sequence	C 494	12	46.2	42	6	AX107449	Sequence
422	12	46.2	25	6	C0627617	Sequence	C 495	12	46.2	43	6	I21480	Sequence 27
423	12	46.2	25	6	C0627618	Sequence	C 496	12	46.2	43	6	AX664845	Sequence
424	12	46.2	25	6	C0627619	Sequence	C 497	12	46.2	43	6	I08940	Sequence 3
425	12	46.2	25	6	C0627620	Sequence	C 498	12	46.2	43	6	A98356	Sequence 30
426	12	46.2	25	6	C0627621	Sequence	C 499	12	46.2	48	6	A98358	Sequence 32
427	12	46.2	25	6	C0627622	Sequence	C 500	12	46.2	48	6	AR078404	Sequence
428	12	46.2	25	6	C0627623	Sequence	C 501	12	46.2	48	6	BD217296	Mammalian
429	12	46.2	25	6	C0627624	Sequence	C 502	12	46.2	48	8	AJ525150	Arabidops
430	12	46.2	25	6	C0627625	Sequence	C 503	12	46.2	48	8	AXH525150	Sequence
431	12	46.2	25	6	I55048	Sequence 14	C 504	12	46.2	49	6	C0815558	Sequence
432	12	46.2	25	6	I78332	Sequence 13	C 505	12	46.2	49	6	AX400956	Sequence
433	12	46.2	25	6	AR468675	Sequence	C 506	12	46.2	50	6	CQ005630	Sequence
434	12	46.2	25	6	AR468676	Sequence	C 507	12	46.2	50	6	CQ008788	Sequence
435	12	46.2	25	6	AR468677	Sequence	C 508	12	46.2	50	6	CQ008807	Sequence
436	12	46.2	25	6	AR468678	Sequence	C 509	12	46.2	50	6	CQ008808	Sequence
437	12	46.2	25	6	AR468679	Sequence	C 510	11.8	45.4	18	9	S81156	T cell anti
438	12	46.2	25	6	AR468680	Sequence	C 511	11.8	45.4	20	6	AR109061	Sequence
439	12	46.2	25	6	AR468681	Sequence	C 512	11.8	45.4	20	6	BD196071	Anti-sense
440	12	46.2	25	6	AR468682	Sequence	C 513	11.8	45.4	20	6	AR200716	Sequence
441	12	46.2	25	6	AR468683	Sequence	C 514	11.8	45.4	20	6	AR311568	Sequence
442	12	46.2	25	6	AR468684	Sequence	C 515	11.8	45.4	20	6	AR313073	Sequence
443	12	46.2	25	6	AR468685	Sequence	C 516	11.8	45.4	20	6	AR382862	Sequence
444	12	46.2	25	6	AR468686	Sequence	C 517	11.8	45.4	21	6	BD013407	Method fo
445	12	46.2	25	6	AR468687	Sequence	C 518	11.8	45.4	22	6	A86925	Sequence 16
446	12	46.2	25	6	AR468688	Sequence	C 519	11.8	45.4	22	6	AR048337	Sequence
447	12	46.2	27	6	A21139	Oligonucleo	C 520	11.8	45.4	22	6	AR079228	Sequence
448	12	46.2	27	6	CQ774577	Sequence	C 521	11.8	45.4	22	6	AR224003	Sequence
449	12	46.2	27	6	E35051	Novel nucle	C 522	11.8	45.4	22	6	AR224003	Sequence
450	12	46.2	27	6	AX259721	Sequence	C 523	11.8	45.4	22	6	AR309659	Sequence
451	12	46.2	29	6	HUMRP20A	Sequence	C 524	11.8	45.4	22	6	AX376674	Sequence
452	12	46.2	30	6	A47694	Homo sapien	C 525	11.8	45.4	24	6	BD234631	Thymidine
453	12	46.2	30	6	BD244422	Mutants o	C 526	11.8	45.4	24	6	BD230227	Sequence
454	12	46.2	30	6	BD244423	Mutants o	C 527	11.8	45.4	25	6	CQ627159	Sequence
455	12	46.2	30	6	AX428067	Sequence	C 528	11.8	45.4	25	6	CQ627160	Sequence
456	12	46.2	30	6	AX027139	Sequence	C 529	11.8	45.4	25	6	AR428019	Sequence
457	12	46.2	30	6	AX027140	Sequence	C 530	11.8	45.4	25	6	AR468222	Sequence

531	11.8	45.4	25	6	AR468223	Sequence	AR468223	Sequence	11.8	45.4	604	42	6	AR222675	Sequence
532	11.8	45.4	25	6	AR468224	Sequence	AR468224	Sequence	11.8	45.4	605	42	6	AR399762	Sequence
533	11.8	45.4	25	6	BD057994	Nucleic a	BD057994	Nucleic a	11.8	45.4	606	42	6	AR474780	Sequence
534	11.8	45.4	26	6	AR072051	Sequence	AR1672051	Sequence	11.8	45.4	607	42	6	AX448991	Sequence
535	11.8	45.4	26	6	AR165219	Sequence	AR165219	Sequence	11.8	45.4	608	42	6	AX555552	Sequence
536	11.8	45.4	26	6	BD244653	Low tempe	BD244653	Low tempe	11.8	45.4	609	42	6	BD070956	Novel hum
537	11.8	45.4	26	6	AR254653	Sequence	AR254653	Sequence	11.8	45.4	610	43	6	AR034922	Sequence
538	11.8	45.4	26	6	AR343261	Sequence	AR343261	Sequence	11.8	45.4	611	44	6	CQ760661	Sequence
539	11.8	45.4	26	6	AR455528	Sequence	AR455528	Sequence	11.8	45.4	612	44	6	AX427216	Sequence
540	11.8	45.4	26	6	AR224994	Sequence	AR224994	Sequence	11.8	45.4	613	46	6	AR175600	Sequence
541	11.8	45.4	27	6	AL7048	Oligonucleo	AL7048	Oligonucleo	11.8	45.4	614	47	6	AR289222	Sequence
542	11.8	45.4	27	6	AL7448	Oligonucleo	AL7448	Oligonucleo	11.8	45.4	615	47	6	AR291247	Sequence
543	11.8	45.4	27	6	AR014423	Sequence	AR014423	Sequence	11.8	45.4	616	47	6	AR291871	Sequence
544	11.8	45.4	27	6	AR137130	Sequence	AR137130	Sequence	11.8	45.4	617	48	6	AX777183	Sequence
545	11.8	45.4	27	6	AR140406	Sequence	AR140406	Sequence	11.8	45.4	618	48	6	AX927790	Sequence
546	11.8	45.4	27	6	IL1866	Sequence 32	IL1866	Sequence 32	11.8	45.4	619	48	8	AX718213	Nicotiana
547	11.8	45.4	27	6	AR277649	Sequence	AR277649	Sequence	11.8	45.4	620	49	6	AR011811	Sequence
548	11.8	45.4	27	6	BD131033	Plant-ori	BD131033	Plant-ori	11.8	45.4	621	49	6	AR129029	Sequence
549	11.8	45.4	28	6	AX591059	Sequence	AX591059	Sequence	11.8	45.4	622	49	6	BD243380	Nucleic a
550	11.8	45.4	28	6	AX712098	Sequence	AX712098	Sequence	11.8	45.4	623	49	6	I77134	Sequence 6
551	11.8	45.4	29	6	AR075128	Sequence	AR075128	Sequence	11.8	45.4	624	49	6	AR239789	Sequence
552	11.8	45.4	29	6	AX098923	Sequence	AX098923	Sequence	11.8	45.4	625	49	6	AX279591	Sequence
553	11.8	45.4	29	6	AX099343	Sequence	AX099343	Sequence	11.8	45.4	626	50	6	CQ004071	Sequence
554	11.8	45.4	29	6	AX275252	Sequence	AX275252	Sequence	11.8	45.4	627	50	6	CQ798735	Sequence
555	11.8	45.4	29	6	AX598462	Sequence	AX598462	Sequence	11.8	45.4	628	50	6	AR356569	Sequence
556	11.8	45.4	30	6	I79319	Sequence 22	I79319	Sequence 22	11.8	45.4	629	50	6	AR381687	Sequence
557	11.8	45.4	31	6	AR084215	Sequence	AR084215	Sequence	11.8	45.4	630	50	6	AR381689	Sequence
558	11.8	45.4	31	6	AR171738	Sequence	AR171738	Sequence	11.8	45.4	631	50	6	AX395198	Sequence
559	11.8	45.4	31	6	I90358	Sequence 2	I90358	Sequence 2	11.8	45.4	632	50	6	AX35201	Sequence
560	11.8	45.4	31	6	BD002681	Gene comp	BD002681	Gene comp	11.8	45.4	633	50	6	BD070868	Insect ex
561	11.8	45.4	32	6	BD211474	Adenovira	BD211474	Adenovira	11.6	44.6	634	18	6	BD274782	CANCER CE
562	11.8	45.4	32	6	AR3430574	Sequence	AR3430574	Sequence	11.6	44.6	635	18	6	AR205248	Sequence
563	11.8	45.4	32	6	AX073434	Sequence	AX073434	Sequence	11.6	44.6	636	19	6	AX138863	Sequence
564	11.8	45.4	33	6	AR368978	Sequence	AR368978	Sequence	11.6	44.6	637	20	6	AX138863	Sequence
565	11.8	45.4	33	6	AR409609	Sequence	AR409609	Sequence	11.6	44.6	638	20	6	AX293770	Sequence
566	11.8	45.4	33	6	AX081230	Sequence	AX081230	Sequence	11.6	44.6	639	20	6	BD015558	Novel pol
567	11.8	45.4	33	6	AX675239	Sequence	AX675239	Sequence	11.6	44.6	640	21	6	E3282	Modified se
568	11.8	45.4	33	6	BD011010	Hiv probe	BD011010	Hiv probe	11.6	44.6	641	22	6	AX343843	Sequence
569	11.8	45.4	35	6	AX39869	Sequence 3	AX39869	Sequence 3	11.6	44.6	642	23	6	AR363348	Sequence
570	11.8	45.4	35	6	A69029	Sequence 17	A69029	Sequence 17	11.6	44.6	643	24	6	AX289137	Sequence
571	11.8	45.4	35	6	AR171740	Sequence	AR171740	Sequence	11.6	44.6	644	24	6	AX444840	Sequence
572	11.8	45.4	35	6	BD211475	Adenovira	BD211475	Adenovira	11.6	44.6	645	24	6	AX937076	Sequence
573	11.8	45.4	35	6	AR193479	Sequence	AR193479	Sequence	11.6	44.6	646	25	6	AX951934	Sequence
574	11.8	45.4	35	6	AX073435	Sequence	AX073435	Sequence	11.6	44.6	647	25	6	AR007404	Sequence
575	11.8	45.4	35	6	BD006106	Feline po	BD006106	Feline po	11.6	44.6	648	25	6	AR007407	Sequence
576	11.8	45.4	36	6	AR119928	Sequence	AR119928	Sequence	11.6	44.6	649	25	6	BD177988	Acylated
577	11.8	45.4	36	6	CQ803276	Sequence	CQ803276	Sequence	11.6	44.6	650	25	6	BD177991	Acylated
578	11.8	45.4	36	6	BD006745	Novel pol	BD006745	Novel pol	11.6	44.6	651	25	6	AX487732	Sequence
579	11.8	45.4	36	6	BD078872	Tumor pro	BD078872	Tumor pro	11.6	44.6	652	26	6	A83432	Sequence 18
580	11.8	45.4	38	6	AR106214	Sequence	AR106214	Sequence	11.6	44.6	653	26	6	CQ778371	Sequence
581	11.8	45.4	38	6	AR178180	Sequence	AR178180	Sequence	11.6	44.6	654	27	6	AR105799	Sequence
582	11.8	45.4	38	6	BD235325	Enzyme fo	BD235325	Enzyme fo	11.6	44.6	655	27	6	AR280223	Sequence
583	11.8	45.4	38	6	AR336455	Sequence	AR336455	Sequence	11.6	44.6	656	27	6	AX081590	Sequence
584	11.8	45.4	38	6	AR473662	Sequence	AR473662	Sequence	11.6	44.6	657	27	6	AX374771	Sequence
585	11.8	45.4	38	6	AX219576	Sequence	AX219576	Sequence	11.6	44.6	658	28	6	A05814	Oligonucleo
586	11.8	45.4	39	6	AR361446	Sequence	AR361446	Sequence	11.6	44.6	659	28	6	I07809	Sequence 5
587	11.8	45.4	39	6	AR361467	Sequence	AR361467	Sequence	11.6	44.6	660	28	6	AX023918	Sequence
588	11.8	45.4	39	6	AX058342	Sequence	AX058342	Sequence	11.6	44.6	661	29	6	AR363828	Sequence
589	11.8	45.4	39	6	AX058364	Sequence	AX058364	Sequence	11.6	44.6	662	30	6	AR118762	Sequence
590	11.8	45.4	39	6	AX062302	Sequence	AX062302	Sequence	11.6	44.6	663	30	6	BD262240	Informati
591	11.8	45.4	40	6	AR146102	Sequence	AR146102	Sequence	11.6	44.6	664	30	6	I06394	Sequence 14
592	11.8	45.4	40	6	AR228736	Sequence	AR228736	Sequence	11.6	44.6	665	30	6	AR308733	Sequence
593	11.8	45.4	40	6	CQ771869	Neisseria	CQ771869	Neisseria	11.6	44.6	666	30	6	AX037663	Sequence
594	11.8	45.4	40	6	AR476110	Sequence	AR476110	Sequence	11.6	44.6	667	30	6	AX298214	Sequence
595	11.8	45.4	40	6	AR27649	Sequence	AR27649	Sequence	11.6	44.6	668	30	6	AX460252	Sequence
596	11.8	45.4	42	6	AR044709	Sequence	AR044709	Sequence	11.6	44.6	669	31	6	A05813	Oligonucleo
597	11.8	45.4	42	6	AR052356	Sequence	AR052356	Sequence	11.6	44.6	670	32	6	AX452011	Sequence
598	11.8	45.4	42	6	AR055154	Sequence	AR055154	Sequence	11.6	44.6	671	32	6	AX538800	Sequence
599	11.8	45.4	42	6	AR089670	Sequence	AR089670	Sequence	11.6	44.6	672	32	6	BD022405	Multi-fun
600	11.8	45.4	42	6	AR158025	Sequence	AR158025	Sequence	11.6	44.6	673	33	6	AX280474	Sequence
601	11.8	45.4	42	6	I13542	Sequence 27	I13542	Sequence 27	11.6	44.6	674	35	6	AR212155	Sequence
602	11.8	45.4	42	6	I15801	Sequence 27	I15801	Sequence 27	11.6	44.6	675	35	6	BD135132	Chitin bi
603	11.8	45.4	42	6	I92505	Sequence 27	I92505	Sequence 27	11.6	44.6	676	36	6	A68640	Sequence 8

C 677	11.6	44.6	36	6	AR048679	Sequence	750	11.4	43.8	25	6	AR468220	Sequence
C 678	11.6	44.6	36	6	AR214446	Sequence	751	11.4	43.8	25	6	AR468221	Sequence
C 679	11.6	44.6	36	6	AR12296	Sequence	C 752	11.4	43.8	25	6	AX119661	Sequence
C 680	11.6	44.6	36	6	AR492783	Sequence	C 753	11.4	43.8	25	6	AX268940	Sequence
C 681	11.6	44.6	36	6	BD070096	Modified	C 754	11.4	43.8	25	6	AX305191	Sequence
C 682	11.6	44.6	37	6	AS9306	Sequence 6	C 755	11.4	43.8	25	6	AX447595	Sequence
C 683	11.6	44.6	37	6	AX063383	Sequence	756	11.4	43.8	25	6	AX688910	Sequence
C 684	11.6	44.6	38	6	AR305250	Sequence	757	11.4	43.8	25	6	AX688911	Sequence
C 685	11.6	44.6	38	6	AR309354	Sequence	758	11.4	43.8	25	6	AX688912	Sequence
C 686	11.6	44.6	38	6	BD106161	Novel LDL	759	11.4	43.8	25	6	AX688913	Sequence
C 687	11.6	44.6	39	6	AR122257	Sequence	760	11.4	43.8	25	6	AX688914	Sequence
C 688	11.6	44.6	39	6	AR131231	Sequence	C 761	11.4	43.8	25	6	BD075788	Sequence
C 689	11.6	44.6	39	6	AR301046	Sequence	C 762	11.4	43.8	25	6	BD075788	Sequence
C 690	11.6	44.6	39	6	AX600082	Sequence	C 763	11.4	43.8	25	6	BD106039	Novel LDL
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C 692	11.6	44.6	41	6	AR141178	Sequence	765	11.4	43.8	26	6	AR087927	Sequence
C 693	11.6	44.6	41	6	AR141189	Sequence	766	11.4	43.8	26	6	I80119	Sequence 8
C 694	11.6	44.6	41	6	AR754917	Sequence	767	11.4	43.8	26	6	I80145	Sequence 34
C 695	11.6	44.6	42	6	AR139460	Sequence	768	11.4	43.8	26	6	AX300582	Sequence
C 696	11.6	44.6	42	6	E25566	Process for	C 769	11.4	43.8	27	6	AR112688	Sequence
C 697	11.6	44.6	42	6	E25724	Method for	770	11.4	43.8	27	6	I07895	Sequence 3
C 698	11.6	44.6	42	6	AX202530	Sequence	771	11.4	43.8	27	6	E0584	DNA encodin
C 699	11.6	44.6	42	6	BD092982	A primer	772	11.4	43.8	27	6	I07895	Sequence 3
C 700	11.6	44.6	43	6	A73753	Sequence 2	773	11.4	43.8	27	6	AR473616	Sequence
C 701	11.6	44.6	43	6	AR059885	Sequence	C 774	11.4	43.8	27	6	AX544271	Sequence 2
C 702	11.6	44.6	43	6	AR059885	Sequence	775	11.4	43.8	27	6	AX544271	Sequence 2
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C 704	11.6	44.6	44	6	AR146157	Sequence	C 777	11.4	43.8	28	6	AR206959	Sequence
C 705	11.6	44.6	46	6	AX026431	Sequence	778	11.4	43.8	28	6	BD107720	Tissue pl
C 706	11.6	44.6	47	6	AX026431	Sequence	C 779	11.4	43.8	28	6	CQ788604	Sequence
C 707	11.6	44.6	47	6	AX057956	Sequence	C 780	11.4	43.8	29	6	AX060666	Sequence
C 708	11.6	44.6	48	6	AR242018	Sequence	C 781	11.4	43.8	30	6	BD184121	Method an
C 709	11.6	44.6	48	6	AX202537	Sequence	C 782	11.4	43.8	30	6	CQ753981	Sequence
C 710	11.6	44.6	48	6	AX957796	Sequence	783	11.4	43.8	30	6	I17184	Sequence 5
C 711	11.6	44.6	48	6	AX958047	Sequence	C 784	11.4	43.8	30	6	AX085877	Sequence
C 712	11.6	44.6	49	6	AX522688	Sequence	C 785	11.4	43.8	30	6	AX742297	Sequence
C 713	11.6	44.6	49	6	AX522688	Sequence	C 786	11.4	43.8	30	6	AX742297	Sequence
C 714	11.6	44.6	50	6	AX157272	Sequence	C 787	11.4	43.8	31	6	CQ7741293	Sequence
C 715	11.6	44.6	50	6	AX160422	Sequence	C 788	11.4	43.8	31	6	CQ7741293	Sequence
C 716	11.6	44.6	50	6	AX160422	Sequence	C 789	11.4	43.8	31	6	AX032925	Sequence
C 717	11.6	44.6	50	6	AX160422	Sequence	790	11.4	43.8	31	6	AX097670	Sequence
C 718	11.6	44.6	50	6	AX160422	Sequence	C 791	11.4	43.8	31	6	AX221332	Sequence
C 719	11.4	43.8	17	6	BD105080	Kit and m	C 792	11.4	43.8	31	6	AX221332	Sequence
C 720	11.4	43.8	17	6	AX211680	Sequence	793	11.4	43.8	31	6	AX221332	Sequence
C 721	11.4	43.8	20	6	AX294646	Sequence	C 794	11.4	43.8	31	6	AX456380	Sequence
C 722	11.4	43.8	20	6	AX785883	Sequence	C 795	11.4	43.8	31	6	AX456380	Sequence
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C 725	11.4	43.8	21	6	AX785883	Sequence	C 798	11.4	43.8	31	6	AX456380	Sequence
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C 845	11.4	43.8	40	6	AX538475	AX538475 Sequence	C 918	11.2	43.1	26	6	AR452184	AR452184 Sequence
C 846	11.4	43.8	41	6	AR084458	AR084458 Sequence	C 919	11.2	43.1	26	6	AX262273	AX262273 Sequence
C 847	11.4	43.8	41	6	I19967	I19967 Sequence 33	C 920	11.2	43.1	26	6	AX719070	AX719070 Sequence
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C 851	11.4	43.8	41	6	AX519259	AX519259 Sequence	C 924	11.2	43.1	27	6	AR143749	AR143749 Sequence
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C 856	11.4	43.8	43	6	AX153783	AX153783 Sequence	C 929	11.2	43.1	28	6	BD243597	BD243597 TNFR rela
C 857	11.4	43.8	44	6	CQ802009	CQ802009 Sequence	C 930	11.2	43.1	28	6	AR197419	AR197419 Sequence
C 858	11.4	43.8	44	6	BD022454	BD022454 Multici-fun	C 931	11.2	43.1	28	6	AR259573	AR259573 Sequence
C 859	11.4	43.8	45	6	AX456429	AX456429 Sequence	C 932	11.2	43.1	28	6	BD138046	BD138046 Expressio
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C 864	11.4	43.8	47	6	AR288883	AR288883 Sequence	C 937	11.2	43.1	30	6	BD262239	BD262239 Informati
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C 866	11.4	43.8	47	6	AR292054	AR292054 Sequence	C 939	11.2	43.1	30	6	AR219295	AR219295 Sequence
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C 874	11.4	43.8	49	6	AR476518	AR476518 Sequence	C 947	11.2	43.1	31	6	AR321954	AR321954 Sequence
C 875	11.4	43.8	49	6	AR487144	AR487144 Sequence	C 948	11.2	43.1	31	6	AR368080	AR368080 Sequence
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C 882	11.4	43.8	50	6	AR372737	AR372737 Sequence	C 955	11.2	43.1	32	6	BD249675	BD249675 DNA seque
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C 887	11.2	43.1	18	6	AX360181	AX360181 Sequence	C 960	11.2	43.1	32	6	AX417736	AX417736 Sequence
C 888	11.2	43.1	20	6	AR088615	AR088615 Sequence	C 961	11.2	43.1	33	6	CQ798273	CQ798273 Sequence
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C 893	11.2	43.1	21	6	AX7938	AX7938 Sequence 5	C 966	11.2	43.1	36	6	BD184735	BD184735 Transcrip
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SOURCE		Unknown.	
ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 26)	
TITLE		Will, S. Gordon.	
JOURNAL		Modified nucleic acid amplification primers	
FEATURES		Patent: US 6001611-A 3 14-DEC-1999;	
		Location/Qualifiers	
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Query Match		100.0%; Score 26; DB 6; Length 26;	
Best Local Similarity		100.0%; Pred. No. 0.091;	
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Db		1 GCAGAAAGCGTCTAGCCATGGCGTTA 26	
RESULT 3			
BD181367		26 bp DNA linear PAT 15-MAY-2003	
LOCUS		A method for determination of a nucleic acid using a control.	
DEFINITION		BD181367	
ACCESSION		BD181367.1 GI:30792285	
VERSION		JP 2002335981-A/6.	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1 (bases 1 to 26)	
AUTHORS		Jaeger, S.	
TITLE		A method for determination of a nucleic acid using a control	
JOURNAL		Patent: JP 2002335981-A 6 26-NOV-2002;	
COMMENT		F HOFFMANN LA ROCHE AG	
		OS Artificial Sequence	
		PN JP 2002335981-A/6	
		PD 26-NOV-2002	
		PF 04-MAR-2002 JP 2002057515	
		PR 02-MAR-2001 EP 01105172.9	
		PI STEPHAN JAEGER	
		PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,	
		PC C12N15/00	
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		CC sequence	
		FH Key	
		FT source	
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FEATURES			
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		/db_xref="taxon:32630"	
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Best Local Similarity		100.0%; Pred. No. 0.091;	
Matches		26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db		1 GCAGAAAGCGTCTAGCCATGGCGTTA 26	
RESULT 4			
AX147021		26 bp DNA linear PAT 08-JUN-2001	
LOCUS		AX147021	
DEFINITION		Sequence 15 from Patent WO0137291.	
ACCESSION		AX147021	
VERSION		AX147021.1 GI:14346292	
KEYWORDS			

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 15 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
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/note="derivatization with a p-(t-butyl)benzyl-residue"
/mod_base=OTHER

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 5
AX523947
LOCUS AX523947 26 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 6 from Patent EP1236804.
ACCESSION AX523947
VERSION AX523947.1 GI:25168878
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 6 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
AX524845
LOCUS AX524845 26 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 6 from Patent EP1236805.
ACCESSION AX524845
VERSION AX524845.1 GI:25169939
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Jaeger,S.

TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 6 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ST280 HCV-specific Primer-sequence"

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Query Match 100.0%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.091;
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Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 7
AR428911
LOCUS AR428911 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6642204.
ACCESSION AR428911
VERSION AR428911.1 GI:40188742
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Llinas-Brunet,M. and Gorys,V.J.
TITLE Hepatitis C inhibitor tri-peptides
JOURNAL Patent: US 6642204-A 1 04-NOV-2003;
FEATURES Location/Qualifiers
source 1..30
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ORIGIN

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Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 8
AR488114
LOCUS AR488114 30 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 17 from patent US 6706874.
ACCESSION AR488114
VERSION AR488114.1 GI:47253862
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kukolj,G. and Pause,A.
TITLE Self-replicating RNA molecule from hepatitis C virus
JOURNAL Patent: US 6706874-A 17 16-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Nov 24 08:46:07 2004

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QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 9
AX472307
LOCUS AX472307 30 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 17 from Patent WO02052015.
ACCESSION AX472307
VERSION AX472307.1 GI:22207326
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE
AUTHORS Beaulieu, P.L., Fazal, G., Kukolj, G., Jolicoeur, E., Gillard, J.,
TITLE Poupart, M.A. and Rancourt, J.
JOURNAL Viral polymerase inhibitors
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1. .30
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RESULT 10
AX696019
LOCUS AX696019 30 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2 from Patent WO03007945.
ACCESSION AX696019
VERSION AX696019.1 GI:29419181
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Beaulieu, P.L., Fazal, G., Goulet, S., Kukolj, G., Poirier, M. and
TITLE Tsantrizos, Y.S.
JOURNAL Viral polymerase inhibitors
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1. .30
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/db_xref="taxon:32630"
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RESULT 11
AX720383
LOCUS AX720383 30 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 2 from Patent WO03010140.
ACCESSION AX720383.1 GI:29892202
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Beaulieu, P.L., Fazal, G., Kukolj, G., Jolicoeur, E., Gillard, J.,
TITLE Poupart, M.A. and Rancourt, J.
JOURNAL Viral polymerase inhibitors
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="Forward Primer"

ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12
AX720387
LOCUS AX720387 30 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 2 from Patent WO03010141.
ACCESSION AX720387
VERSION AX720387.1 GI:29892207
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Beaulieu, P.L., Fazal, G., Goulet, S., Kukolj, G., Poirier, M.,
TITLE Tsantrizos, Y.S., Jolicoeur, E., Gillard, J., Poupart, M.A. and
JOURNAL Rancourt, J.
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES
source 1. .30
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/Note="Forward Primer"

ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
   |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 13
AX814298
LOCUS AX814298 30 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 1 from Patent WO03064455.
ACCESSION AX814298
VERSION AX814298.1 GI:39103539
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

```

```
artificial sequences.
1
REFERENCE
AUTHORS      Llinas-Brunet,M. and Gorys,V.J.
TITLE        Macrocyclic peptides active against the hepatitis c virus
JOURNAL      Patent: WO 03064455-A 1 07-AUG-2003;
BOEHRINGER  BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES     Location/Qualifiers
source       1..30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Forward primer"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 14
AX814301
LOCUS          AX814301          30 bp      DNA          linear          PAT 05-DEC-2003
DEFINITION     Sequence 1 from Patent WO03064456.
ACCESSION      AX814301
VERSION        AX814301.1 GI:39103542
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Llinas-Brunet,M. and Gorys,V.J.
TITLE          Tripeptides having a hydroxyproline ether of a substituted
                quinoline for the inhibition of ns3 (hepatitis c)
JOURNAL        Patent: WO 03064456-A 1 07-AUG-2003;
                Boehringer Ingelheim International GmbH (DE)
FEATURES       Location/Qualifiers
source         1..30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Forward primer"

ORIGIN
Query Match      100.0%; Score 26; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 15
AR411537
LOCUS          AR411537          28 bp      DNA          linear          PAT 18-DEC-2003
DEFINITION     Sequence 1 from patent US 6638714.
ACCESSION      AR411537
VERSION        AR411537.1 GI:40163881
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Linnen,J.M. and Gorman,K.M.
TITLE          Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof
JOURNAL        Patent: US 6638714-A 1 28-OCT-2003;
                Location/Qualifiers
FEATURES       1..28
source

artificial sequences.
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      96.2%; Score 25; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 16
BD000263
LOCUS          BD000263          28 bp      DNA          linear          PAT 31-JAN-2002
DEFINITION     Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof.
ACCESSION      BD000263
VERSION        BD000263.1 GI:18623342
KEYWORDS       JP 2000279200-A/1.
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Lynen,J.M. and Gorman,K.M.
TITLE          Oligonucleotide primers for efficient detection of hepatitis C
                virus (HCV) and methods of use thereof
JOURNAL        Patent: JP 2000279200-A 1 10-OCT-2000;
                ORTHO CLINICAL DIAGNOSTICS INC
COMMENT        OS Artificial Sequence
                PN JP 2000279200-A/1
                PD 10-OCT-2000
                PF 03-FEB-2000 JP 2000032656
                PR 03-FEB-1999 US 60/118497
                PI JEFFREY M LYNNEN, KEVIN M GORMAN
                PC C12Q1/68; C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00,
                PC C12R1:92)
                CC
                FH Key
                FT source
                FT Location/Qualifiers
                /organism="Artificial Sequence".
FEATURES       Location/Qualifiers
source         1..28
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      96.2%; Score 25; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 17
CQ830529
LOCUS          CQ830529          37 bp      DNA          linear          PAT 12-JUL-2004
DEFINITION     Sequence 3 from Patent WO2004055210.
ACCESSION      CQ830529
VERSION        CQ830529.1 GI:50250862
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Balakireva,L.
TITLE          Molecules inhibiting hepatitis c virus protein synthesis and method
                for screening same
JOURNAL        Patent: WO 2004055210-A 3 01-JUL-2004;
                Location/Qualifiers
FEATURES       1..28
source
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PD	10-DEC-2002	JP 2001334894	01106308.8 PI
PF	31-OCT-2001	EP 00123728.8, 15-MAR-2001 EP	
PP	31-OCT-2000	EP 00123728.8, 15-MAR-2001 EP	

EBERHARD RUSSMANN, THOMAS MAIER, RAINER SCHMUCK, JOHNNY STABEELS, PI
UWE WEHNES
PC C12Q1/37, C12N9/54, C12N15/09, C12N15/09, C12Q1/68//C12N9/54, PC
C12R1-07),

PC C12N15/00, C12N15/00
CC Method for analyzing non-protein component
using protease from
CC bacillus

CC strain Location/Qualifiers
FH Key 1..24
FT source /organism='Hepatitis virus (hepatitis C FT
FT virus)'

FEATURES
source
Location/Qualifiers
1..24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN

Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 22

BD194954
LOCUS
DEFINITION Method of specifically and highly sensitively detecting nucleic
acid.
ACCESSION BD194954
VERSION BD194954.1 GI:33004707
KEYWORDS JP 2002509694-A/1.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler, C., Harverhuizen, G., Bartl, K. and Orumu, H.
TITLE Method of specifically and highly sensitively detecting nucleic
acid
JOURNAL Patent: JP 2002509694-A 1 02-APR-2002;
COMMENT ROCHE DIAGNOSTICS GMBH
OS Unidentified
PN JP 2002509694-A/1
PD 02-APR-2002
PF 03-NOV-1998 JP 2000519104
PR 04-NOV-1997 DE 197 48 690.8, 28-MAR-1998 DE 198 14 001.0 PR
02-APR-1998 DE 198 14 828.3
PI CHRISTOPHE KESSLER, GERU TO HARVERHUIZEN, KNUD BARTL, HENRICK PI
ORUMU

PC C12Q1/68//C12N15/09, C12N15/00

CC Strandedness: Single;
CC Topology: Linear;
CC Method of specifically and highly sensitively detecting CC
nucleic acid Location/Qualifiers
FH Key 1..24
FT source /organism='Unidentified'.
FT Location/Qualifiers
1..24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

FEATURES
source
Location/Qualifiers
1..24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN

Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 23

BD195155
LOCUS
DEFINITION 24 bp DNA linear PAT 17-JUL-2003
ACCESSION Ribonuclease resistant RNA preparation and utilization.
VERSION BD195155
KEYWORDS BD195155.1 GI:33004915
SOURCE JP 2002514905-A/7.
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dubois, D.B., Winkler, M.M., Pasloske, B.L. and Brown, D.
TITLE Ribonuclease resistant RNA preparation and utilization
JOURNAL Patent: JP 2002514905-A 7 21-MAY-2002;
AMBION INC, CENETRON DIAGNOSTICS LLC

COMMENT

OS Unidentified
PN JP 2002514905-A/7
PD 21-MAY-2002
PF 02-JUL-1997 JP 1998504527
PR 03-JUL-1996 US 08/675153, 03-JUL-1996 US 60/021145 PR
24-JUN-1997 US 08/881571
PI DWIGHT B DUBOIS, MATTHEW M WINKLER, BRITTAN L PASLOSKE, DAVID PI
BROWN
PC C12N15/40, C12N15/48, C12N15/51, C12N15/10, C12N15/88, C12N7/04, PC
C12Q1/68,
PC C12Q1/70, C12P19/34
CC Strandedness: Single;
CC Topology: Linear;
CC Ribonuclease resistant RNA preparation and utilization FH
Key Location/Qualifiers
FT source 1..24
/organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1..24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN

Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 24

I22146
LOCUS
DEFINITION Sequence 5 from patent US 5527669.
ACCESSION I22146
VERSION I22146.1 GI:1602500
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick, R.M. and Young, K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel
variants
JOURNAL Patent: US 5527669-A 5 18-JUN-1996;
FEATURES
source
Location/Qualifiers
1..24
/organism='unknown'
/mol_type='unassigned DNA'

ORIGIN

Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 25
I26949 24 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 17 from patent US 5561058.
DEFINITION 126949
ACCESSION 126949 GI:1606819
VERSION 126949.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gelfand,D.H., Myers,T.W. and Sigua,C.L.
TITLE Methods for coupled high temperatures reverse transcription and
polymerase chain reactions
JOURNAL Patent: US 5561058-A 17 01-OCT-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 26
I40301 24 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 9 from patent US 5620852.
DEFINITION 140301
ACCESSION 140301 GI:2082593
VERSION 140301.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin,L., Cimino,G. and Zhu,Y.S.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5620852-A 9 15-APR-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 27
I59678 24 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 9 from patent US 5654179.
DEFINITION

ACCESSION I59678 GI:2478310
VERSION I59678.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin,L.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5654179-A 9 05-AUG-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 28
I68634 24 bp DNA linear PAT 04-FEB-1998
LOCUS Sequence 7 from patent US 5677124.
DEFINITION 168634
ACCESSION 168634 GI:2830756
VERSION 168634.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS DuBois,D.B., Winkler,M.M. and Pasloske,B.L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 7 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 29
AR211384 24 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 7 from patent US 6399307.
DEFINITION AR211384
ACCESSION AR211384
VERSION AR211384.1 GI:21514692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Pasloske,B.L., DuBois,D.B., Brown,D.M. and Winkler,M.M.
TITLE Methods of quantifying viral load in an animal with a ribonuclease
resistant RNA preparation
JOURNAL Patent: US 6399307-A 7 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN	Query Match Best Local Similarity 92.3%; Score 24; DB 6; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
Db	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
RESULT 30		
AX003941	LOCUS	AX003941
DEFINITION	Sequence 1 from Patent WO9223249.	DNA
ACCESSION	AX003941	linear
VERSION	AX003941.1 GI:9927601	PAT 07-SEP-2000
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1	
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.	
TITLE	Specific and sensitive method for detecting nucleic acids	
JOURNAL	Patent: WO 9223249-A 1 14-MAY-1999;	
	KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);	
	ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)	
FEATURES	Location/Qualifiers	
source	1..24	
	/organism="synthetic construct"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32630"	
	/note="KY80"	
ORIGIN	Query Match Best Local Similarity 92.3%; Score 24; DB 6; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
Db	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
RESULT 31		
AX021563	LOCUS	AX021563
DEFINITION	Sequence 1 from Patent WO9224606.	DNA
ACCESSION	AX021563	linear
VERSION	AX021563.1 GI:10044847	PAT 07-SEP-2000
KEYWORDS	Hepatitis C virus	
SOURCE	Hepatitis C virus	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	
REFERENCE	1	
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.	
TITLE	Specific and sensitive nucleic acid detection method	
JOURNAL	Patent: WO 9224606-A 1 20-MAY-1999;	
	KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);	
	ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)	
FEATURES	Location/Qualifiers	
source	1..24	
	/organism="Hepatitis C virus"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:11103"	
ORIGIN	Query Match Best Local Similarity 92.3%; Score 24; DB 6; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
Db	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
RESULT 32		
AX021622	LOCUS	AX021622
DEFINITION	Sequence 1 from Patent WO923250.	DNA
ACCESSION	AX021622	linear
VERSION	AX021622.1 GI:10044905	PAT 07-SEP-2000
KEYWORDS	Hepatitis C virus	
SOURCE	Hepatitis C virus	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	
REFERENCE	1	
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.	
TITLE	Specific and sensitive method for detecting nucleic acids	
JOURNAL	Patent: WO 923250-A 1 14-MAY-1999;	
	KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);	
	ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)	
FEATURES	Location/Qualifiers	
source	1..24	
	/organism="Hepatitis C virus"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:11103"	
ORIGIN	Query Match Best Local Similarity 92.3%; Score 24; DB 6; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
Db	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
RESULT 33		
AX147011	LOCUS	AX147011
DEFINITION	Sequence 5 from Patent WO0137291.	DNA
ACCESSION	AX147011	linear
VERSION	AX147011.1 GI:14346282	PAT 08-JUN-2001
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1	
AUTHORS	Weindel,K., Riedling,M. and Geiger,A.	
TITLE	Magnetic glass particles, method for their preparation and uses thereof	
JOURNAL	Patent: WO 0137291-A 5 25-MAY-2001;	
	Roche Diagnostics GmbH (DE)	
FEATURES	Location/Qualifiers	
source	1..24	
	/organism="synthetic construct"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32630"	
	/note="Synthetic oligonucleotide primer (HCV forward)"	
ORIGIN	Query Match Best Local Similarity 92.3%; Score 24; DB 6; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
Db	1 GCAGAAAGCGTCTAGCCATGGCGT 24 	
RESULT 34		
AX250664	LOCUS	AX250664
		24 bp DNA
		linear
		PAT 05-OCT-2000

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DEFINITION Sequence 60 from Patent WO0168921.
ACCESSION AX250664
VERSION AX250664.1 GI:15984408
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Koshinsky,H., Zwick,M.S. and McCue,K.F.
TITLE Compositions and methods for simultaneous detection of multiple
JOURNAL biological entities
Patent: WO 0168921-A 60 20-SEP-2001;
Investigen (US)

FEATURES
source
1..24
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 35
AX428908
LOCUS AX428908 24 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 4 from Patent EP1201752.
ACCESSION AX428908
VERSION AX428908.1 GI:21540298
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Schmuck,R., Staepels,J., Meier,T., Wehnes,U. and Russmann,E.
TITLE Methods for the analysis of non-proteinaceous components using a
JOURNAL protease from a bacillus strain
Patent: EP 1201752-A 4 02-MAY-2002;
Roche Diagnostics GmbH (DE)

FEATURES
source
1..24
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 36
AX428981
LOCUS AX428981 24 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 4 from Patent EP1201753.
ACCESSION AX428981
VERSION AX428981.1 GI:21540352
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Schmuck,R., Staepels,J., Meier,T., Wehnes,U. and Russmann,E.
TITLE Methods for the analysis of non-proteinaceous components using a
JOURNAL protease from a bacillus strain
Patent: EP 1201752-A 4 02-MAY-2002;
Roche Diagnostics GmbH (DE)

FEATURES
source
1..24
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 37
BD138662
LOCUS BD138662 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Specific and sensitive method for detecting nucleic acids.
ACCESSION BD138662
VERSION BD138662.1 GI:23233607
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1
AUTHORS Kessler,C., Haberhausen,G., Bartl,K. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: JP 2002505071-A 1 19-FEB-2002;
ROCHE DIAGNOSTICS GMBH

COMMENT OS HCV
PN JP 2002505071-A/1
PD 19-FEB-2002
PF 03-NOV-1998 JP 2000519105
PR 04-NOV-1997 DE 197 48 690.8,28-MAR-1998 DE 198 14 001.0 PR
PI 02-APR-1998 DE 198 14 828.3
PI CHRISTOPHE KESSLER,GERD HABERHAUSEN,KNUD BARTL,HENRIK ORUM PC
C12Q1/68,C12N15/09,C12N15/00
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FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 38
122147
LOCUS 122147 26 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5527669.
ACCESSION 122147
VERSION 122147.1 GI:1602501

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 139.543 Seconds
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978.085 Million cell updates/sec

Title: US-10-087-631B-6

Perfect score: 26

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Scoring table: IDENTITY NUC

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Maximum Match 100%

Listing first 1000 summaries

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2: Geneseq1990s:*

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4: Geneseq2001as:*

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6: Geneseq2002as:*

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11: Geneseq2003ds:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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SUMMARIES

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5	26	100.0	27	6	AAD43287 HCV DNA a
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8	26	100.0	30	8	ACC48582 Hepatitis
9	26	100.0	30	8	AAD51019 Hepatitis
10	26	100.0	30	8	ACC43164 PCR prime
11	26	100.0	30	9	ACF36230 HCV 5' IR
12	26	100.0	30	10	ACF36227 HCV 5' IR
13	26	100.0	30	10	ACF36280 HCV 5' IR
14	26	100.0	30	10	ABZ76307 HCV RNA 5
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16	24	92.3	24	2	AAT37573 HCV conse
17	24	92.3	24	2	AAQ79964 Primer KY
18	24	92.3	24	2	AAT93541 Sense pri
19	24	92.3	24	2	AAT87096 HCV gene
20	24	92.3	24	2	AAT64887 Hepatitis
21	24	92.3	24	2	AAV15320 Hepatitis

22	24	92.3	24	2	AAV18849	AAV18849 Primer KY
23	24	92.3	24	2	AAZ23336	AAZ23336 HCV wild
24	24	92.3	24	2	AAZ23968	AAZ23968 PCR prime
25	24	92.3	24	2	AAZ78451	AAZ78451 HCV PCR p
26	24	92.3	24	2	AAZ09797	AAZ09797 HCV PCR p
27	24	92.3	24	4	AAH25403	AAH25403 PCR prime
28	24	92.3	24	4	AAH19056	AAH19056 Hepatitis
29	24	92.3	24	6	ABN83648	ABN83648 Hepatitis
30	24	92.3	24	6	ABK51599	ABK51599 Hepatitis
31	24	92.3	24	8	ABZ75890	ABZ75890 HCV RNA d
32	24	92.3	24	10	ADC54067	ADC54067 HCV 5'UTR
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37	24	92.3	24	12	ADO05656	ADO05656 HCV 5' NC
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39	24	92.3	25	10	ADD67940	ADD67940 Hepatitis
40	24	92.3	25	10	ABX10612	ABX10612 Light Cyc
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42	24	92.3	26	2	AAT64888	AAT64888 Hepatitis
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44	24	92.3	37	2	AAQ85920	AAQ85920 Hepatitis
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46	23	88.5	24	5	AAH79081	AAH79081 HCV PCR p
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51	21	80.8	21	2	AAV70448	AAV70448 HCV targe
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55	21	80.8	21	6	ABA01127	ABA01127 HCV prime
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69	20	76.9	46	2	AAV54438	AAV54438 Nucleotid
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71	19	73.1	19	6	ABN80472	ABN80472 DNA-RNA h
72	19	73.1	19	10	ADF51511	ADF51511 Hepatitis
73	19	73.1	19	10	ADF52207	ADF52207 Hepatitis
74	19	73.1	19	10	ADF51523	ADF51523 Hepatitis
75	19	73.1	19	10	ADF51525	ADF51525 Hepatitis
76	19	73.1	19	10	ADF52208	ADF52208 Hepatitis
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91	19	73.1	27	4	AAF23734	AAF23734 plus sens
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246	14	53.8	28	10	ADD12206	Add12206 Human DVL	C 319	13	50.0	21	12	ADQ25845	Adq25845 Chimaeric
247	14	53.8	30	2	AQ93151	Aq93151 Growth ho	C 320	13	50.0	22	4	ABA03375	Abao3375 Human gen
248	14	53.8	30	10	ADE48252	Ade48252 Primer of	C 321	13	50.0	22	6	ABKS2661	Abks2661 Hepatitis
249	14	53.8	33	2	AAV14925	Aav14925 psbL and	C 322	13	50.0	24	6	ABL55376	AbL55376 Human eer
250	14	53.8	42	10	ACF04691	Acf04691 Human bre	C 323	13	50.0	24	6	ABQ78213	Abq78213 Sense PCR
251	13.8	53.1	23	2	AAQ54364	Aaq54364 Primer/pr	C 324	13	50.0	25	9	ACI41689	AcI41689 Human mic
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253	13.8	53.1	25	12	ADP17385	Adp17385 Renal cel	C 326	13	50.0	27	2	AAx99917	Aax99917 Probe 3 r
254	13.8	53.1	25	12	ADP17386	Adp17386 Renal cel	C 327	13	50.0	28	3	AAx82590	Aax82590 Hammerhea
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256	13.8	53.1	27	2	AAQ79948	Aaq79948 Tth polym	C 329	13	50.0	31	2	AAQ65584	Aaq65584 Bacillus
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260	13.8	53.1	31	8	ABZ63831	Abz63831 Human H-R	C 333	13	50.0	33	2	AAAX24771	Aax24771 Human gla
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267	13.6	52.3	24	6	ABL54619	AbL54619 Human DNA	C 340	13	50.0	40	6	ABA98145	AbA98145 Oligonuc
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275	13.6	52.3	41	4	AAH50085	Aah50085 Bacterial	C 348	12.8	49.2	30	6	AAAL39273	Aal39273 Murine To
276	13.6	52.3	41	4	AAH50064	Aah50064 Bacterial	C 349	12.8	49.2	30	6	AAAL39272	Aal39272 Murine To
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278	13.4	51.5	29	10	ADC24678	Adc24678 HIV gp41	C 351	12.8	49.2	30	10	ACF36728	Acf36728 Murine To
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282	13.4	51.5	38	8	ACD23124	Acd23124 Human LDL	C 355	12.8	49.2	34	2	AAQ58020	Aaq58020 Sequence
283	13.4	51.5	40	5	AAH45393	Aah45393 Synthetic	C 356	12.8	49.2	35	2	AAAT38863	Aat38863 Primer fo
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291	13.2	50.8	20	12	ADP77219	Adp77219 Chimeric	C 364	12.8	49.2	39	6	AAQ73321	Abq73321 TPO mimet
292	13.2	50.8	22	3	AAZ50168	Aaz50168 3' PCR pri	C 365	12.8	49.2	39	12	ADQ16658	Adq16658 Human Kap
293	13.2	50.8	24	6	ABZ25749	Abz25749 Human cel	C 366	12.8	49.2	41	6	ABQ75868	Abq75868 Human cYC
294	13.2	50.8	25	12	ADP14367	Adp14367 Renal cel	C 367	12.6	48.5	22	12	ADN27381	Adn27381 Plasminog
295	13.2	50.8	27	8	ABT43607	Abt43607 RS4 PCR p	C 368	12.6	48.5	24	6	AB184686	Abi84686 Capture o
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297	13.2	50.8	39	2	AAV13448	Aav13448 Primer fo	C 370	12.6	48.5	25	9	ACI03940	AcI03940 Human mic
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302	13.2	50.8	44	12	ADH42836	Adh42836 Novel hum	C 375	12.6	48.5	29	10	ABZ75148	Abz75148 Murine in
303	13.2	50.8	47	12	ADM67674	Adm67674 Rice Bhdl	C 376	12.6	48.5	30	2	AAQ63067	Aaq63067 Random re
304	13	50.0	13	8	ABZ81784	Abz81784 HCV 5' UT	C 377	12.6	48.5	30	4	AAQ98345	Aaq98345 bFGF fami
305	13	50.0	13	8	ACD65985	Acd65985 Anti-HCV	C 378	12.6	48.5	30	4	AAAF70581	Aaf70581 SELEX exp
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309	13	50.0	13	12	ADI87553	Adi87553 Anti-HCV	C 382	12.6	48.5	34	2	AAQ71180	Aaq71180 Ribonucle
310	13	50.0	13	12	ADI87554	Adi87554 Anti-HCV	C 383	12.6	48.5	34	4	AAAD02841	Aad02841 A. thalia
311	13	50.0	15	8	ACD65928	Acd65928 Anti-HCV	C 384	12.6	48.5	36	3	AAAS35626	Aas35626 Permutain
312	13	50.0	15	12	ADI87527	Adi87527 Anti-HCV	C 385	12.6	48.5	37	2	AAQ72197	Aaq72197 Rat PACAP
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395	12.4	47.7	24	6	AB190734	Capture o	C 468	12.2	46.9	18	12	ADP83278
396	12.4	47.7	25	2	ABQ88306	Yeast ret	C 469	12.2	46.9	20	2	AAQ54916
397	12.4	47.7	25	2	AAV64007	Mycobacte	C 470	12.2	46.9	20	2	AAX88344
398	12.4	47.7	25	2	AAV22972	PCR prime	C 471	12.2	46.9	20	2	AAX88342
399	12.4	47.7	25	2	AAV70646	PCR prime	C 472	12.2	46.9	20	3	AAA38181
400	12.4	47.7	25	2	AAX81059	PCR prime	C 473	12.2	46.9	20	6	AB194058
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404	12.4	47.7	27	3	AAA39597	M. tuberc	C 477	12.2	46.9	20	10	ABZ91563
405	12.4	47.7	27	6	AAU50061	Murine al	C 478	12.2	46.9	20	11	ABD29206
406	12.4	47.7	28	2	AQ85575	B. subtil	C 479	12.2	46.9	20	11	ABD27993
407	12.4	47.7	28	2	AQ85574	B. subtil	C 480	12.2	46.9	20	12	ADP77963
408	12.4	47.7	28	3	AAD00987	Primer #1	C 481	12.2	46.9	20	12	ADP76905
409	12.4	47.7	28	10	ADH62365	CAPS mark	C 482	12.2	46.9	21	10	ADH34377
410	12.4	47.7	30	2	AAQ20963	HTLV-1 pr	C 483	12.2	46.9	22	3	AAC95442
411	12.4	47.7	30	2	AAQ58132	cbhl1-ph 2	C 484	12.2	46.9	24	6	AAS18076
412	12.4	47.7	30	2	AAQ98754	Primer fo	C 485	12.2	46.9	24	6	ADB25884
413	12.4	47.7	30	2	AAQ26610	PCR prime	C 486	12.2	46.9	25	3	AAZ35206
414	12.4	47.7	30	2	AAAX26609	PCR prime	C 487	12.2	46.9	25	4	AAH37735
415	12.4	47.7	30	10	ADE48262	Primer of	C 488	12.2	46.9	25	9	ACI87911
416	12.4	47.7	30	12	ADK98502	Osteoclas	C 489	12.2	46.9	25	9	ACI87911
417	12.4	47.7	30	12	ADK98503	Osteoclas	C 490	12.2	46.9	25	10	AAAD44807
418	12.4	47.7	31	3	AAAG4772	C. tracho	C 491	12.2	46.9	25	12	ADP17384
419	12.4	47.7	31	6	AAU592504	Chlamydia	C 492	12.2	46.9	26	8	ACD17038
420	12.4	47.7	31	6	AAU592504	Chlamydia	C 493	12.2	46.9	26	8	ACD17038
421	12.4	47.7	31	6	ACN32543	WNV minus	C 494	12.2	46.9	29	3	AAW76232
422	12.4	47.7	31	8	ACD58203	HCV DNaz	C 495	12.2	46.9	29	6	ABK15617
423	12.4	47.7	31	9	ACF04099	E coli Xa	C 496	12.2	46.9	30	3	ABC87815
424	12.4	47.7	31	10	ABT17604	Invader d	C 497	12.2	46.9	30	4	AAF55288
425	12.4	47.7	31	12	AD188228	HCV DNaz	C 498	12.2	46.9	30	6	AAAD24036
426	12.4	47.7	32	2	AAQ93887	Pas-delta	C 499	12.2	46.9	30	12	ADE11127
427	12.4	47.7	32	2	AAQ26369	HGH end o	C 500	12.2	46.9	30	12	ADO56416
428	12.4	47.7	33	2	AAV14923	pSBL and	C 501	12.2	46.9	32	4	AAQ02216
429	12.4	47.7	33	10	ADE48269	Primer of	C 502	12.2	46.9	32	4	AAQ36850
430	12.4	47.7	34	2	AAAT73600	Primer us	C 503	12.2	46.9	33	2	AAV64966
431	12.4	47.7	35	1	AAAN94216	Sequence	C 504	12.2	46.9	33	5	AAV76922
432	12.4	47.7	35	4	AAAF56601	Human gro	C 505	12.2	46.9	33	6	AAAD24097
433	12.4	47.7	36	2	AAQ88333	Maize alp	C 506	12.2	46.9	33	6	AAI72787
434	12.4	47.7	37	10	ADJ81800	Primer Ta	C 507	12.2	46.9	33	12	ADP04388
435	12.4	47.7	38	2	AAT858586	Secretory	C 508	12.2	46.9	34	10	ABZ83362
436	12.4	47.7	38	11	ADL56467	Human PKR	C 509	12.2	46.9	35	4	AAK94943
437	12.4	47.7	39	2	AAT59803	Hepatitis	C 510	12.2	46.9	35	10	ADB65795
438	12.4	47.7	39	12	ADP18478	S pneumon	C 511	12.2	46.9	35	10	ADA55723
439	12.4	47.7	40	2	AAX18398	Primer MI	C 512	12.2	46.9	35	12	ADL32155
440	12.4	47.7	40	6	ABR39472	A. thalia	C 513	12.2	46.9	36	6	ABS71041
441	12.4	47.7	40	12	ADP43301	Human pit	C 514	12.2	46.9	36	6	ABS66467
442	12.4	47.7	41	6	ABV75544	Alcohol d	C 515	12.2	46.9	36	8	ABZ25338
443	12.4	47.7	41	6	ABZ50760	Human gly	C 516	12.2	46.9	36	8	ABZ25338
444	12.4	47.7	41	6	ABZ44550	Human gly	C 517	12.2	46.9	36	9	ADA74114
445	12.4	47.7	41	6	ABL96060	Brassica	C 518	12.2	46.9	36	12	ADI40789
446	12.4	47.7	42	2	AAQ05717	BPI prote	C 519	12.2	46.9	37	2	AAZ19821
447	12.4	47.7	42	9	ADB75662	PCR prime	C 520	12.2	46.9	37	2	AAV19348
448	12.4	47.7	42	12	ADL80491	Human mut	C 521	12.2	46.9	38	6	ABS66468
449	12.4	47.7	43	9	ADB75660	PCR prime	C 522	12.2	46.9	38	6	ABS66468
450	12.4	47.7	43	9	ADB75663	PCR prime	C 523	12.2	46.9	38	10	ADP60079
451	12.4	47.7	44	9	ADB75659	PCR prime	C 524	12.2	46.9	38	12	ADK10790
452	12.4	47.7	44	9	ADB75658	PCR prime	C 525	12.2	46.9	38	12	ADK19382
453	12.4	47.7	45	6	ABA91338	Streptoco	C 526	12.2	46.9	39	4	AAK94944
454	12.4	47.7	45	6	ADB75661	PCR prime	C 527	12.2	46.9	39	8	ACD23106
455	12.4	47.7	45	6	ABK40880	Human obe	C 528	12.2	46.9	39	10	ADB65796
456	12.4	47.7	47	8	AAD50914	Oligonucl	C 529	12.2	46.9	39	10	ADA55724
457	12.4	47.7	47	12	ADF47514	Pir-GILT	C 530	12.2	46.9	39	11	ADM06211
458	12.4	47.7	47	12	ADJ58620	GILT 9 ol	C 531	12.2	46.9	39	12	ADL32156
459	12.4	47.7	48	5	AAF16712	dGMP-spec	C 532	12.2	46.9	42	8	ACD23104

C 533	12.2	46.9	44	8	ACA14542	Aca14542	Prokaryot	606	12	46.2	25	9	ACH61325	Ach61325	DNA target
C 534	12.2	46.9	48	2	AAQ49569	Aaq49569	Corynebac	607	12	46.2	25	12	ADP87775	Adp87775	Hepatitis
C 535	12.2	46.9	48	2	AAQ49459	Aaq49459	dapA gene	C 608	12	46.2	27	2	AAQ10740	Aaq10740	Oligonucle
C 536	12.2	46.9	48	2	AAV35800	Aav35800	PCR primer	C 609	12	46.2	27	3	AZ44696	Aaz44696	Human bra
C 537	12.2	46.9	48	2	AAV99495	Aav99495	Corynebac	C 610	12	46.2	27	12	ADL22791	Adl22791	Wheat RAF
C 538	12.2	46.9	48	2	AAZ22624	Aaz22624	CBD_alpha	C 611	12	46.2	29	3	AAZ99862	Aaz99862	Nucleosid
C 539	12.2	46.9	48	6	ADA16019	Ada16019	Human chi	C 612	12	46.2	29	8	ABZ59146	Abz59146	Human ak
C 540	12.2	46.9	48	8	ADA16019	Ada16019	Corynebac	C 613	12	46.2	30	2	AAT10255	Aat10255	Human lip
C 541	12.2	46.9	48	9	ACH03665	Ach03665	Corynebac	C 614	12	46.2	30	2	AAV64016	Aav64016	Mycobacte
C 542	12.2	46.9	48	10	AAD62878	Aad62878	Human chi	C 615	12	46.2	30	2	AAV81107	Aav81107	PCR prime
C 543	12.2	46.9	50	4	AAL28718	Aal28718	Human SNP	C 616	12	46.2	30	3	AAA64835	Aaa64835	PCR prime
C 544	12.2	46.9	50	6	ABZ05594	Abz05594	Human leu	C 617	12	46.2	30	3	AAA64836	Aaa64836	PCR prime
C 545	12	46.2	13	8	ACD65986	Acd65986	Anti-HCV	C 618	12	46.2	30	5	AAAD16849	Aaad16849	Mutagenic
C 546	12	46.2	13	12	ADP87555	Adp87555	Anti-HCV	C 619	12	46.2	30	5	AAAD16848	Aaad16848	Mutagenic
C 547	12	46.2	17	6	ABN07470	Abn07470	Human GDM	C 620	12	46.2	31	9	ACF04106	Acf04106	RBS regio
C 548	12	46.2	17	6	ABN07472	Abn07472	Human GDM	C 621	12	46.2	32	2	AAV55001	Aav55001	Sense PCR
C 549	12	46.2	17	6	ABN07468	Abn07468	Human GDM	C 622	12	46.2	32	2	AAV58473	Aav58473	Primer fo
C 550	12	46.2	17	6	ABN07473	Abn07473	Human GDM	C 623	12	46.2	32	8	ABX79057	Abx79057	PCR prime
C 551	12	46.2	17	6	ABN07469	Abn07469	Human GDM	C 624	12	46.2	33	1	AAAN90583	Aaan90583	DNA 57SLE
C 552	12	46.2	17	6	ABN07471	Abn07471	Human GDM	C 625	12	46.2	33	2	AAT95709	Aat95709	DNA from
C 553	12	46.2	17	8	ACD56822	Acd56822	HCV DNazzy	C 626	12	46.2	33	2	AAV04924	Aav04924	Primer LR
C 554	12	46.2	17	12	ADI82772	Adi82772	HCV DNazzy	C 627	12	46.2	33	2	AAV09865	Aav09865	Primer LR
C 555	12	46.2	18	2	AAQ22068	Aaq22068	Sequence	C 628	12	46.2	33	2	AAV15222	Aav15222	PCR prime
C 556	12	46.2	18	3	AAZ22625	Aaz22625	Arabidops	C 629	12	46.2	33	3	AAA90158	Aaa90158	PCR prime
C 557	12	46.2	19	10	ADF51547	Adf51547	Hepatitis	C 630	12	46.2	33	6	AAI72531	Aai72531	Nested PC
C 558	12	46.2	19	10	ADF51513	Adf51513	Hepatitis	C 631	12	46.2	33	6	ABQ73389	Abq73389	Human cut
C 559	12	46.2	19	10	ADF52209	Adf52209	Hepatitis	C 632	12	46.2	33	6	ABA95866	Abaa95866	Human zin
C 560	12	46.2	19	10	ADF52243	Adf52243	Hepatitis	C 633	12	46.2	33	8	ABX11224	Abx11224	HIV-1 PCR
C 561	12	46.2	20	2	AAQ58394	Aaq58394	Antisense	C 634	12	46.2	33	10	ADB61440	Adb61440	GPR40 DNA
C 562	12	46.2	20	2	AAQ58394	Aaq58394	Hepatitis	C 635	12	46.2	33	12	ADG17542	Adg17542	Human GPR
C 563	12	46.2	20	2	AAZ04594	Aaz04594	PCR prime	C 636	12	46.2	33	12	ADO21539	Ado21539	Human GPR
C 564	12	46.2	20	6	ABS57333	Abs57333	PCR prime	C 637	12	46.2	34	6	AAAD40546	Aaad40546	hGH signa
C 565	12	46.2	20	10	ABT3602	Abt3602	Stabilisi	C 638	12	46.2	35	2	AAQ99919	Aaq99919	HIV-1 mRN
C 566	12	46.2	20	10	ABZ86738	Abz86738	Human oli	C 639	12	46.2	35	3	AAZ44695	Aaz44695	Human bra
C 567	12	46.2	20	10	ABZ88229	Abz88229	Human oli	C 640	12	46.2	35	8	ABX08330	Abx08330	Forward R
C 568	12	46.2	20	10	ABZ92975	Abz92975	Human oli	C 641	12	46.2	35	9	ACD26444	Acd26444	HIV-1 gen
C 569	12	46.2	20	11	ABD29205	Abd29205	AA150500-	C 642	12	46.2	36	2	AAZ78065	Aaz78065	Rat DTDT
C 570	12	46.2	20	11	ABD24459	Abd24459	AI652901-	C 643	12	46.2	36	2	AAZ08739	Aaz08739	HCNV/HIV-
C 571	12	46.2	20	11	ABD22968	Abd22968	Human myo	C 644	12	46.2	37	3	AAA94001	Aaa94001	Antiviral
C 572	12	46.2	21	2	AAV40611	Aav40611	Human TSC	C 645	12	46.2	37	4	AAAC86895	Aaac86895	PCR prime
C 573	12	46.2	21	4	AAF84798	Aaf84798	PCR prime	C 646	12	46.2	37	4	AAH20082	Aah20082	Asp 1 gen
C 574	12	46.2	21	12	ADE52353	Ade52353	Inhibitor	C 647	12	46.2	37	12	ADO59185	Ado59185	PCR prime
C 575	12	46.2	21	12	ADE52352	Ade52352	Inhibitor	C 648	12	46.2	38	2	AAV49359	Aav49359	Primer AB
C 576	12	46.2	22	2	AAT45327	Aat45327	Mycoplasma	C 649	12	46.2	39	2	AAH85413	Aah85413	RNA ligan
C 577	12	46.2	23	2	AAAT65095	Aaat65095	Hepatitis	C 650	12	46.2	39	12	ADL64466	Adl64466	Human sin
C 578	12	46.2	23	3	AAAG4218	Aaag4218	Primer fo	C 651	12	46.2	39	12	ADL64467	Adl64467	Human sin
C 579	12	46.2	23	5	AAAF56559	Aaaf56559	HIV-1 det	C 652	12	46.2	40	4	AAH50076	Aah50076	Bacterial
C 580	12	46.2	23	9	ACF05116	Acf05116	Retrovira	C 653	12	46.2	40	10	ADC46975	Adc46975	Synthesis
C 581	12	46.2	24	2	AAQ75820	Aaq75820	Sense pri	C 654	12	46.2	40	10	ADC46977	Adc46977	Synthesis
C 582	12	46.2	24	2	AAAT51431	Aaat51431	Primer Ab	C 655	12	46.2	40	10	ADC56755	Adc56755	Self asse
C 583	12	46.2	24	3	AAZ45815	Aaz45815	PCR prime	C 656	12	46.2	40	10	ADC56758	Adc56758	Self asse
C 584	12	46.2	24	3	AAZ45809	Aaz45809	PCR prime	C 657	12	46.2	41	2	AAV44490	Aav44490	tRNA-Lys3
C 585	12	46.2	24	5	AAAF56557	Aaaf56557	HIV-1 det	C 658	12	46.2	41	4	AAH49842	Aah49842	Bacterial
C 586	12	46.2	24	10	ADE36828	Ade36828	Rhesus ro	C 659	12	46.2	41	4	AAH50072	Aah50072	Bacterial
C 587	12	46.2	24	10	ABX13008	Abx13008	Oxidative	C 660	12	46.2	41	12	ADH06159	Adh06159	Gene poly
C 588	12	46.2	25	2	AAQ81978	Aaq81978	Human sol	C 661	12	46.2	41	12	ADH05486	Adh05486	Gene poly
C 589	12	46.2	25	6	ABN12363	Abn12363	Human GDM	C 662	12	46.2	41	12	ADH91273	Adh91273	1-beta-me
C 590	12	46.2	25	6	ABN12368	Abn12368	Human GDM	C 663	12	46.2	41	12	ADH91946	Adh91946	1-beta-me
C 591	12	46.2	25	6	ABN12365	Abn12365	Human GDM	C 664	12	46.2	42	4	AAH50073	Aah50073	Bacterial
C 592	12	46.2	25	6	ABN12366	Abn12366	Human GDM	C 665	12	46.2	42	4	AAH49844	Aah49844	Bacterial
C 593	12	46.2	25	6	ABN12360	Abn12360	Human GDM	C 666	12	46.2	43	2	AAQ38111	Aaq38111	Mycobacte
C 594	12	46.2	25	6	ABN12367	Abn12367	Human GDM	C 667	12	46.2	43	6	ABK96447	Abk96447	PCR prime
C 595	12	46.2	25	6	ABN12373	Abn12373	Human GDM	C 668	12	46.2	43	10	AAD53316	Aad53316	Bovine ma
C 596	12	46.2	25	6	ABN12372	Abn12372	Human GDM	C 669	12	46.2	47	3	AAZ67089	Aaz67089	Human map
C 597	12	46.2	25	6	ABN12371	Abn12371	Human GDM	C 670	12	46.2	48	2	AAZ28179	Aaz28179	Murine al
C 598	12	46.2	25	6	ABN12362	Abn12362	Human GDM	C 671	12	46.2	48	3	AAZ56997	Aaz56997	Forward a
C 599	12	46.2	25	6	ABN12364	Abn12364	Human GDM	C 672	12	46.2	48	3	AAZ99162	Aaz99162	Murine pe
C 600	12	46.2	25	6	ABN12369	Abn12369	Human GDM	C 673	12	46.2	49	5	AAAF56560	Aaaf56560	HIV-1 det
C 601	12	46.2	25	6	ABN12370	Abn12370	Human GDM	C 674	12	46.2	50	4	AAAL31062	Aaal31062	Human SNP
C 602	12	46.2	25	6	ABN12361	Abn12361	Human GDM	C 675	12	46.2	50	4	AAAL34220	Aaal34220	Human SNP
C 603	12	46.2	25	9	ACK15513	Ack15513	Human mic	C 676	12	46.2	50	4	AAAL34240	Aaal34240	Human SNP
C 604	12	46.2	25	9	ACH53993	Ach53993	DNA target	C 677	12	46.2	50	4	AAAL34239	Aaal34239	Human SNP
C 605	12	46.2	25	9	ACH53993	Ach53993	DNA target	C 678	11.8	45.4	17	6	ACN01221	Acn01221	WNV Hamme

C 679	11.8	45.4	17	6	ACN12457	ACN12457 WNV minus	C 752	11.8	45.4	36	5	AAC90748	AAC90748 Human sec
C 680	11.8	45.4	17	6	ACN04523	ACN04523 WNV Zinz	C 753	11.8	45.4	36	8	AAD55014	AAD55014 VEGF alte
C 681	11.8	45.4	17	6	ACN09924	ACN09924 WNV minus	C 754	11.8	45.4	36	12	ADP20784	ADP20784 CD40ex-F1
C 682	11.8	45.4	20	2	AAX38389	AAX38389 E. coli K	C 755	11.8	45.4	37	10	ADF89504	ADF89504 PCR prime
C 683	11.8	45.4	20	2	AAX92804	AAX92804 PCR prime	C 756	11.8	45.4	38	2	AAQ58536	AAQ58536 LFA-3 sen
C 684	11.8	45.4	20	2	AAX94284	AAX94284 PCR prime	C 757	11.8	45.4	38	2	AAQ36524	AAQ36524 PCR prime
C 685	11.8	45.4	20	6	ABL95993	ABL95993 Brassica	C 758	11.8	45.4	38	2	AAZ98262	AAZ98262 Z. ramige
C 686	11.8	45.4	20	12	ADP78056	ADP78056 Chimeric	C 759	11.8	45.4	38	3	AAA63922	AAA63922 PCR prime
C 687	11.8	45.4	20	12	ADP78163	ADP78163 Chimeric	C 760	11.8	45.4	38	4	ABK05018	ABK05018 Human NOG
C 688	11.8	45.4	21	9	AAD58224	AAD58224 Cytokine	C 761	11.8	45.4	38	6	ABA92848	ABA92848 Transmem
C 689	11.8	45.4	21	12	ADH50962	ADH50962 Endotheli	C 762	11.8	45.4	38	6	ACN29529	ACN29529 WNV minus
C 690	11.8	45.4	22	2	AAT75365	AAT75365 cDNA synt	C 763	11.8	45.4	38	11	ADL54071	ADL54071 Human IKK
C 691	11.8	45.4	22	2	AAV59947	AAV59947 PCR prime	C 764	11.8	45.4	38	12	ADF47532	ADF47532 IGF-II ta
C 692	11.8	45.4	22	6	ABK10153	ABK10153 Douglas f	C 765	11.8	45.4	39	5	ADO26075	ADO26075 Arabidops
C 693	11.8	45.4	22	10	ADC39505	ADC39505 PmbIP pro	C 766	11.8	45.4	39	5	AAC85342	AAC85342 cDNA prim
C 694	11.8	45.4	23	3	AAA40595	AAA40595 Human Arp	C 767	11.8	45.4	39	5	AAC85321	AAC85321 Primer Sa
C 695	11.8	45.4	24	4	AHH44338	AHH44338 Human par	C 768	11.8	45.4	39	5	AAF63974	AAF63974 Human tan
C 696	11.8	45.4	24	6	ABL52682	ABL52682 Insulin-1	C 769	11.8	45.4	39	6	ABS61220	ABS61220 Human pol
C 697	11.8	45.4	24	9	ABX04799	ABX04799 Guanylate	C 770	11.8	45.4	40	2	AAV49999	AAV49999 PCR prime
C 698	11.8	45.4	24	9	ACF05089	ACF05089 Bovine th	C 771	11.8	45.4	40	2	AAV55934	AAV55934 Primer us
C 699	11.8	45.4	25	2	AAV64007	AAV64007 Mycobacte	C 772	11.8	45.4	40	2	AAV57583	AAV57583 Primer us
C 700	11.8	45.4	25	2	AAH81059	AAH81059 PCR prime	C 773	11.8	45.4	40	3	AAZ95996	AAZ95996 Polynucle
C 701	11.8	45.4	25	6	ABN11908	ABN11908 Human GDM	C 774	11.8	45.4	40	3	AAZ38920	AAZ38920 Neisseria
C 702	11.8	45.4	25	6	ABN11909	ABN11909 Human GDM	C 775	11.8	45.4	42	2	AAQ91729	AAQ91729 Alpha-d 3
C 703	11.8	45.4	25	6	ABN11907	ABN11907 Human GDM	C 776	11.8	45.4	42	2	AAQ91729	AAQ91729 Alpha-d 3
C 704	11.8	45.4	25	9	ACT97410	ACT97410 Human mic	C 777	11.8	45.4	42	2	AAV65896	AAV65896 IT3-8 inv
C 705	11.8	45.4	25	9	ACK16141	ACK16141 Human mic	C 778	11.8	45.4	42	2	AAV31554	AAV31554 Beta2 int
C 706	11.8	45.4	25	9	ACK103835	ACK103835 Human mic	C 779	11.8	45.4	42	2	AAV35250	AAV35250 Human bet
C 707	11.8	45.4	25	9	ACK15012	ACK15012 Human mic	C 780	11.8	45.4	42	2	AAV63796	AAV63796 Human alp
C 708	11.8	45.4	25	9	ACK126150	ACK126150 Human mic	C 781	11.8	45.4	42	2	AAV08460	AAV08460 Primer fo
C 709	11.8	45.4	25	9	ACH59996	ACH59996 DNA targ	C 782	11.8	45.4	42	3	AAA60028	AAA60028 Human alp
C 710	11.8	45.4	26	2	AAT16230	AAT16230 Primer #6	C 783	11.8	45.4	42	6	AAV75505	AAV75505 Prospero
C 711	11.8	45.4	26	3	AAZ50993	AAZ50993 PCR prime	C 784	11.8	45.4	42	6	ABK82418	ABK82418 Human bet
C 712	11.8	45.4	26	4	AAD15663	AAD15663 PCR prime	C 785	11.8	45.4	42	6	ADE52965	ADE52965 FEN-1 rel
C 713	11.8	45.4	26	8	ACDI17031	ACDI17031 Sample pr	C 786	11.8	45.4	42	6	ADP38652	ADP38652 Synchroni
C 714	11.8	45.4	26	8	ADA89432	ADA89432 Rice hype	C 787	11.8	45.4	43	2	AAQ1306	AAQ1306 PCR prime
C 715	11.8	45.4	26	9	ADA89432	ADA89432 Interfero	C 788	11.8	45.4	43	2	AAZ5349	AAZ5349 Antisense
C 716	11.8	45.4	27	2	AAX32410	AAX32410 Plant lum	C 789	11.8	45.4	43	2	AAZ5349	AAZ5349 Antisense
C 717	11.8	45.4	27	3	AAZ36882	AAZ36882 PCR prime	C 790	11.8	45.4	43	2	AAZ66271	AAZ66271 Human map
C 718	11.8	45.4	27	3	ABZ79464	ABZ79464 mGRR1a re	C 791	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 719	11.8	45.4	28	8	ABZ79464	ABZ79464 mGRR1a re	C 792	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 720	11.8	45.4	28	8	AAQ81250	AAQ81250 Ribozyme	C 793	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 721	11.8	45.4	29	2	AAQ59802	AAQ59802 Hepatitis	C 794	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 722	11.8	45.4	29	2	AAQ76036	AAQ76036 TK-(tetO)	C 795	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 723	11.8	45.4	29	2	AAQ501429	AAQ501429 Unknown p	C 796	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 724	11.8	45.4	29	5	AAV57566	AAV57566 Calcium p	C 797	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 725	11.8	45.4	29	6	AAV57566	AAV57566 Calcium p	C 798	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 726	11.8	45.4	29	6	AAV57566	AAV57566 Calcium p	C 799	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 727	11.8	45.4	30	10	ADP48270	ADP48270 Primer of	C 800	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 728	11.8	45.4	30	12	ADJ63957	ADJ63957 Plant lip	C 801	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 729	11.8	45.4	31	2	AAV14924	AAV14924 pBL and	C 802	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 730	11.8	45.4	31	6	AAV78977	AAV78977 Human gen	C 803	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 731	11.8	45.4	31	6	ACN32015	ACN32015 WNV minus	C 804	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 732	11.8	45.4	31	6	ACN32800	ACN32800 WNV minus	C 805	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 733	11.8	45.4	32	3	AAZ47085	AAZ47085 Primer alb	C 806	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 734	11.8	45.4	32	4	AAV31194	AAV31194 Oligonuc	C 807	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 735	11.8	45.4	32	6	ABN84385	ABN84385 Mouse alb	C 808	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 736	11.8	45.4	32	6	AAQ46728	AAQ46728 HIV ampli	C 809	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 737	11.8	45.4	33	2	AAQ89504	AAQ89504 Human imm	C 810	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 738	11.8	45.4	33	3	AAA08646	AAA08646 Primer GV	C 811	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 739	11.8	45.4	33	3	AAQ85512	AAQ85512 Primer #9	C 812	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 740	11.8	45.4	33	6	ABO75561	ABO75561 Xenopus l	C 813	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 741	11.8	45.4	33	11	ADM77930	ADM77930 Acetylglu	C 814	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 742	11.8	45.4	34	4	AAV81340	AAV81340 Rubisco S	C 815	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 743	11.8	45.4	34	9	ADA44835	ADA44835 PCR prime	C 816	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 744	11.8	45.4	35	2	AAV1719	AAV1719 Primer fo	C 817	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 745	11.8	45.4	35	2	AAV14926	AAV14926 pBL and	C 818	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 746	11.8	45.4	35	2	AAV49277	AAV49277 Primer AB	C 819	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 747	11.8	45.4	35	3	AAZ47086	AAZ47086 Primer Su	C 820	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 748	11.8	45.4	35	3	AAV31195	AAV31195 Oligonuc	C 821	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 749	11.8	45.4	36	2	AAV02899	AAV02899 Alpha gal	C 822	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 750	11.8	45.4	36	2	AAV21835	AAV21835 Primer EB	C 823	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map
C 751	11.8	45.4	36	2	AAV21835	AAV21835 Primer EB	C 824	11.8	45.4	47	3	AAZ66271	AAZ66271 Human map

C 825	11.6	44.6	22	12	ADIS3310	Adi53310 CXCR4 RT-	C 898	11.6	44.6	39	2	AAQ90912	AaQ90912 hMLH1 gen
C 826	11.6	44.6	23	12	ADI60025	Adi60025 SIKNA -ve	C 899	11.6	44.6	39	3	AAAS0248	AaAS0248 Maize hea
C 827	11.6	44.6	24	3	AAZ57985	Aaz57985 T cell re	C 900	11.6	44.6	39	4	AAAF32320	AaAF32320 E. coli A
C 828	11.6	44.6	24	6	ABQ06527	Abq06527 Oligonuc1	C 901	11.6	44.6	39	4	AAH26481	AaH26481 Maize hea
C 829	11.6	44.6	24	6	ABQ06486	Abq06486 Oligonuc1	C 902	11.6	44.6	39	6	ABQ73325	Abq73325 TPO minet
C 830	11.6	44.6	24	6	ABQ01288	Abq01288 Oligonuc1	C 903	11.6	44.6	39	6	ABQ73320	Abq73320 TPO minet
C 831	11.6	44.6	24	6	ABQ01288	Abq01288 Oligonuc1	C 904	11.6	44.6	39	8	AAAS0761	AaAS0761 Arabidops
C 832	11.6	44.6	24	6	ABQ01288	Abq01288 Oligonuc1	C 905	11.6	44.6	39	9	ACA62043	AaCA62043 Maize mit
C 833	11.6	44.6	24	6	ABQ01288	Abq01288 Oligonuc1	C 906	11.6	44.6	39	10	ABV75300	AaBV75300 AANT1 cod
C 834	11.6	44.6	24	10	ADBE6775	Adbe6775 Pax5-lacz	C 907	11.6	44.6	39	12	ADQ16662	AaDQ16662 Human Kap
C 835	11.6	44.6	25	2	AAQ86410	Aaq86410 Human ins	C 908	11.6	44.6	39	12	ADQ16657	AaDQ16657 Human Kap
C 836	11.6	44.6	25	2	AAQ86401	Aaq86401 Human ins	C 909	11.6	44.6	40	5	AA91413	Aa91413 R. renifo
C 837	11.6	44.6	25	6	ABZ30813	Abz30813 Candida a	C 910	11.6	44.6	40	5	AA91413	Aa91413 R. renifo
C 838	11.6	44.6	25	9	ACK10759	Ack10759 Human mic	C 911	11.6	44.6	40	9	ACD32772	AaCD32772 Backtrans
C 839	11.6	44.6	25	9	ACT00461	Act00461 Human mic	C 912	11.6	44.6	40	9	ACD32772	AaCD32772 Backtrans
C 840	11.6	44.6	25	9	ACH22159	Ach22159 Human mic	C 913	11.6	44.6	40	9	ACD32799	AaCD32799 Backtrans
C 841	11.6	44.6	25	9	ACH22159	Ach22159 Human mic	C 914	11.6	44.6	40	10	ADD24544	AaD24544 DNA polym
C 842	11.6	44.6	26	2	AAV65088	Aav65088 Human ZPB	C 915	11.6	44.6	40	10	ADG79087	AaD79087 Schizophr
C 843	11.6	44.6	26	12	ADJ76805	Adj76805 FETUB rev	C 916	11.6	44.6	40	10	ABZ72394	Abz72394 Tomato sp
C 844	11.6	44.6	27	2	AAT18018	Aat18018 Chemokine	C 917	11.6	44.6	41	2	AAAX5892	AaAX5892 Primer us
C 845	11.6	44.6	27	3	AA898797	Aa898797 Mutagenic	C 918	11.6	44.6	41	4	AAAC87946	AaAC87946 Oligonuc1
C 846	11.6	44.6	27	4	AA812797	Aa812797 Mutagenic	C 919	11.6	44.6	41	4	AAAC87935	AaAC87935 B43 scFv
C 847	11.6	44.6	27	4	AA812797	Aa812797 Mutagenic	C 920	11.6	44.6	41	8	ACD23093	AaCD23093 Human LPL
C 848	11.6	44.6	27	4	AA812797	Aa812797 Mutagenic	C 921	11.6	44.6	42	2	AAAX27116	AaX27116 Primer P5
C 849	11.6	44.6	27	4	AA812797	Aa812797 Mutagenic	C 922	11.6	44.6	42	2	AAAX84825	AaX84825 PCR prime
C 850	11.6	44.6	27	6	ABK37882	Abk37882 Promoter	C 923	11.6	44.6	42	4	AAAF55358	AaAF55358 PCR prime
C 851	11.6	44.6	27	6	ABK37882	Abk37882 Promoter	C 924	11.6	44.6	42	4	AAAF55358	AaAF55358 PCR prime
C 852	11.6	44.6	28	3	AAZ55351	Aaz55351 Neisseria	C 925	11.6	44.6	42	4	AAH23279	AaH23279 3x2F ZGS
C 853	11.6	44.6	28	3	AAZ55351	Aaz55351 Neisseria	C 926	11.6	44.6	44	10	ADD41404	AaD41404 Recombina
C 854	11.6	44.6	28	10	ADJ33191	Adj33191 Primer se	C 927	11.6	44.6	45	4	AAH70659	AaH70659 Human cer
C 855	11.6	44.6	30	3	AA30758	Aa30758 Human G p	C 928	11.6	44.6	47	3	AAA48364	AaA48364 Fungal xy
C 856	11.6	44.6	30	5	AA16886	Aa16886 Informati	C 929	11.6	44.6	47	3	AAA48338	AaA48338 Thermomyc
C 857	11.6	44.6	30	6	ABK97364	Abk97364 Stratum c	C 930	11.6	44.6	47	3	AAZ67840	AaZ67840 Human map
C 858	11.6	44.6	30	6	ABK97364	Abk97364 Stratum c	C 931	11.6	44.6	47	3	AAZ66849	AaZ66849 Human map
C 859	11.6	44.6	30	10	ADC22767	Adc22767 Human G p	C 932	11.6	44.6	47	9	AAAC86569	AaAC86569 Primer us
C 860	11.6	44.6	30	10	ADH14240	Adh14240 Human GPR	C 933	11.6	44.6	47	9	AAFT43504	AaFT43504 PCR prime
C 861	11.6	44.6	31	2	AAQ52229	Aaq52229 Neuroblas	C 934	11.6	44.6	48	4	AAH79981	AaH79981 EST polym
C 862	11.6	44.6	31	3	AAZ50968	Aaz50968 E. haloch	C 935	11.6	44.6	48	12	ADG15848	AaD15848 Insect de
C 863	11.6	44.6	31	4	AAI30936	Aai30936 Human sin	C 936	11.6	44.6	48	12	ADG15848	AaD15848 Insect de
C 864	11.6	44.6	31	6	ACN32043	Acn32043 WNV minus	C 937	11.6	44.6	49	8	ABZ09198	Abz09198 Human oli
C 865	11.6	44.6	31	8	ACD43766	Acd43766 Human gen	C 938	11.6	44.6	49	10	ABZ78651	Abz78651 Tumour su
C 866	11.6	44.6	31	8	ACD56868	Acd56868 HCV DNaz	C 939	11.6	44.6	50	2	AAQ80312	AaQ80312 Primer PC
C 867	11.6	44.6	31	12	ADM62947	Adm62947 Hepatitis	C 940	11.6	44.6	50	3	AAZ48338	AaZ48338 Primer sp
C 868	11.6	44.6	31	12	ADM62947	Adm62947 Hepatitis	C 941	11.6	44.6	50	3	AAZ48338	AaZ48338 Primer sp
C 869	11.6	44.6	32	2	AAI76809	Aai76809 Human sil	C 942	11.6	44.6	50	4	AAI76811	AaI76811 Human sil
C 870	11.6	44.6	32	2	AAI76809	Aai76809 Human sil	C 943	11.6	44.6	50	4	AAI76809	AaI76809 Human sil
C 871	11.6	44.6	32	2	AAI76809	Aai76809 Human sil	C 944	11.6	44.6	50	6	ABZ05181	Abz05181 Human leu
C 872	11.6	44.6	32	2	AAV55454	Aav55454 Interleuk	C 945	11.6	44.6	50	6	ABZ03212	Abz03212 Human leu
C 873	11.6	44.6	32	6	AAAD4047	Aaad4047 Rubisco-R	C 946	11.6	44.6	50	6	ABZ03262	Abz03262 Human leu
C 874	11.6	44.6	32	6	ABR00192	Ab00192 Probe Rub	C 947	11.6	44.6	50	12	ADJ87546	AaD87546 Human cyt
C 875	11.6	44.6	33	5	ABR00192	Ab00192 Probe Rub	C 948	11.6	44.6	50	12	ADJ87546	AaD87546 Human cyt
C 876	11.6	44.6	33	6	ABR05764	Ab05764 Telomeric	C 949	11.6	44.6	50	17	ABL31695	AaB31695 Human HLA
C 877	11.6	44.6	33	6	ABR05764	Ab05764 Telomeric	C 950	11.6	44.6	50	18	AAA67000	AaA67000 Human leu
C 878	11.6	44.6	33	6	ABR05764	Ab05764 Telomeric	C 951	11.6	44.6	50	4	AAH26389	AaH26389 Chloromph
C 879	11.6	44.6	33	10	ADC47066	Adc47066 Polypepti	C 952	11.6	44.6	50	5	AAAF54653	AaAF54653 Human HLA
C 880	11.6	44.6	33	10	ADC47066	Adc47066 Polypepti	C 953	11.6	44.6	50	6	AB194688	Ab194688 Capture o
C 881	11.6	44.6	35	2	AAZ20958	Aaz20958 Primer SE	C 954	11.6	44.6	50	10	ADC26395	AaD26395 NOV prote
C 882	11.6	44.6	35	6	ADAD2633	Adad2633 PCR prime	C 955	11.6	44.6	50	10	ADD42530	AaD42530 Human inf
C 883	11.6	44.6	35	8	ACN10046	Acn10046 Necrosis	C 956	11.6	44.6	50	10	ADD42531	AaD42531 Human inf
C 884	11.6	44.6	35	10	ADG62862	Adg62862 Secreted	C 957	11.6	44.6	50	11	ADH52817	AaH52817 PCR prime
C 885	11.6	44.6	36	2	AAV59926	Aav59926 Sense pri	C 958	11.6	44.6	50	11	ADM07049	AaM07049 Aspergill
C 886	11.6	44.6	36	2	AAV58458	Aav58458 Primer OM	C 959	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 887	11.6	44.6	36	2	AAV10641	Aav10641 A. thalia	C 960	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 888	11.6	44.6	36	2	AAV10641	Aav10641 A. thalia	C 961	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 889	11.6	44.6	36	3	AA35749	Aa35749 Forward P	C 962	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 890	11.6	44.6	36	3	AA35749	Aa35749 Forward P	C 963	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 891	11.6	44.6	36	3	AA35749	Aa35749 Forward P	C 964	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 892	11.6	44.6	37	8	ABX79063	Abx79063 Human ret	C 965	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 893	11.6	44.6	37	8	ABX79063	Abx79063 Human ret	C 966	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 894	11.6	44.6	37	8	ABX79063	Abx79063 Human ret	C 967	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 895	11.6	44.6	37	5	ABL58057	AbL58057 Human Apo	C 968	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 896	11.6	44.6	38	2	AAQ92449	Aaq92449 CD3 epsil	C 969	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I
C 897	11.6	44.6	38	2	AAV85709	Aav85709 LRP5 exon	C 970	11.6	44.6	50	12	ADQ80724	AaQ80724 Porcine I

CC Amplification of HCV nucleic acid using this primer is up to 100 times
CC more efficient than amplification with prior art primers
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
RESULT 2
AAV59058
ID AAV59058 standard; DNA; 26 BP.
XX AAV59058
AC AAV59058;
XX 07-JAN-1999 (first entry)
DT Primer ST280A for HCV fragment.
DE PCR primer; HCV; nucleic acid amplification; ss.
XX Synthetic.
OS Human herpesvirus 5.
XX Key Location/Qualifiers
FT modified_base 26
FT /*tag= a
FT /note= "optionally benzylated, methylated, or
FT nitrobenzylated"
XX EP866071-A2.
XX 23-SEP-1998.
XX 12-MAR-1998; 98EP-00104461.
XX 20-MAR-1997; 97US-0041127P.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Will SG, Young KKY;
XX WPI; 1998-482929/42.
XX Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
XX primers for nucleic acid amplification.
XX Example 6; Page 16; 38pp; English.
XX This sequence represents a primer for a fragment of HCV, and is an
XX example of an oligonucleotide of the invention. The oligonucleotides of
XX the invention are of the formula 5'-Sl-Nu-3' or 5'-Sl-Nu-S2-3', where S1
XX is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3 nucleotides;
XX and Nu is a nucleotide with a purine or pyrimidine base having an
XX exocyclic amino group substituted by CHIR2; R1, R2 are H, 1-10C alkyl,
XX alkoxy, optionally substituted phenyl, phenoxy or optionally substituted
XX naphthyl. The oligonucleotides are useful as primers for nucleic acid
XX amplification, preferably by polymerase chain reaction. Use of the
XX modified primers reduces non-specific amplification, especially primer
XX dimer formation, with a concomitant increase in the yield of the intended
XX target
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Abq00061 Oligonucle
Abq04137 Oligonucle
AbL53747 Human fas
Aal42862 Survivin-
Aal45956 Human bre
Ab555957 Human RNA
Ab182908 Capture o
Ab192174 Capture o
Ab192175 Capture o
Ab185947 Capture o
Ab182909 Capture o
Ab185946 Capture o
Ab56981 PCR prime
Adp82650 Cy5/FAM p
Aav85586 LRPS PCR
Aax24032 Human AOM
Aax23979 Human HG3
Aax50784 PCR prime
Aax23582 Primer us
Aax36406 Probe PBS
Aax39403 Human G-p
Aax14843 PCR prime
Aac64397 Human KCN
Aas57806 Antisense
Aac66606 Human kin
Aas15266 Mouse VHC
Aaf83350 Human SAP
Aaf85384 PCR prime
Abn11905 Human GDM
Abn11906 Human GDM

ALIGNMENTS

RESULT 1
AAT67193
ID AAT67193 standard; DNA; 26 BP.
XX AC
AC AAT67193;
XX 13-FEB-1998 (first entry)
DT Hepatitis C virus (HCV) RNA amplification primer ST280A.
DE Hepatitis C virus; HCV; ST280A; reverse transcription PCR; RT-PCR;
XX PCR primer; ss.
XX Synthetic.
XX EP776981-A2.
XX 04-JUN-1997.
XX 21-NOV-1996; 96EP-00118704.
XX 29-NOV-1995; 95US-0007739P.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Tsang SY;
XX WPI; 1997-291296/27.
XX Oligonucleotide primers for hepatitis C virus RNA amplification - by
XX polymerase chain reaction.
XX Claim 1; Page 11; 16pp; English.
XX This upstream primer ST280A is used in the amplification of the Hepatitis
XX C virus (HCV) RNA by reverse transcription PCR. This is used to amplify a
XX 250 base pair product from the 5' untranslated region of the HCV genome.
XX This can be used to detect HCV in a sample with increased sensitivity.

```

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 3
AAH25413
ID AAH25413 standard; DNA; 26 BP.
XX
AC AAH25413;
XX
DT 22-AUG-2001 (first entry)
XX
DE Forward PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT modified_base 26
FT /*tag= a
FT /*note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
FN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP011459.
XX
PR 17-NOV-1999; 99EP-00122853.
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
XX
PS Example 7; Page 98; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. PCR primers AAH25413-
CC 14 were used to amplify HCV DNA fragments. The amplified fragment can be
CC purified using the method of the invention
XX
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
    Query Match 100.0%; Score 26; DB 4; Length 26;
    Best Local Similarity 100.0%; Pred. No. 0.0052;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 4
ADC84692
ID ADC84692 standard; DNA; 26 BP.
XX
AC ADC84692;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer, #1, used to amplify HCV 5' UTR cDNA.

```

```

XX RNA purification; undegraded RNA; RNA binding solution;
KW RNA-complexing salt; chaotropic substance; non-silica solid support;
KW RNA lysing solution; amphiphilic reagent; PCR; ss; primer; 5' UTR;
KW untranslated region.
XX
OS Hepatitis C virus.
XX
PN US2003073830-A1.
XX
PD 17-APR-2003.
XX
PF 12-OCT-2001; 2001US-00974798.
XX
PR 12-OCT-2001; 2001US-00974798.
XX
PA (HEAT/) HEATH E M.
PA (WAGE/) WAGES J M.
XX
PI Heath EM, Wages JM;
XX
DR WPI; 2003-786889/74.
XX
PT Purifying substantially pure and undegraded RNA from biological material
PT involves use of high pH- and strong chaotropic substance-free RNA binding
PT solution that allows RNA to preferentially bind to a solid support.
XX
PS Example 10; Page 11; 14pp; English.
XX
CC The invention discloses a method for purifying substantially pure and
CC undegraded RNA from biological material (B). The method comprises mixing
CC (B) with RNA binding solution (I) that has RNA-complexing salt and is
CC free of strong chaotropic substance, to form a mixture which is contacted
CC with to a non-silica solid support (SS) such that nucleic acids
CC comprising substantially undegraded RNA in mixture preferentially bind to
CC SS, washing SS and eluting bound substantially undegraded RNA from SS.
CC The method may also comprise mixing (B), with an RNA lysing solution (II)
CC buffered at a pH of greater than about 7, and comprising an amphiphilic
CC reagent, and RNA-complexing salt, and is free of a strong chaotropic
CC substance, lysing (B) with (II) to form a lysate comprising nucleic acids
CC comprising substantially undegraded RNA and non-nucleic acid biological
CC matter, contacting the lysate to an immobilised non-silica SS such that
CC the nucleic acids comprising substantially undegraded RNA in the lysate
CC preferentially bind to SS, washing SS and eluting bound substantially
CC undegraded RNA. The methods are useful for purifying substantially pure
CC and undegraded RNA (e.g. total RNA chosen from mRNA, tRNA, rRNA and viral
CC RNA, or its combinations) from biological material containing RNA. The
CC method is useful for purifying RNA from crude and partially purified
CC mixtures of nucleic acids, from (B) such as eukaryotic, prokaryotic,
CC microbial, bacterial or plant cells, mycoplasma, protozoa, bacteria,
CC fungi, viruses, yeasts, rickettsia or their homogenates. The method is
CC also useful for purifying RNA from (B) such as whole blood, bone marrow,
CC blood spots, blood serum, blood plasma, buffy coat preparations, saliva,
CC cerebrospinal fluid, solid animal tissues, faeces, urine, tears, sweat or
CC from environmental samples taken from air, water sediment or soil. The
CC purified RNA is useful in analytical and diagnostic methods such as
CC reverse transcriptase-PCR and micro array analyses. The method purifies
CC RNA from a variety of biological materials without the use of hazardous
CC substances such as phenol and chloroform or hazardous chaotropic
CC substances such as guanidinium salts, urea, etc. The method allows the
CC elution of RNA in low salt reagents thus eliminating tedious desalting
CC steps. The method is versatile and effective. The sequence presented is a
CC PCR primer which was used to amplify Hepatitis C virus (HCV) 5'
CC untranslated region (UTR) to demonstrate the integrity of the purified
CC mRNA.
XX
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
    Query Match 100.0%; Score 26; DB 10; Length 26;
    Best Local Similarity 100.0%; Pred. No. 0.0052;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

```

ID	AA43739	standard; DNA; 27 BP.
XX	AA43739;	
XX	07-AUG-2003	(revised)
XX	14-NOV-2002	(first entry)
XX	HCV DNA amplifying PCR primer, ST280.	
XX	Amplification; target nucleic acid; control nucleic acid; PCR; primer;	
XX	ss.	
XX	Hepatitis C virus.	
XX	Key	Location/Qualifiers
XX	stem_loop	1..16
XX		/*tag= a
XX	misc_binding	1..5
XX		/*tag= b
XX		/bound_moiety= "Nucleotides 16-11"
XX	misc_binding	11..16
XX		/*tag= c
XX		/bound_moiety= "Nucleotides 5-1"
XX	EP1236804-A1.	
XX	PN	
XX	04-SEP-2002.	
XX	PD	
XX	02-MAR-2001;	2001EP-00105172.
XX	PF	
XX	02-MAR-2001;	2001EP-00105172.
XX	PR	
XX	(HOFF) ROCHE DIAGNOSTICS GMBH.	
XX	(HOFF) HOFFMANN LA ROCHE & CO AG F.	
XX	Jaeger S;	
XX	PI	
XX	WPI;	2002-610694/66.
XX	DR	
XX	Amplification of a target nucleic acid region using control sequences.	
XX	PT	
XX	PS	Example 2; Fig 3; 29pp; English.
XX	XX	The invention relates to a method for amplification of a target nucleic acid region. The method is useful for amplification of a nucleic acid molecule using control nucleic acid sequences. The control nucleic acid sequences are at least in part parallel-complementary to the sequence of the target nucleic acid. The present sequence is HCV DNA amplifying PCR primer. Note: This sequence is stated to be same as that shown as SEQ ID NO:6 in sequence listing. However this sequence has additional A at its 3' end. (Updated on 07-AUG-2003 to correct OS field.)
XX	Sequence	27 BP; 8 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
XX	Query Match	100.0%; Score 26; DB 6; Length 27;
XX	Best Local Similarity	100.0%; Pred. No. 0.0053;
XX	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1	GCAGAAAGCGTCTAGCCATGCGTTA 26
Db	1	GCAGAAAGCGTCTAGCCATGCGTTA 26
RESULT 7		
ABK88588		
ID	ABK88588	standard; DNA; 30 BP.
XX	AC	ABK88588;
XX	21-OCT-2002	(first entry)
XX	Hepatitis C virus (HCV) forward RT-PCR primer.	

KW Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor;
 KW cell culture replication; reverse transcriptase PCR; RT-PCR; primer; ss.
 OS Hepatitis C virus.
 XX
 XX
 FN WO200252015-A2.
 XX
 XX
 PD 04-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-CA001843.
 XX
 XX 22-DEC-2000; 2000US-0257857P.
 PR
 XX
 PA (BOEH) BOEHRINGER INGELHEIM CANADA LTD.
 XX
 XX Kukolj G, Pause A;
 PI
 XX WPI; 2002-575382/61.
 DR
 XX
 PT New self-replicating RNA molecules from Hepatitis C virus (HCV), which
 PT possess enhanced transduction or replication efficiency, useful for
 PT evaluating potential inhibitors of HCV replication.
 XX
 XX Example 9; Page 24; 140pp; English.
 PS
 CC The invention describes a self-replicating hepatitis C virus (HCV)
 CC polynucleotide molecule comprising a 5'-non translated region (NTR),
 CC where guanine at position 1 is substituted for adenine, a HCV polypeptide
 CC region coding for a HCV polypeptide; and a 3'-NTR region. The self-
 CC replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating
 CC potential inhibitors of HCV replication. The HCV RNA molecule is also
 CC useful for efficiently establishing cell culture replication. The self-
 CC replicating polynucleotide molecule contains a 5'-NTR, where G at
 CC position 1 is substituted for A, and therefore provides an alternative to
 CC existing systems comprising a self-replicating HCV RNA molecule that, in
 CC conjunction with mutations in the HCV non-structural region, such as the
 CC G2042C/R mutations, transduces and/or replicates with greater
 CC efficiency. This sequence represents a reverse transcriptase PCR primer
 CC used to amplify HCV RNA during testing of replicon RNA levels in cell
 CC lines
 XX
 SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 26; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
 RESULT 8
 ACC48582
 ID ACC48582 standard; DNA; 30 BP.
 XX
 AC ACC48582;
 XX
 XX 11-AUG-2003 (first entry)
 DT
 DE Hepatitis C virus 5' untranslated region forward PCR primer.
 XX
 XX HCV; RNA polymerase; enzyme; inhibitor; virucide; hepatotropic;
 KW antinflammatory; heterocycle; PCR; primer; ss.
 KW
 XX Hepatitis c virus.
 OS
 XX WO2003010140-A2.
 FN
 XX
 PD 06-FEB-2003.
 XX
 PF 18-JUL-2002; 2002WO-CA001127.
 XX

PR 25-JUL-2001; 2001US-0307674P.
 PR 07-DEC-2001; 2001US-0338061P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM CANADA LTD.
 XX
 PI Beaulieu PL, Fazal G, Kukolj G, Jolicoeur E, Gillard J;
 PI Poupart M, Rancourt J;
 XX
 XX WPI; 2003-342387/32.
 DR
 XX
 PT New heterocyclic compounds are viral polymerase inhibitors, useful for
 PT treating hepatitis C virus.
 XX
 XX Example 25; Page 74; 112pp; English.
 PS
 CC The invention provides novel heterocyclic compounds that have inhibitory
 CC activity against the RNA-dependent RNA polymerase NSSB (see ABR41892) of
 CC hepatitis C virus (HCV). The present sequence is a forward primer for the
 CC 5' untranslated region of HCV. This forward primer, the reverse primer
 CC given in ACC48583 and the fluorescent probe given in ACC48584 were used
 CC for real-time RT-PCR in a cell-based HCV RNA replication assay. RT-PCR
 CC data allowed the HCV RNA copy number in each well of a cell culture plate
 CC to be determined, and this was used as a measure of the amount of
 CC replicating HCV RNA in the presence of various concentrations of
 CC different HCV RNA polymerase inhibitors. The cell-based HCV RNA
 CC replication assay showed that selected compounds had IC50 values of less
 CC than 500 nM to over 1 uM. These compounds can be used in the treatment or
 CC prevention of HCV infection
 XX
 SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 26; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
 Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
 RESULT 9
 AAD51019
 ID AAD51019 standard; DNA; 30 BP.
 XX
 AC AAD51019;
 XX
 XX 02-APR-2003 (first entry)
 DT
 DE Hepatitis C virus (HCV) E2 cDNA specific probe.
 XX
 XX Transmembrane protein; extracellular domain; rous sarcoma virus; RSV;
 KW intracellular internalisation signal; vaccine; therapy; viral infection;
 KW hepatitis C virus; HCV; human immunodeficiency virus; herpes B virus;
 KW HBV; HIV; gene therapy; virucide; probe; ss.
 XX
 OS Hepatitis C virus.
 XX
 XX WO200294874-A2.
 FN
 XX 28-NOV-2002.
 PD
 XX
 XX 24-MAY-2002; 2002WO-CA000762.
 PF
 XX 24-MAY-2001; 2001GB-00012652.
 PR
 XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 PA
 XX Tan YH, Tan YJ, Lim SP, Lim SG, Hong WJ, Goh PY;
 PI
 XX WPI; 2003-120788/11.
 DR
 XX Chimeric transmembrane protein for manufacturing a medicament for
 PT treating or preventing viral infection, comprises an extracellular domain

PT capable of binding a virus and an intracellular internalization signal.

XX Example 1; Col 23; 33pp; English.

PS The invention relates to a chimeric transmembrane protein comprising an

CC extracellular domain capable of binding a virus and an intracellular

CC internalisation signal. The protein is useful for identifying an

CC antiviral agent or a vaccine, which is useful for manufacturing a

CC medicament for treating or preventing viral infection. The viral

CC infections are hepatitis C virus (HCV), human immunodeficiency virus

CC (HIV), herpes B virus (HBV), rous sarcoma virus (RSV), influenza virus,

CC herpes simplex virus, rabies virus, coxsackie virus, or rhinovirus. The

CC invention is also used in gene therapy. The present sequence is a probe

CC specific for HCV E2 cDNA. This sequence is used in the exemplification of

CC the invention

XX

SQ Sequence 30 BP; 8 A; 6 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

RESULT 10

ACC43164

ID ACC43164 standard; DNA; 30 BP.

AC ACC43164;

XX 17-JUN-2003 (first entry)

DT PCR primer used to amplify a 256 bp region of the 5' UTR of HCV.

DE HCV; viral polymerase inhibitor; HCV replication; HCV infection; PCR;

KW primer; ss.

XX Hepatitis C virus.

OS WO2003010141-A2.

PN 06-FEB-2003.

PD 18-JUL-2002; 2002WO-CA001128.

PF 25-JUL-2001; 2001US-0307674P.

PR 07-DEC-2001; 2001US-0338061P.

XX (BOEH) BOEHRINGER INGELHEIM CANADA LTD.

PA Beaulieu PL, Fazal G, Goulet S, Kukolj G, Poirier M;

XX Tsantrizos YS, Jolicoeur E, Gillard J, Poupard M, Rancourt J;

PI WPI; 2003-300442/29.

DR New viral polymerase inhibitors, useful in the treatment of hepatitis C

XX virus.

XX Example 48; Page 146; 336pp; English.

PS PCR primers ACC43164-65 and probe ACC43166 were used to amplify and

CC detect, respectively, a 256 bp fragment of the 5' untranslated region (5'

CC UTR) of Hepatitis C virus (HCV). The primers and probe were used to

CC determine the effect on HCV replication of compounds of the invention.

CC The specification describes viral polymerase inhibitor compounds, and

CC their isomers, enantiomers, diastereomers or tautomers. The compounds are

CC of a formula given in the specification. Viral polymerase inhibitor

CC compounds of the invention are inhibitors of HCV replication, and are

CC used in the treatment or prevention of HCV infection

XX

SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 11

ACF36230

ID ACF36230 standard; DNA; 30 BP.

XX ACF36230;

XX 04-DEC-2003 (first entry)

DT HCV 5' IRES quantifying forward primer.

DE HCV; hepatotropic; antiinflammatory; virucide. NS3 protease; RT-PCR;

KW RNA replication; IRES; primer; ss.

XX Hepatitis C virus.

OS WO2003064455-A2.

PN 07-AUG-2003.

PD 24-JAN-2003; 2003WO-CA000089.

PF 30-JAN-2002; 2002CA-02369711.

PR (BOEH) BOEHRINGER INGELHEIM CANADA LTD.

PA Llinas-Brunet M, Gorys VJ;

XX WPI; 2003-663463/62.

DR New heterocyclic tripeptides are Hepatitis C Virus (HCV) NS3 protease

PT inhibitors, used in treatment of hepatitis C viral infection and

PT producing fewer side effects.

XX Example 10; Page 34; 21pp; English.

PS The invention relates to heterocyclic tripeptides of specified formula.

CC The compounds inhibit the activity of Hepatitis C virus (HCV) NS3

CC protease activity and also inhibit HCV RNA replication. The compounds

CC show good pharmacokinetic properties and can be used in the manufacture

CC of a medicament for the treatment or prevention of HCV infection in

CC mammals. The present sequence represents a primer used for amplifying a

CC 5' UTR fragment of HCV, used in a RT-PCR quantification of HCV 5' IRES

CC sequence

XX

SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26

DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12

ACF36227

ID ACF36227 standard; DNA; 30 BP.

XX ACF36227;

XX 04-DEC-2003 (first entry)

DT

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XX HCV 5' IRES quantifying forward primer.
XX HCV; hepatotropic; antiinflammatory; virucide. NS3 protease; RT-PCR;
XX RNA replication; IRES; primer; ss.
XX Hepatitis C virus.
XX WO2003064416-A1.
XX 07-AUG-2003.
XX 24-JAN-2003; 2003WO-CA000091.
XX 01-FEB-2002; 2002CA-02369970.
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX Llinas-Brunet M, Bailey MD, Ghire E;
XX WPI; 2003-663458/62.
XX New heterocyclic tripeptides useful for the treatment of hepatitis C
XX viral infection.
XX Example 10; Page 32; 21pp; English.
XX The invention relates to heterocyclic tripeptides of specified formula.
XX The compounds inhibit the activity of Hepatitis C virus (HCV) NS3
XX protease activity and also inhibit HCV RNA replication. The compounds
XX show good pharmacokinetic properties and can be used in the manufacture
XX of a medicament for the treatment or prevention of HCV infection in
XX mammals. The present sequence represents a primer used for amplifying a
XX 5' UTR fragment of HCV, used in in a RT-PCR quantification of HCV 5' IRES
XX sequence
XX SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 26; DB 10; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.0054;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
XX |||||||||||||||||||||||||||
XX Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
XX |||||||||||||||||||||||||||
XX
XX RESULT 13
XX ID ACF36280 standard; DNA; 30 BP.
XX AC ACF36280;
XX AC ACF36280;
XX DT 04-DEC-2003 (first entry)
XX DE HCV 5' IRES quantifying forward primer.
XX KW HCV; hepatotropic; antiinflammatory; virucide; NS3 protease; RT-PCR;
XX KW RNA replication; IRES; primer; ss.
XX OS Hepatitis C virus.
XX OS WO2003064456-A1.
XX PN 07-AUG-2003.
XX PD 24-JAN-2003; 2003WO-CA000090.
XX PF 01-FEB-2002; 2002CA-02370396.
XX PR (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PA Llinas-Brunet M, Gorys VJ;
XX PI

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XX WPI; 2003-671487/63.
XX New tripeptides (having substituted quinoline with hydroxyproline ether
XX side chain) derivatives are Hepatitis C virus (HCV) NS3 protease activity
XX inhibitors useful in treatment of hepatitis C viral infection with fewer
XX side effects.
XX Example 11; Page 43; 28pp; English.
XX The invention relates to tripeptides (having substituted quinoline with
XX hydroxyproline ether side chain) derivatives of specified formula. The
XX compounds inhibit the activity of Hepatitis C virus (HCV) NS3 protease
XX activity and also inhibit HCV RNA replication. The compounds show good
XX pharmacokinetic properties and can be used in the manufacture of a
XX medicament for the treatment or prevention of HCV infection in mammals.
XX The present sequence represents a primer used for amplifying a 5' UTR
XX fragment of HCV, used in in a RT-PCR quantification of HCV 5' IRES
XX sequence
XX SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 26; DB 10; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.0054;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
XX |||||||||||||||||||||||||||
XX Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
XX |||||||||||||||||||||||||||
XX
XX RESULT 14
XX ID ABZ76307 standard; DNA; 30 BP.
XX AC ABZ76307;
XX AC ABZ76307;
XX DT 12-JUN-2003 (first entry)
XX DE HCV RNA 5' IRES quantifying forward primer.
XX KW NS3; benzimidazole; viral polymerase; virucide; hepatotropic; IRES;
XX KW antiinflammatory; RT-PCR; primer; ss.
XX OS Hepatitis C virus.
XX OS WO2003007945-A1.
XX PN 30-JAN-2003.
XX PD 18-JUL-2002; 2002WO-CA001129.
XX PF 20-JUL-2001; 2001US-0306669P.
XX PR 07-DEC-2001; 2001US-0338324P.
XX PA (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
XX PI Beaulieu PL, Fazal G, Goulet S, Kukolj G, Poirier M;
XX PI Tsantrizos YS;
XX DR WPI; 2003-289764/28.
XX PT New 5-substituted benzimidazole derivatives, useful for treating
XX PT hepatitis C virus infection by inhibiting viral polymerase, and their
XX PT intermediates are new.
XX PS Example 24; Page 161; 166pp; English.
XX The invention relates to isomers, diastereoisomers, enantiomers and
XX tautomers of 5-substituted benzimidazole compounds of specified formula.
XX The compounds are viral polymerase inhibitors, especially they are potent
XX inhibitors of HCV NS5B polymerase. The compounds are used to treat or
XX prevent infection by hepatitis C virus. The present sequence represents a
XX

```

CC primer used in real-time RT-PCR quantification of the 5' IRES (internal
CC ribosome entry sequence) of HCV RNA
XX
SQ Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 26; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
DB 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28
RESULT 15
ADP20412
ID ADP20412 standard; DNA; 37 BP.
XX
XX
AC ADP20412;
XX 09-SEP-2004 (first entry)
DT
DE Hepatitis C virus IRES region II consensus sequence, SEQ ID 3.
XX
XX Virucide; Cytostatic; p110 subunit;
KW eukaryotic translation initiation factor eIF3; region II;
KW internal ribosome entry site; IRES; aminoglycoside;
KW hepatitis C infection; swine fever; bovine diarrhoea; viral infection;
KW cancer; ds.
XX
OS Hepatitis C virus.
XX
XX FR2848572-A1.
XX
XX 18-JUN-2004.
XX 12-DEC-2002; 2002FR-00015718.
XX 12-DEC-2002; 2002FR-00015718.
PR
XX (UYFO-) UNIV FOURIER JOSEPH.
XX Balakireva L;
XX
XX WPI; 2004-452919/43.
XX
XX In vitro screening for antiviral agents, from ability to inhibit complex
XX formation between the p110 subunit of translation initiation factor eIF3
XX and region II of the viral internal ribosome binding site.
XX
XX Claim 3; SEQ ID NO 3; 45pp; French.
XX
XX The present invention relates to an in vitro method of screening for
XX compounds (A) that inhibit the formation of a complex between the p110
XX subunit (ADP20413) of the eukaryotic translation initiation factor eIF3
XX and region II of the internal ribosome entry site (IRES; ADP20411) of
XX hepatitis C virus (HCV). Preferably the p110 recognition motif (ADP20414)
XX and the region II consensus sequence (ADP20412), or fragment of it
XX containing at least 8 consecutive nucleotides, are used. (A) is
XX especially an aminoglycoside, specifically tobramycin or an
XX oligonucleotide antisense to consensus sequence ADP20412, or parts of it.
XX (A) are used for treating infection by hepatitis C, swine fever and
XX bovine diarrhoea viruses, also for treating viral or non-viral diseases
XX which involve proteins synthesis of which is initiated from an IRES, e.g.
XX cancer.
XX
XX Sequence 37 BP; 8 A; 10 C; 9 G; 10 T; 0 U; 0 Other;
SQ
Query Match 96.2%; Score 25; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTT 25

DB 13 GCAGAAAGCGTCTAGCCATGGCGTT 37
RESULT 16
AAQ37573
ID AAQ37573 standard; DNA; 24 BP.
XX
XX AC AAQ37573;
XX
XX 25-MAR-2003 (revised)
DT 23-JUN-1993 (first entry)
DT
DE HCV conserved region upstream primer/probe KY80, position 56-79.
XX
XX Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
XX EP529493-A2.
XX
XX 03-MAR-1993.
XX
XX 19-AUG-1992; 92EP-00114115.
XX
XX 27-AUG-1991; 91US-00751305.
PR
PR 21-JUL-1992; 92US-00918844.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Resnick RM, Young KKY;
XX
XX WPI; 1993-068572/09.
XX
XX Compsn. comprising oligo:nucleotide probe-primer - used for detecting
XX hepatitis C virus strains Japan, US and C9.
XX
XX Claim 4; Page 7; 43pp; English.
XX
XX The sequences given in AAQ37569-96 are oligonucleotides which can be used
XX as primers or probes which hybridise to the conserved region at the 5'-
XX end of the hepatitis C virus (HCV) genome. HCV is a small RNA virus
XX containing a small, positive sense, molecule of RNA about 10,000
XX nucleotides in length. the genome contains a single, long, open reading
XX frame believed to translated in to a single, large polyprotein and
XX subsequently processed. The open reading frame begins at nucleotide 343
XX (using the numbering system from the prototype virus) following an
XX untranslated region (UTR) the 5'UTR sequence is relatively conserved and
XX may be important in viral replication and regulation. The 5' end of the
XX coding region is also conserved. These primer/probes can be used to
XX identify different HCV isolates such as US, Japan and C9 (see also
XX AAQ37597-601). (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGTT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGTT 24
RESULT 17
AAQ79964
ID AAQ79964 standard; DNA; 24 BP.
XX
XX AC AAQ79964;
XX

DT 25-MAR-2003 (revised)
 DT 01-AUG-1995 (first entry)
 XX
 DE Primer KY90 for HCV RNA.
 XX
 KW Primer; PCR; polymerase chain reaction; amplification; RNA detection;
 KW reverse transcription; hepatitis C virus; HCV; ss.
 XX
 OS Synthetic.
 XX
 PN EP632134-A2.
 XX
 PD 04-JAN-1995.
 XX
 PP 20-JUN-1994; 94EP-00109468.
 XX
 PR 01-JUL-1993; 93US-00086483.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Gelfand DH, Myers TW, Sigua CL;
 XX
 DR WPI; 1995-037815/06.
 XX
 PT Improved amplification method for target RNA - using buffering agent
 PT which buffers both pH and divalent cation concn.
 XX
 PS Example 6; Page 22; 37pp; English.
 XX
 CC The primers given in AAQ79963-64 were used to amplify HCV templates for
 CC use in a novel method of RNA amplification involving high-temp. reverse
 CC transcription and PCR. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 RESULT 18
 AAT93541
 ID AAT93541 standard; DNA; 24 BP.
 XX
 AC AAT93541;
 XX
 DT 19-FEB-1998 (first entry)
 XX
 DE Sense primer KY80 for amplification of HCV RNA.
 XX
 KW Armoured RNA; bacteriophage M2; RT-PCR; ribonuclease; recombinant;
 KW Human immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;
 KW detection; quantification standard; maturase protein; coat protein;
 KW PCR primer; OS RNA; reverse transcriptase-PCR; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus; Virus.
 XX
 PN US5677124-A.
 XX
 PD 14-OCT-1997.
 XX
 PF 03-JUL-1996; 96US-00675153.
 XX
 PR 03-JUL-1996; 96US-00675153.
 XX
 PA (AMEI-) AMEION INC.
 PA (CENE-) CENETRON DIAGNOSTICS LLC.
 XX

PI Pasloske BL, Dubois DB, Winkler MM;
 DR WPI; 1997-511866/47.
 XX
 PT Recombinant RNA segment encapsidated in bacteriophage viral coat protein
 PT - RNA detection and/or quantification standard.
 XX
 PS Example 5; Col 22; 23pp; English.
 XX
 CC This sense primer is used in the RT-PCR amplification of HCV RNA to
 CC create a quantitative HCV "armoured RNA" standard. An "armoured RNA" is a
 CC recombinant RNA segment encapsidated in bacteriophage viral coat protein.
 CC The recombinant RNA segment comprises an operator coding sequence, a
 CC viral maturase protein binding site, and a non-bacteriophage sequence.
 CC The recombinant RNA in its packaged form is highly resistant to
 CC ribonucleases, insuring that the RNA standard is not compromised by
 CC inadvertent ribonuclease contamination. The armoured RNA standards are
 CC ideal as RNA standards for the quantification of RNA viruses such as HIV
 CC and HCV from human body fluids such as blood and cerebrospinal fluid
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 |||||
 RESULT 19
 AAT87096
 ID AAT87096 standard; DNA; 24 BP.
 XX
 AC AAT87096;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-JAN-1998 (first entry)
 XX
 DE HCV gene PCR primer KY80.
 XX
 KW RNA; plasma; hepatitis C virus; HCV; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN US5654179-A.
 XX
 PD 05-AUG-1997.
 XX
 PF 03-OCT-1994; 94US-00317220.
 XX
 PR 14-NOV-1990; 90US-00614921.
 PR 19-JUN-1992; 92US-00901545.
 PR 08-APR-1993; 93US-00044649.
 XX
 PA (HYDS) HRI RES INC.
 XX
 PI Lin L;
 XX
 DR WPI; 1997-401849/37.
 XX
 PT Preparation of RNA samples from plasma - by alcohol precipitation after
 PT lysis with guanidinium thiocyanate.
 XX
 PS Disclosure; Col 47; 60pp; English.
 XX
 CC Primer KY80 (AAT87096) and primer KY78 (AAT87095) were used for the PCR
 CC amplification of a 305 bp hepatitis C virus gene product (see AAT87088).
 CC A claimed method for preparing RNA samples comprises: (a) mixing plasma
 CC with an aqueous buffer solution containing guanidinium thiocyanate and
 CC beta-mercaptoethanol; (b) heating the mixture; (c) adding an equal volume

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CC of an alcohol to precipitate RNA; and (d) recovering the RNA. The method
 CC can be used to prepare RNA samples for subsequent amplification.
 CC especially for detecting pathogens, e.g. hepatitis C virus or HIV.
 CC Compared with the known 'Isoquick' and 'RNazol' methods, the method
 CC uses fewer tubes (just one), requires fewer steps, takes less time and
 CC produces no toxic waste. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 20
 AAT64887
 ID AAT64887 standard; DNA; 24 BP.
 XX
 AC AAT64887;
 XX
 AC
 XX 25-MAR-2003 (revised)
 DT 12-MAR-1998 (first entry)
 XX
 DE Hepatitis C virus (HCV) oligonucleotide KY80.
 XX
 XX Hepatitis C virus; reverse transcription; probe; PCR primer; detection;
 KW ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN EP787807-A2.
 XX
 PD 06-AUG-1997.
 XX
 PF 19-AUG-1992; 97EP-00106534.
 XX
 PR 27-AUG-1991; 91US-00751305.
 PR 21-JUL-1992; 92US-00918844.
 PR 19-AUG-1992; 92EP-00114115.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 PI Resnick RM, Young KKY;
 XX
 DR WPI; 1997-387489/36.
 XX
 XX Oligo:nucleotide probes and primers for detecting hepatitis C virus
 PT nucleic acid - from many different strains without loss of specificity,
 PT allow single step reverse transcription and amplification.
 XX
 XX Claim 2 and 5; Page 7; 35pp; English.
 PS
 XX This oligonucleotide KY80 can be used as a probe for detecting hepatitis
 CC C virus (HCV) nucleic acid from a Japanese or US prototype strain. This
 CC oligonucleotide can also be used as a primer for amplifying HCV nucleic
 CC acid. This primer is capable of amplifying HCV C9 prototype strains also.
 CC The sequence of this oligonucleotide is contained in a specific region of
 CC the HCV genomic nucleic acid. The probe or the primer is preferably labelled.
 CC The probe is used to detect HCV nucleic acid, preferably after this has
 CC been amplified using the new primer in reverse transcription polymerase
 CC chain reaction (RT-PCR), for both diagnostic and epidemiological
 CC applications. The primer is effective for both reverse transcription and
 CC PCR, eliminating the need to open the reaction tube during the procedure.
 CC Amplification is effective (no need for a second round of PCR with nested
 CC primers) and provides high sensitivity. The probe is directed to
 CC conserved regions and so can detect many different strains without loss
 CC of specificity. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
 CC 25-MAR-2003 to correct PR field.)

XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 21
 AAV15320
 ID AAV15320 standard; DNA; 24 BP.
 XX
 AC AAV15320;
 XX
 AC
 XX 25-MAR-2003 (revised)
 DT 28-MAY-1998 (first entry)
 XX
 DE Hepatitis C virus PCR primer PKY80.
 XX
 XX Hepatitis C virus; HCV; PCR primer; detection; reverse transcription;
 KW enzyme immunoassay; viral RNA; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN WO9746716-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 03-JUN-1997; 97WO-IT000128.
 XX
 PR 07-JUN-1996; 96IT-RM000404.
 XX
 PA (WESA) WABCO BV.
 XX
 PI Bosio P, Strumia C, Clemenza F;
 XX
 DR WPI; 1998-042222/04.
 XX
 XX Detection of hepatitis C virus - by reverse transcription, single-step
 PT PCR and detection by DNA enzyme immunoassay.
 XX
 PS Disclosure; Page 4; 26pp; English.
 XX
 XX The present sequence represents a PCR primer involved in the method of
 CC the present invention for detecting hepatitis C virus (HCV). The method
 CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
 CC resulting cDNA by a single polymerase chain reaction in a reaction
 CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
 CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
 CC immunoassay) using an oligonucleotide probe. The sensitivity of this
 CC method is at least equal to that achievable by more complicated assays
 CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 92.3%; Score 24; DB 2;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 22
 AAV18849
 ID AAV18849 standard; DNA; 24 BP.
 XX

CC veterinary medicine, e.g. for detecting human immune deficiency virus,
CC hepatitis B or C viruses, or Chlamydia, in blood screening. The method
CC provides target-dependent, exponential amplification for highly specific
CC and sensitive, reproducible and quantitative detection of one or more
CC nucleic acids (single or double stranded). The design of primers and
CC probes is sufficiently flexible to allow many nucleic acids to be
CC detected in a standardized reaction format using partly the same primers
CC and probes. Only small amplicons are produced (requiring short
CC amplification cycles), there is no competition/displacement between the
CC short counter-strand of the amplicon and the detection probe, and
CC specificity is high because the relative proportion of the internal
CC detection region is increased with respect to the total amplicon length,
CC allowing better differentiation between (viral) subtypes. Also short
CC amplicons are less likely to undergo non-specific hybridization, so
CC background is low, and short RNA sequences are more stable, with reduced
CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
CC PCR primers and probes used in the method of the invention
CC
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||

RESULT 25
AAX78451
ID AAX78451 standard; DNA; 24 BP.
XX
AC AAX78451;
XX
XX
DT 26-AUG-1999 (first entry)
XX
DE HCV PCR primer 1.
XX
XX RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
KW ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV; HTLV-1;
KW HTLV-2; hepatitis 6; enterovirus; blood-borne pathogen; ss.
XX
XX Synthetic.
OS Hepatitis C virus.
XX
XX US5919625-A.
XX
XX 06-JUL-1999.
XX
XX 29-APR-1997; 97US-00841252.
XX
XX 03-JUL-1996; 96US-00675153.
XX (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX
XX Pasloske BL, Dubois DB, Winkler MM;
XX
XX WPI; 1999-394617/33.
XX
XX Ribonuclease resistant viral RNA standards.
PT
XX Example V; Col 31-32; 22pp; English.
XX
XX This invention describes the construction of novel RNA standards for the
CC quantification of human immunodeficiency virus (HIV) and hepatitis C
CC virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
CC obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
CC RNA standard, encapsulated in a bacteriophage viral coat protein, which
CC comprises an RNA segment having a segment encoding a sequence that serves
CC as a standard in detection or quantification of the RNA of interest; (3)
CC mixing the sample with the standard; (4) isolating RNA from the mixture,

CC and (5) assaying for the presence of the RNA. The method is useful for
CC the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1, HTLV-2,
CC hepatitis G, an enterovirus or a blood-borne pathogen. This sequence
CC represents a PCR primer used to amplify a region of the Hepatitis C
CC genome which is used in the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||

RESULT 26
AAZ09797
ID AAZ09797 standard; DNA; 24 BP.
XX
AC AAZ09797;
XX
XX 26-NOV-1999 (first entry)
DT
XX HCV PCR primer KY80.
DE
XX Probe; amplification; primer; reporter group; quencher group; PCR;
KW amplicon; detection; ss.
XX
XX Synthetic.
OS Hepatitis C virus.
XX
XX DE19814001-A1.
XX
XX 30-SEP-1999.
XX
XX 28-MAR-1998; 98DE-01014001.
XX
XX 28-MAR-1998; 98DE-01014001.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA
XX Kessler C, Haberhausen G, Batz H, Orum H;
PI
XX WPI; 1999-552213/47.
XX
XX Fluorescent nucleic acid amplification assay, useful for detection of
PT viral, bacterial, cellular, yeast or fungal nucleic acids.
XX
XX Example 1; Page 19; 16pp; German.
XX
XX This invention describes a novel assay for a nucleic acid which comprises
CC an amplification reaction using two non-overlapping primers, a polymerase
CC with 5'-nuclease activity and a probe with reporter groups and quencher
CC groups that binds a region other than that bound by the primers. The
CC reaction generates products of less than 100 nucleotides. The assay is
CC useful for detection of viral, bacterial, cellular, yeast or fungal
CC nucleic acids in human, animal, bacterial, plant, yeast or tissue, cell
CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC or liquid biopsy samples. Compared with assays in which longer
CC amplification products are generated, the assay can be performed more
CC rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC may be increased due to reduced competition between the short
CC counterstrand of the amplicon and the detector probe. Specificity may
CC also be increased because of the increased relative length of sequence B
CC compared with the total length of the amplicon and the differentiability
CC of subtypes may be increased. In addition signal-to-noise ratios may be
CC increased with the new method because short amplicons have reduced
CC potential for nonspecific hybridization. In addition reproducibility may
CC be increased because small target regions on RNA genomes are less
CC sensitive to RNA degradation, and the possibilities for secondary
CC structure formation are reduced. This sequence represents a PCR primer

CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 27
AAH25403
ID AAH25403 standard; DNA; 24 BP.
XX
AC AAH25403;
XX
DT 22-AUG-2001 (first entry)
XX
DE PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP011459.
XX
PR 17-NOV-1999; 99EP-00122853.
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
WPI; 2001-381247/40.
DR
XX
PT Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
XX
PS Example 7; Page 94; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. PCR primers AAH25403-
CC 04 were used to amplify HCV DNA fragments. The amplified fragment can be
CC purified using the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 28
AAD19056
ID AAD19056 standard; DNA; 24 BP.
XX
AC AAD19056;

CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 29
ABN83648
ID ABN83648 standard; DNA; 24 BP.
XX
AC ABN83648;
XX
DT 27-AUG-2002 (first entry)
XX
DE Hepatitis C virus PCR primer KY80.
XX
KW Nucleic acid detection; infection; subtilisin; esperase; diagnosis; PCR;
XX primer; ss.
XX
OS Hepatitis C virus.
XX

XX
DT 18-DEC-2001 (first entry)
XX
DE Hepatitis viral DNA amplifying forward PCR primer #30.
XX
KW Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.
XX
OS Hepatitis virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US008110.
XX
PR 14-MAR-2000; 2000US-0189344P.
XX
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, Mccue KF;
XX
WPI; 2001-611396/70.
DR
XX
PT Simultaneous detection of biological entities such as bacteria, fungi and
PT viruses by specific nucleic acid amplification.
XX
PS Disclosure; Page 31; 55pp; English.
XX
CC The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a
CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC caused by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (Staphylococcus, Pneumococcus,
CC Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis,
CC dermatitis, Candida albicans) or protozoa (Entamoeba histolytica). The
CC present sequence is a PCR primer used for amplifying Hepatitis viral DNA
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 29
ABN83648
ID ABN83648 standard; DNA; 24 BP.
XX
AC ABN83648;
XX
DT 27-AUG-2002 (first entry)
XX
DE Hepatitis C virus PCR primer KY80.
XX
KW Nucleic acid detection; infection; subtilisin; esperase; diagnosis; PCR;
XX primer; ss.
XX
OS Hepatitis C virus.
XX

PN EP1201752-A1.
XX
PD 02-MAY-2002.
XX
PF 31-OCT-2000; 2000EP-00123728.
XX
PR 31-OCT-2000; 2000EP-00123728.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Schmuck R, Staepels J, Meier T, Wehnes U, Russmann E;
XX WPI; 2002-396808/43.
DR
XX
XX Use of Bacillus lentus subtilisin 147 to analyze one or more target non-
PT proteinaceous components from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically.
XX
PS Example; Page 22; 36pp; English.
XX
CC The present sequence is hepatitis C virus (HCV) PCR primer KY80. This was
CC used with biotinylated primer KY78 (see ABN83649) and a capture probe
CC (see ABN83650) in an example from the invention for the amplification and
CC detection of HCV RNA in a plasma sample. The invention provides a method
CC for the analysis of non-proteinaceous components, especially DNA and/or
CC RNA, in a mixture of proteinaceous and non-proteinaceous components in a
CC biological sample. The sample is incubated with protease subtilisin 147
CC (see ABN76400) of Bacillus lentus variant 147 (NCIB 10147), and the
CC target DNA or RNA is then amplified by PCR and determined or detected. In
CC the present example, the ruthenium-tris(bipyridyl)-labeled capture probe
CC provided a sensitive nonisotopic approach to detection based on
CC electrochemiluminescence following specific hybridisation to biotinylated
CC denatured HCV amplicons. The method is useful in environmental, food and
CC medical analysis, e.g. to detect viral infection, and in molecular
CC biological research, and can be performed using a high throughput format
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 30
ABK51599
ID ABK51599 standard; DNA; 24 BP.
XX
AC ABK51599;
XX
DT 13-AUG-2002 (first entry)
XX
DE Hepatitis C virus protease, PCR primer KY80.
XX
KW Subtilisin 147; medical analysis; environmental analysis; food analysis;
KW diagnostic; virus infection; PCR; primer; ss; hepatitis C virus;
KW protease.
XX
OS Hepatitis C virus.
XX
FN EP1201753-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001EP-00125322.
XX
PR 31-OCT-2000; 2000EP-00123728.
PR 15-MAR-2001; 2001EP-00106308.
XX

PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Russmann E, Schmuck R, Meier T, Staepels J, Wehnes U;
XX WPI; 2002-428566/46.
DR
XX
XX Use of Bacillus lentus subtilisin 147 to analyze a target non-
PT proteinaceous component from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically to detect viruses.
XX
PS Example 2; Page 24; 38pp; English.
XX
CC The invention describes a target non-proteinaceous component is analysed
CC from a mixture of non-proteinaceous and proteinaceous components derived
CC from a biological sample by incubating the mixture with a protease having
CC at least 80 % identity to the known amino acid sequence for subtilisin
CC 147 from Bacillus lentus. The methods are useful for analysis of
CC biological samples e.g. in medical, environmental or food analysis or in
CC molecular biological research. They are especially useful in diagnostics
CC e.g. to detect virus infections. They can be used to enrich a mixture for
CC a target non-proteinaceous component or purify/isolate the component, the
CC component can especially be a nucleic acid, e.g. from a
CC virus/microorganism. The methods can be used to isolate non-proteinaceous
CC components useful as substrates in enzymatic reactions, or (in the case
CC of nucleic acids) for sequencing, as probes etc. They can be used in high
CC throughput formats, enabling analysis of large numbers of samples in a
CC short time. Kits for undertaking the methods, comprising the preferred
CC polypeptide, optionally a material with an affinity to nucleic acids
CC (especially preferred materials as above) and/or optionally lysis,
CC washing and elution buffers are provided. This sequence represents a
CC primer used to isolate DNA sequences encoding Hepatitis C virus proteases
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 92.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 31
ABZ75890
ID ABZ75890 standard; DNA; 24 BP.
XX
AC ABZ75890;
XX
DT 15-MAY-2003 (first entry)
XX
DE HCV RNA detecting RT-PCR primer RJD-1 (KY80) .
XX
KW HCV; hepatic disorder; envelope glycoprotein; DC-SIGN; DC-SIGNR; primer;
KW hepatoprotective; virucide; cytostatic; protein therapy; RT-PCR; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003000024-A2.
XX
PD 03-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-US020875.
XX
PR 26-JUN-2001; 2001US-00891894.
XX
PA (PROG-) PROGENICS PHARM INC.
XX
PI Olson WC, Maddon PJ;
XX WPI; 2003-267852/26.
DR

XX Treating hepatitis, cirrhosis or hepatocellular carcinoma by inhibiting
PT binding between HCV envelope glycoproteins and DC-SIGN/DC-SIGNR proteins
PT on the surface of cells.
XX
XX Disclosure; Page 119; 165pp; English.
XX
XX The invention relates to methods and agents for diagnosing and treating
CC Hepatitis C Virus (HCV) infections and other hepatic disorders based on
CC binding between HCV envelope glycoproteins and DC-SIGN and DC-SIGNR
CC proteins on the surface of cells. The methods may be used to identify
CC agents (antibodies, peptides and other non-peptidyl agents) that may be
CC administered to treat hepatitis, cirrhosis or hepatocellular carcinomas
CC and to diagnose these disease. The present sequence represents a primer
CC used in a RT-PCR assay for the detection of HCV RNA
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 92.3%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Dd 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 32
ADC54067
ID ADC54067 standard; DNA; 24 BP.
XX
XX ADC54067;
XX
XX 18-DEC-2003 (first entry)
XX
XX HCV 5'UTR PCR primer, SEQ ID NO:19.
DE
XX HCV; hepatitis C virus; classification; interferon therapy; 5'UTR; PCR;
XX primer; ss.
KW
XX Hepatitis C virus.
OS
XX
XX JP2002345467-A.
FN
XX
XX 03-DEC-2002.
PD
XX
XX 17-APR-2001; 2001JP-00118810.
PF
XX
XX 23-OCT-2000; 2000JP-00322567.
PR
XX
XX (SRLS-) SRL KK.
PA
XX
XX WPI; 2003-460879/44.
DR
XX
XX Probe and method for classification of hepatitis C virus (HCV) types used
PT for forecast of therapeutic effect of interferon administration.
PT
XX
XX Example 1; SEQ ID NO 18; 15pp; Japanese.
PS
XX
XX The invention relates to a nucleic acid probe for the classification of
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1Ami
CC (type 1), MH2Ami (type 2) and MHCG3C-MHCG3C' (type 3). The probe can be
CC used to classify HCV type to enable prediction of the success or
CC otherwise of interferon therapy in a patient. Sequences ADC54066-ADC54067
CC represent PCR primers used to amplify a region of the HCV 5'UTR in an
CC example of the invention.
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 92.3%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Dd 1 GCAGAAAGCGTCTAGCCATGGCGT 24
RESULT 33
ADD5635
ID ADD5635 standard; DNA; 24 BP.
XX
XX ADD5635;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX PCR primer, RD1, used to amplify HCV nucleic acid.
DE
XX
XX HCV; fluorescent dye; fluorescent molecular beacon pair; lambda phage;
KW lambda phage-HCV hybrid amplicon; detection; diagnosis; HCV infection;
KW hepatitis; cirrhosis; antiviral therapy; PCR; primer; ss.
XX
XX Hepatitis C virus.
OS
XX
XX US2003104582-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 04-DEC-2001; 2001US-00011855.
PF
XX
XX 04-DEC-2001; 2001US-00011855.
PR
XX
XX (BAUM/) BAUMANN R.
PA (HAMD/) HAMMAN H.
PA (LEWI/) LEWINSKI M.
XX
XX Baumann R, Hamdan H, Lewinski M;
PI
XX
XX WPI; 2003-801237/75.
DR
XX
XX Detecting hepatitis C virus (HCV) nucleic acid in a sample comprises
PT reverse transcribing and amplifying HCV nucleic acids with primer pair,
PT hybridizing amplicons with a labeled probe, and detecting a signal.
XX
XX Claim 8; Page 6; 11pp; English.
PS
XX
XX The invention discloses a method for detecting the presence or amount of
CC Hepatitis C virus (HCV) nucleic acids in a sample comprising reverse
CC transcribing and amplifying any HCV nucleic acid present, reacting the
CC amplified nucleic acids with a probe in the presence of an enzyme that
CC cleaves the probe if specifically hybridised to HCV nucleic acids, and
CC detecting a signal from the probe. The detectable label is a fluorescent
CC dye or a fluorescent molecular beacon pair. Lambda phage HCV nucleic acid
CC hybrids are introduced into the test sample, reverse transcribed and
CC amplified using the pair of oligonucleotide primers to produce lambda
CC phage-HCV hybrid amplicons. The hybrids are hybridised to a control
CC oligonucleotide sequence (ADD55640) which is conjugated to 6-
CC carboxyfluorescein (FAM) and 6-carboxytetramethylrhodamine (TAMRA). The
CC test sample is chosen from serum, blood, plasma, cerebral spinal fluid,
CC synovial fluid, and urine. The nucleic acids are purified from the sample
CC prior to the reverse transcription and amplification step. The lambda
CC phage-HCV ribonucleic acid hybrids may be introduced into the test sample
CC prior to isolating nucleic acids from the sample. The method is useful
CC for detecting the presence or amount of hepatitis C virus (HCV) nucleic
CC acids in a test sample, for diagnosing HCV infection, which can lead to
CC chronic hepatitis and cirrhosis, for identification of individuals with
CC high viral replication, for monitoring patients on therapy and for
CC predicting whether antiviral therapy will be successful. The method is
CC specific and sensitive and exhibits a broad dynamic range of detection of
CC HCV nucleic acids and provides quantitative as well as qualitative
CC results. The sequence presented is a primer used to amplify HCV nucleic
CC acid.
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 92.3%; Score 24; DB 10; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 34
ADM24824
ID ADM24824 standard; DNA; 24 BP.
XX AC ADM24824;
XX DT 20-MAY-2004 (first entry)
XX DE Hepatitis C virus (HCV) RNA specific RT-PCR primer, RJD-1.
XX KW Hepatotropic; virucide; antiinflammatory; cytostatic; Hepatitis C virus;
KW HCV; HCV infection; DC-SIGN; DC-SIGN related; DC-SIGNR; therapy;
KW liver disease; hepatitis; cirrhosis; hepatocellular carcinoma;
KW reverse transcription; RT; PCR; primer; ss.
XX OS Hepatitis C virus.
XX PN US2003134297-A1.
XX PD 17-JUL-2003.
XX PF 26-JUN-2002; 2002US-00184150.
XX PR 26-JUN-2001; 2001US-0300971P.
XX PA (OLSO/) OLSON W C.
XX PA (MADD/) MADDON P J.
XX PI Olson WC, Maddon PJ;
XX DR WPI; 2003-829636/77.
XX QY Inhibiting hepatitis C virus infection of susceptible cell or target cell
PT comprises contacting cell with compound to inhibit binding of hepatitis C
PT virus envelope glycoprotein to specified intracellular adhesion proteins.
PS Disclosure; Page 31; 47pp; English.
XX CC The invention relates to a method for inhibiting Hepatitis C virus (HCV)
CC infection using dendritic cell-specific intracellular adhesion molecule 3
CC -grabbing nonintegrin (DC-SIGN) or DC-SIGN related (DC-SIGNR) protein.
CC The method is useful for inhibiting HCV infection of a susceptible cell
CC or a target cell, e.g. a primary cell, a dendritic cell, endometrial cell
CC in liver or placenta cell. It is useful for diagnosing and treating HCV
CC infection. The method is useful for treating or preventing a liver
CC disease, e.g., hepatitis, cirrhosis and hepatocellular carcinoma. The
CC present sequence is HCV RNA specific reverse transcription (RT)-PCR
CC primer. This sequence is used to illustrate the method of the invention.
XX QY Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX Query Match 92.3%; Score 24; DB 11; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 0.051;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 35
ADE91309
ID ADE91309 standard; DNA; 24 BP.
XX AC ADE91309;

XX DT 12-FEB-2004 (first entry)
XX DE PCR primer #1 for hepatitis C virus (HCV) polyprotein gene.
XX KW Hepatitis C virus infection; HCV infection; clinical diagnosis;
KW polyprotein; PCR; primer; ss.
XX OS Hepatitis C virus.
XX PN US2003124654-A1.
XX PD 03-JUL-2003.
XX PF 03-JAN-2002; 2002US-00037990.
XX PR 03-JAN-2002; 2002US-00037990.
XX PA (RELI-) RELIANCE LIFE SCI PRIVATE LTD.
XX PI Sharma V, Kondiboyina VR;
XX DR WPI; 2004-009143/01.
XX QY Detecting hepatitis C virus by amplification using primers which amplify
PT transcripts of the polyprotein gene of hepatitis C virus is useful for
PT clinical diagnosis of hepatitis C virus.
XX PS Claim 1; Page 5; 7pp; English.
XX CC The present invention relates to a method for detecting hepatitis C virus
CC (HCV) in a biological sample. The method comprises amplification using
CC PCR primers which amplify the HCV polyprotein gene and detection with an
CC oligonucleotide probe. The method is useful for rapid clinical diagnosis
CC of HCV infection. Also disclosed is a kit for carrying out the detection
CC method. The present sequence represents a PCR primer used in the method
XX QY Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX Query Match 92.3%; Score 24; DB 12; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 0.051;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
DB 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 36
ADH79950
ID ADH79950 standard; DNA; 24 BP.
XX AC ADH79950;
XX DT 22-APR-2004 (first entry)
XX DE HCV RT-PCR primer RJD-1 (KY80).
XX KW DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGNR; HCV envelope glycoprotein; cytostatic;
KW antiinflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-1; KY80.
XX OS Hepatitis C virus.
XX PN US2003232745-A1.
XX PD 18-DEC-2003.
XX PF 24-DEC-2002; 2002US-00328997.
XX PR 26-JUN-2001; 2001US-0300971P.

PR 26-JUN-2002; 2002US-00184150.
 XX (OLSO/) OLSON W C.
 PA (MADD/) MADDON P J.
 PA (GARD/) GARDNER J P.
 XX Olson WC, Maddon PJ, Gardner JP;
 XX WPI; 2004-061306/06.
 DR Use of DC-SIGN and DC-SIGNR proteins for inhibiting, preventing or
 PT treating HCV infection and liver disease e.g. hepatitis or cirrhosis or
 PT hepatocellular carcinoma.
 XX Disclosure; Page 33; 55pp; English.
 XX The invention relates to the use of DC-SIGN and DC-SIGNR proteins for
 CC inhibiting, treating or preventing HCV infection and liver diseases such
 CC as hepatocellular carcinoma, hepatitis or cirrhosis. The DC-SIGN and DC-
 CC SIGNR protein are useful for inhibiting HCV infection, treating HCV
 CC infection or treating or preventing liver disease e.g. hepatitis,
 CC cirrhosis or hepatocellular carcinoma. Antibodies to the polypeptides,
 CC the polypeptides or non-peptidyl agents can be used for inhibiting
 CC binding of a DC-SIGN or DC-SIGNR protein to an HCV envelope glycoprotein.
 CC This sequence represents an HCV reverse transcriptase PCR (RT-PCR) primer
 CC used in the scope of the invention.
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 SQ Query Match 92.3%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 37
 ADO05656
 ID ADO05656 standard; DNA; 24 BP.
 AC ADO05656;
 XX 15-JUL-2004 (first entry)
 DT HCV 5' NCR (non coding region) fragment amplifying forward primer 7.
 DE Nucleic acid amplification; mutation detection; cytostatic;
 XX antiinflammatory; hepatotropic; virucide; cancer; PCR; primer; ss.
 KW Hepatitis C virus.
 XX Synthetic.
 OS WO2004035832-A1.
 XX 29-APR-2004.
 PD 17-OCT-2003; 2003WO-KR002179.
 XX 18-OCT-2002; 2002KR-00063832.
 PR 02-SEP-2003; 2003KR-00061066.
 XX (GENE-) GENEMATRIX INC.
 PA Kim N, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;
 PI Jee M, Hwang S, Hong S;
 XX WPI; 2004-348478/32.
 DR Detecting a mutation, useful in diagnosing and treating e.g. cancer or
 PT hepatitis, comprises generating fragments of polynucleotides using
 PT specific primers and measuring molecular weight of cleaved fragments.

XX Claim 13; SEQ ID NO 17; 58pp; English.
 PS The invention relates to detecting a mutation. The method involves
 XX amplifying a target polynucleotide using a forward primer and a reverse
 CC primer; generating fragments of two or more single-stranded
 CC polynucleotides including one or more mutations sequence having the size
 CC of 2-32 bases by cleaving the amplified target polynucleotide with
 CC restriction enzymes, where the second restriction enzyme does not react
 CC while a first restriction enzyme is reacted with the amplified
 CC polynucleotide; and measuring the molecular weight of the cleaved
 CC fragments. The polynucleotide is cleaved to include one mutation among
 CC two or more different mutations in only one single stranded
 CC polynucleotide fragment and all mutations in the other single stranded
 CC nucleotide fragment. Restrictions enzyme treatment step is performed
 CC using restriction enzymes having different optimum temperatures. The
 CC method is useful in detecting a mutation. The method and primer are
 CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.
 CC cancer or hepatitis B or C virus. The present sequence represents a
 CC primer for amplifying the HCV 5' NCR (non coding region) DNA fragment.
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 SQ Query Match 92.3%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24
 RESULT 38
 ADO52627
 ID ADO52627 standard; DNA; 24 BP.
 XX ADO52627;
 AC ADO52627;
 XX 26-AUG-2004 (first entry)
 DT HCV real time, RT-PCR primer KV80.
 DE HCV; ss; acute hepatitis; chronic liver disease; cirrhosis; liver cancer;
 XX real time PCR; reverse transcriptase PCR; PCR; primer; RT-PCR.
 KW Hepatitis C virus.
 OS US2004106099-A1.
 XX 03-JUN-2004.
 PD 02-DEC-2002; 2002US-00307523.
 XX 02-DEC-2002; 2002US-00307523.
 PR (LEET/) LEE T H.
 XX Lee TH;
 PI WPI; 2004-460064/43.
 DR Detecting hepatitis C virus in sample such as serum collected from humans
 PT infected with HCV, by performing real time PCR and detecting amplified
 PT product using nucleic acid binding fluorescent entity.
 XX Disclosure; Page 4; 5pp; English.
 PS The invention relates to detecting hepatitis C virus (HCV) in a sample,
 XX involving extracting RNA and synthesizing cDNA using reverse
 CC transcriptase, forming an amplification medium along with a nucleic acid
 CC binding fluorescent entity and thermally cycling it, illuminating the
 CC medium, determining amount of fluorescence generated, and detecting
 CC presence of target nucleic acid by analysing amount of luminescence

CC The invention describes a method of identifying a compound that inhibits
CC replication of a hepatitis C virus (HCV) RNA. The method comprises
CC

xx CC The invention discloses a replication competent hepatitis C virus (HCV)
CC comprising a HCV virus genome and a heterologous polynucleotide, where
CC the HCV genome comprises a 3' non-translated RNA and the heterologous
CC polynucleotide is present in the 3' non-translated RNA. HCV is a cause of
CC chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the
CC development of hepatocellular carcinoma. A cell comprising the HCV is
CC useful for selecting or detecting a replication competent HCV, for
CC identifying a compound that inhibits replication of HCV, for producing

CC infectious viral particles which are useful as a source of virus
CC particles for various assays, including evaluating methods for
CC inactivating particles, excluding particles from serum, identifying a
CC neutralising compound and as an antigen for use in detecting anti-HCV
CC antibodies in an animal. The cell comprising the HCV is also useful for
CC identifying a variant HCV. An HCV particle is useful as an antigen, as a
CC positive-control in assays that test for the presence of anti-HCV
CC antibodies, to produce antibodies to detect the presence of viral
CC particles in biological samples (e.g. blood products and cell-free blood
CC products) and as a source of viral antigen to measure the presence and
CC amount of antibody present in an animal. The sequence presented is the
CC Light Cycler fluor PCR probe which was used to detect viral RNA in Huh-
CC secretory alkaline phosphatase (SEAP)-o10 cell lines
XX
SQ Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGCGGTTA 26
|||||
Db 1 AGAAGCGTCTAGCCATGCGGTTA 24

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102	13.2	50.8	33	1	US-08-285-936-14	Sequence 14, Appli	Sequence 14, Appli	20	1	US-08-231-990-8	Sequence 8, Appli
103	13.2	50.8	33	1	US-08-487-860-14	Sequence 14, Appli	Sequence 14, Appli	20	1	US-08-367-122-8	Sequence 8, Appli
104	13.2	50.8	36	4	US-10-083-304-11	Sequence 11, Appli	Sequence 11, Appli	20	3	US-09-165-264-9	Sequence 9, Appli
105	13.2	50.8	40	3	US-09-147-550-1	Sequence 1, Appli	Sequence 1, Appli	20	3	US-09-600-932-22	Sequence 22, Appli
106	13.2	50.8	40	3	US-09-557-917-1	Sequence 1, Appli	Sequence 1, Appli	20	4	US-09-600-932-24	Sequence 24, Appli
107	13.2	50.8	40	3	US-09-355-947-1	Sequence 1, Appli	Sequence 1, Appli	20	4	US-09-657-472-1474	Sequence 1474, Ap
108	13.2	50.8	44	3	US-08-484-661A-3	Sequence 3, Appli	Sequence 3, Appli	21	4	US-10-083-304-8	Sequence 8, Appli
109	13.2	50.8	44	3	US-08-656-664-3	Sequence 3, Appli	Sequence 3, Appli	21	4	US-09-623-326-26	Sequence 26, Appli
110	13.2	50.8	44	3	US-09-422-978-1436	Sequence 1436, Ap	Sequence 1436, Ap	27	4	US-09-386-642-31	Sequence 31, Appli
111	13.2	50.8	47	4	US-09-284-832-45	Sequence 45, Appli	Sequence 45, Appli	30	4	US-07-829-461A-18	Sequence 18, Appli
112	13	50.0	27	3	US-09-308-759A-48	Sequence 48, Appli	Sequence 48, Appli	33	3	US-09-197-649-19	Sequence 19, Appli
113	13	50.0	31	1	US-08-446-486-27	Sequence 27, Appli	Sequence 27, Appli	33	3	US-09-894-799-1	Sequence 1, Appli
114	13	50.0	31	1	US-08-463-308-27	Sequence 27, Appli	Sequence 27, Appli	37	4	US-08-889-841B-51	Sequence 51, Appli
115	13	50.0	31	1	US-09-946-678-27	Sequence 27, Appli	Sequence 27, Appli	37	4	US-09-419-362-51	Sequence 51, Appli
116	13	50.0	31	6	5254799-27	Patent No. 5254799	Patent No. 5254799	38	4	US-08-484-661A-6	Sequence 6, Appli
117	13	50.0	31	6	US-08-379-057-9	Sequence 9, Appli	Sequence 9, Appli	44	3	US-08-656-664-6	Sequence 6, Appli
118	13	50.0	32	2	US-08-425-684-48	Sequence 48, Appli	Sequence 48, Appli	44	5	PCT-US96-09641-6	Sequence 6, Appli
119	13	50.0	40	2	US-08-575-502-48	Sequence 48, Appli	Sequence 48, Appli	47	4	US-09-422-978-1691	Sequence 1691, Ap
120	13	50.0	40	2	US-09-245-802-48	Sequence 48, Appli	Sequence 48, Appli	47	4	US-08-474-633A-4	Sequence 4, Appli
121	13	50.0	40	4	US-08-411-796-48	Sequence 48, Appli	Sequence 48, Appli	48	1	US-09-267-574-38	Sequence 38, Appli
122	13	50.0	42	1	US-08-471-039-48	Sequence 48, Appli	Sequence 48, Appli	48	3	US-08-823-771-4	Sequence 4, Appli
123	13	50.0	42	3	US-08-559-390-48	Sequence 48, Appli	Sequence 48, Appli	48	4	PCT-US93-02480-4	Sequence 4, Appli
124	13	50.0	42	4	PCT-US93-11198-48	Sequence 48, Appli	Sequence 48, Appli	48	5	US-09-474-432B-3	Sequence 3, Appli
125	13	50.0	42	5	US-09-081-385-30	Sequence 30, Appli	Sequence 30, Appli	48	5	US-09-476-387-3	Sequence 3, Appli
126	12.8	49.2	20	4	US-08-389-564B-7	Sequence 7, Appli	Sequence 7, Appli	16	4	US-09-866-108A-7460	Sequence 7460, Ap
127	12.8	49.2	34	2	US-08-466-047B-7	Sequence 7, Appli	Sequence 7, Appli	16	4	US-09-866-108A-7461	Sequence 7461, Ap
128	12.8	49.2	34	2	US-08-738-944-49	Sequence 49, Appli	Sequence 49, Appli	17	4	US-09-866-108A-7462	Sequence 7462, Ap
129	12.8	49.2	37	1	US-09-263-352-39	Sequence 39, Appli	Sequence 39, Appli	17	4	US-09-866-108A-7463	Sequence 7463, Ap
130	12.8	49.2	37	3	US-08-384-708A-43	Sequence 43, Appli	Sequence 43, Appli	17	4	US-09-866-108A-7464	Sequence 7464, Ap
131	12.6	48.5	30	1	US-08-687-421-43	Sequence 43, Appli	Sequence 43, Appli	17	4	US-09-866-108A-7465	Sequence 7465, Ap
132	12.6	48.5	30	3	PCT-US94-00844-3	Sequence 3, Appli	Sequence 3, Appli	17	4	US-07-971-819A-19	Sequence 19, Appli
133	12.6	48.5	30	4	US-08-811-897A-48	Sequence 48, Appli	Sequence 48, Appli	18	1	US-08-475-231-19	Sequence 19, Appli
134	12.6	48.5	34	5	US-08-855-213-48	Sequence 48, Appli	Sequence 48, Appli	18	1	US-08-397-220B-32	Sequence 32, Appli
135	12.6	48.5	37	2	US-09-201-474-48	Sequence 48, Appli	Sequence 48, Appli	20	3	US-08-650-093C-32	Sequence 32, Appli
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152	12.4	47.7	30	3	US-09-620-412C-204	Sequence 204, App	Sequence 204, App	25	4	US-09-866-108A-12362	Sequence 12362, A
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160	12.4	47.7	34	3	US-08-399-412A-115	Sequence 9, Appli	Sequence 9, Appli	33	3	US-08-185-827-1	Sequence 1, Appli
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163	12.4	47.7	41	3	US-09-464-453-87	Sequence 9, Appli	Sequence 9, Appli	36	1	US-09-552-950-22	Sequence 31, Appli
164	12.4	47.7	41	3	US-09-434-122-9	Sequence 87, Appli	Sequence 87, Appli	37	4	US-09-936-572-31	Sequence 27, Appli
165	12.4	47.7	41	3	US-08-878-766A-6	Sequence 6, Appli	Sequence 6, Appli	37	4	US-09-232-479-27	Sequence 27, Appli
166	12.4	47.7	41	3	US-10-170-097-1257	Sequence 1257, Ap	Sequence 1257, Ap	38	4	US-09-784-990-27	Sequence 27, Appli
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171	12.4	47.7	41	3				38	4		
172	12.4	47.7	41	3				38	4		
173	12.4	47.7	41	3				38	4		

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C 248	12	46.2	48	3	US-09-303-862-23	Sequence 23, Appl	321	11.8	45.4	47	4	US-09-422-978-257	Sequence 957, App
C 249	12	46.2	49	4	US-09-611-627-28	Sequence 28, Appl	C 322	11.8	45.4	47	4	US-09-422-978-257	Sequence 2682, Ap
C 250	11.8	45.4	20	3	US-08-813-507-20	Sequence 20, Appl	C 323	11.8	45.4	47	4	US-09-422-978-257	Sequence 3606, Ap
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C 258	11.8	45.4	22	4	US-09-168-595-16	Sequence 16, Appl	C 331	11.8	45.4	49	5	US-08-956-171E-2687	Sequence 2687, Ap
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C 261	11.8	45.4	25	4	US-09-050-739-106	Sequence 106, App	C 334	11.8	45.4	50	4	US-08-781-986A-2687	Sequence 2687, Ap
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C 265	11.8	45.4	26	2	US-08-502-535B-9	Sequence 9, Appli	C 338	11.6	44.6	25	1	US-08-400-256-8	Sequence 8, Appli
C 266	11.8	45.4	26	2	US-08-908-005A-9	Sequence 9, Appli	C 339	11.6	44.6	25	3	US-08-975-365-5	Sequence 5, Appli
C 267	11.8	45.4	26	3	US-09-253-523-9	Sequence 9, Appli	C 340	11.6	44.6	25	3	US-08-975-365-8	Sequence 8, Appli
C 268	11.8	45.4	26	3	US-09-251-911-9	Sequence 9, Appli	C 341	11.6	44.6	27	3	US-08-651-472-68	Sequence 68, Appl
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C 277	11.8	45.4	27	4	US-09-711-899-9	Sequence 9, Appli	C 350	11.6	44.6	36	1	US-07-934-373C-12	Sequence 12, Appl
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C 284	11.8	45.4	31	2	US-08-995-161-2	Sequence 2, Appli	C 357	11.6	44.6	38	4	US-09-402-923A-204	Sequence 103, App
C 285	11.8	45.4	31	2	US-09-063-927-2	Sequence 2, Appli	C 358	11.6	44.6	39	3	US-09-810-103	Sequence 103, App
C 286	11.8	45.4	31	3	US-09-202-316-38	Sequence 38, Appl	C 359	11.6	44.6	39	3	US-08-352-902D-103	Sequence 103, App
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C 288	11.8	45.4	32	4	US-09-150-811-1	GENERAL INFORMA	C 361	11.6	44.6	39	4	US-03-245-503B-103	Sequence 103, App
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C 305	11.8	45.4	40	4	US-09-777-157A-7	Sequence 7, Appli	C 378	11.4	43.8	25	4	US-09-402-923A-82	Sequence 82, Appl
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C 313	11.8	45.4	42	2	US-08-943-363-27	Sequence 27, Appl	C 386	11.4	43.8	26	2	US-09-003-067-34	Sequence 34, Appl
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C 317	11.8	45.4	42	4	US-09-350-259-27	Sequence 27, Appl	C 390	11.4	43.8	28	3	US-09-155-758-8	Sequence 8, Appli
C 318	11.8	45.4	42	4	US-09-940-244-147	Sequence 147, App	C 391	11.4	43.8	28	3	US-09-411-977-11	Sequence 11, Appl
C 319	11.8	45.4	43	2	US-08-846-338-16	Sequence 16, Appl	C 392	11.4	43.8	29	4	US-09-304-232-91	Sequence 91, Appl

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394	11.4	43.8	30	6	5487973-5	Patent No. 5487973	c 467	11.2	43.1	26	4	US-09-225-201B-1139	Sequence 1139, Ap
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C 399	11.4	43.8	33	1	US-08-485-978-3	Sequence 3, Appli	c 472	11.2	43.1	27	3	US-09-253-396A-11	Sequence 11, Appli
C 400	11.4	43.8	33	2	US-08-486-814-3	Sequence 3, Appli	c 473	11.2	43.1	27	3	US-09-687-230A-3	Sequence 3, Appli
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C 402	11.4	43.8	33	3	US-08-485-740-3	Sequence 3, Appli	c 475	11.2	43.1	28	3	US-09-225-928-504	Sequence 504, App
C 403	11.4	43.8	33	3	US-09-162-184-3	Sequence 3, Appli	c 476	11.2	43.1	28	4	US-09-225-201B-504	Sequence 23, Appl
C 404	11.4	43.8	33	3	US-09-161-902-3	Sequence 3, Appli	c 477	11.2	43.1	28	4	US-09-894-799-23	Sequence 13, Appl
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C 406	11.4	43.8	33	5	PCT-US95-08179-3	Sequence 3, Appli	c 479	11.2	43.1	30	2	US-08-779-596A-3	Sequence 3, Appli
C 407	11.4	43.8	34	2	US-09-913-524-33	Sequence 33, Appl	c 480	11.2	43.1	30	2	US-08-814-567A-13	Sequence 13, Appl
C 408	11.4	43.8	35	2	US-08-696-834-40	Sequence 40, Appl	c 481	11.2	43.1	30	3	US-09-185-501B-11	Sequence 11, Appl
C 409	11.4	43.8	35	2	US-09-270-140A-3	Sequence 3, Appli	c 482	11.2	43.1	30	4	US-09-386-642-24	Sequence 24, Appl
C 410	11.4	43.8	36	2	US-08-585-684B-430	Sequence 430, App	c 483	11.2	43.1	31	4	US-09-556-877-206	Sequence 206, App
C 411	11.4	43.8	36	3	US-08-491-954-49	Sequence 49, Appl	c 484	11.2	43.1	31	4	US-09-620-412C-206	Sequence 206, App
C 412	11.4	43.8	37	3	US-09-038-073-430	Sequence 35, Appl	c 485	11.2	43.1	31	4	US-09-598-419-206	Sequence 2, Appli
C 413	11.4	43.8	37	3	US-09-202-316-35	Sequence 76, Appl	c 486	11.2	43.1	31	4	US-07-775-786-2	Sequence 2, Appli
C 414	11.4	43.8	37	4	US-08-728-742A-76	Sequence 9690, Ap	c 487	11.2	43.1	32	4	US-09-558-133-2	Sequence 36, Appl
C 415	11.4	43.8	38	4	US-09-371-772B-9690	Sequence 9731, Ap	c 488	11.2	43.1	32	4	US-09-736-116-36	Sequence 4, Appli
C 416	11.4	43.8	38	4	US-09-371-772B-9731	Sequence 9773, Ap	c 489	11.2	43.1	32	4	US-09-864-866-4	Sequence 8, Appli
C 417	11.4	43.8	39	3	US-08-785-668-33	Sequence 33, Appl	c 490	11.2	43.1	35	4	US-09-864-866-8	Sequence 13, Appl
C 418	11.4	43.8	39	3	US-08-471-112A-12	Sequence 12, Appl	c 491	11.2	43.1	39	1	US-08-147-000B-13	Sequence 5, Appli
C 419	11.4	43.8	39	4	US-09-912-733-34	Sequence 34, Appl	c 492	11.2	43.1	39	3	US-08-484-661A-5	Sequence 5, Appli
C 420	11.4	43.8	39	4	US-10-001-052-77	Sequence 77, Appl	c 493	11.2	43.1	39	3	US-08-656-664-5	Sequence 5, Appli
C 421	11.4	43.8	39	4	US-09-950-634-12	Sequence 60, Appl	c 494	11.2	43.1	39	5	PCT-US96-09641-5	Sequence 31, Appl
C 422	11.4	43.8	40	1	US-08-399-696-60	Sequence 12, Appl	c 495	11.2	43.1	41	3	US-09-413-452-31	Sequence 31, Appl
C 423	11.4	43.8	40	2	US-08-425-684-132	Sequence 132, App	c 496	11.2	43.1	41	3	US-09-413-452-31	Sequence 31, Appl
C 424	11.4	43.8	40	2	US-08-675-502-132	Sequence 132, App	c 497	11.2	43.1	41	3	US-09-413-452-31	Sequence 31, Appl
C 425	11.4	43.8	40	2	US-09-245-802-132	Sequence 132, App	c 498	11.2	43.1	42	3	US-08-335-844A-70	Sequence 70, Appl
C 426	11.4	43.8	40	4	US-08-252-057-33	Sequence 33, Appl	c 499	11.2	43.1	42	4	US-09-129-366-70	Sequence 25, Appl
C 427	11.4	43.8	41	1	US-08-786-555-5	Sequence 5, Appli	c 500	11.2	43.1	43	3	US-09-351-814-25	Sequence 265, App
C 428	11.4	43.8	41	2	US-08-375-116A-13	Sequence 13, Appl	c 501	11.2	43.1	46	1	US-08-171-389-265	Sequence 265, App
C 429	11.4	43.8	42	2	US-08-930-274-16	Sequence 16, Appl	c 502	11.2	43.1	46	1	US-08-123-326-265	Sequence 265, App
C 430	11.4	43.8	46	2	US-08-093-884-31	Sequence 31, Appl	c 503	11.2	43.1	46	2	US-08-482-080A-265	Sequence 265, App
C 431	11.4	43.8	47	1	US-09-526-542-7	Sequence 7, Appli	c 504	11.2	43.1	46	3	US-09-354-947-265	Sequence 265, App
C 432	11.4	43.8	47	4	US-09-422-978-618	Sequence 618, App	c 505	11.2	43.1	46	3	PCT-US93-12388-265	Sequence 832, App
C 433	11.4	43.8	47	4	US-09-422-978-1451	Sequence 1451, Ap	c 506	11.2	43.1	46	5	US-09-641-638-832	Sequence 1125, App
C 434	11.4	43.8	47	4	US-09-422-978-3789	Sequence 3789, Ap	c 507	11.2	43.1	47	4	US-09-641-638-832	Sequence 1125, App
C 435	11.4	43.8	47	4	US-10-117-087-7	Sequence 7, Appli	c 508	11.2	43.1	47	4	US-08-422-978-927	Sequence 927, App
C 436	11.4	43.8	47	3	US-09-025-769B-70	Sequence 70, Appl	c 509	11.2	43.1	47	4	US-09-422-978-1196	Sequence 1196, Ap
C 437	11.4	43.8	49	4	US-09-490-153-70	Sequence 70, Appl	c 510	11.2	43.1	47	4	US-09-422-978-2187	Sequence 2187, Ap
C 438	11.4	43.8	49	4	US-09-627-465B-41	Sequence 41, Appl	c 511	11.2	43.1	47	4	US-09-422-978-2388	Sequence 832, App
C 439	11.4	43.8	49	4	US-08-229-279-14	Sequence 14, Appl	c 512	11.2	43.1	47	4	US-10-170-097-832	Sequence 1125, Ap
C 440	11.4	43.8	50	1	US-08-701-269-14	Sequence 14, Appl	c 513	11.2	43.1	47	4	US-08-171-389-404	Sequence 404, App
C 441	11.4	43.8	50	2	US-08-821-559A-17	Sequence 17, Appl	c 514	11.2	43.1	50	1	US-08-171-389-404	Sequence 526, App
C 442	11.4	43.8	50	2	US-08-821-559A-18	Sequence 18, Appl	c 515	11.2	43.1	50	1	US-08-123-936-404	Sequence 53, Appl
C 443	11.4	43.8	50	3	US-09-400-541-17	Sequence 17, Appl	c 516	11.2	43.1	50	1	US-08-123-936-404	Sequence 404, App
C 444	11.4	43.8	50	3	US-09-400-541-18	Sequence 18, Appl	c 517	11.2	43.1	50	1	US-08-123-936-404	Sequence 526, App
C 445	11.4	43.8	50	3	US-09-899-999-17	Sequence 17, Appl	c 518	11.2	43.1	50	1	US-08-475-228A-404	Sequence 404, App
C 446	11.4	43.8	50	3	US-09-899-999-18	Sequence 18, Appl	c 519	11.2	43.1	50	2	US-08-475-228A-526	Sequence 526, App
C 447	11.4	43.8	50	3	US-09-075-395-1	Sequence 1, Appli	c 520	11.2	43.1	50	2	US-08-482-080A-404	Sequence 404, App
C 448	11.4	43.8	50	3	US-09-075-395-1	Sequence 1, Appli	c 521	11.2	43.1	50	3	US-08-482-080A-526	Sequence 526, App
C 449	11.2	43.1	20	2	US-09-887-145-31	Sequence 5, Appli	c 522	11.2	43.1	50	3	US-09-423-439-21	Sequence 21, Appl
C 450	11.2	43.1	20	3	US-08-765-332-5	Sequence 5, Appli	c 523	11.2	43.1	50	3	US-09-354-947-404	Sequence 404, App
C 451	11.2	43.1	21	3	US-09-448-894-5	Sequence 5, Appli	c 524	11.2	43.1	50	3	US-09-354-947-404	Sequence 526, App
C 452	11.2	43.1	21	3	US-08-983-605-451	Sequence 451, App	c 525	11.2	43.1	50	3	US-09-354-947-404	Sequence 138, App
C 453	11.2	43.1	21	3	US-08-451-691-2	Sequence 2, Appli	c 526	11.2	43.1	50	4	US-09-621-976-14914	Sequence 14914, A
C 454	11.2	43.1	23	1	US-08-528-363-2	Sequence 2, Appli	c 527	11.2	43.1	50	4	US-09-905-125A-138	Sequence 138, App
C 455	11.2	43.1	23	1	US-08-451-318-2	Sequence 2, Appli	c 528	11.2	43.1	50	4	US-09-905-125A-138	Sequence 138, App
C 456	11.2	43.1	23	4	US-08-191-225-2	Sequence 5, Appli	c 529	11.2	43.1	50	4	US-09-906-700-138	Sequence 138, App
C 457	11.2	43.1	24	1	US-08-485-602-5	Sequence 79, Appl	c 530	11.2	43.1	50	4	PCT-US93-12388-404	Sequence 404, App
C 458	11.2	43.1	24	1	US-08-485-602-5	Sequence 5, Appli	c 531	11.2	43.1	50	4	PCT-US93-12388-404	Sequence 526, App
C 459	11.2	43.1	24	1	US-08-757-180-5	Sequence 78, Appl	c 532	11.2	43.1	50	5	US-09-474-432B-2	Sequence 2, Appli
C 460	11.2	43.1	24	1	US-08-757-180-78	Sequence 78, Appl	c 533	11.2	43.1	50	5	US-09-474-432B-2	Sequence 4, Appli
C 461	11.2	43.1	24	1	US-08-745-638-5	Sequence 5, Appli	c 534	11.2	43.1	16	4	US-09-476-387-2	Sequence 2, Appli
C 462	11.2	43.1	24	1	US-08-745-638-5	Sequence 5, Appli	c 535	11.2	43.1	16	4	US-09-476-387-2	Sequence 4, Appli
C 463	11.2	43.1	25	4	US-09-050-739-104	Sequence 104, App	c 536	11.2	43.1	16	4	US-09-476-387-4	Sequence 4, Appli
C 464	11.2	43.1	25	4	US-08-859-998-1139	Sequence 1139, Ap	c 537	11.2	43.1	16	4	US-09-476-387-4	Sequence 4, Appli
C 465	11.2	43.1	26	2			c 538	11.2	43.1	16	4		

c 685	10.8	41.5	28	3	US-09-218-444-4	Sequence 4, Appli	758	10.8	41.5	35	2	US-07-829-461A-14	Sequence 14, Appl
c 686	10.8	41.5	28	4	US-09-248-998-57	Sequence 57, Appl	759	10.8	41.5	35	2	US-08-948-176-18	Sequence 18, Appl
c 687	10.8	41.5	28	4	US-09-853-666-4	Sequence 4, Appli	c 760	10.8	41.5	35	3	US-08-691-045-38	Sequence 38, Appl
c 688	10.8	41.5	28	4	US-09-610-651-57	Sequence 57, Appl	c 761	10.8	41.5	35	3	US-09-197-649-15	Sequence 15, Appl
c 689	10.8	41.5	30	2	US-08-670-175-5	Sequence 5, Appli	c 762	10.8	41.5	35	3	US-09-232-477-14	Sequence 14, Appl
c 690	10.8	41.5	30	2	US-09-038-227-39	Sequence 39, Appl	c 763	10.8	41.5	35	4	US-09-532-594B-21	Sequence 21, Appl
c 691	10.8	41.5	30	2	US-08-993-927-8	Sequence 8, Appli	c 764	10.8	41.5	35	4	US-09-784-982-14	Sequence 14, Appl
c 692	10.8	41.5	30	3	US-09-582-096-8	Sequence 8, Appli	c 765	10.8	41.5	35	5	PCT-US91-09160-18	Sequence 18, Appl
c 693	10.8	41.5	30	4	US-09-553-690-45	Sequence 45, Appl	c 766	10.8	41.5	35	5	PCT-US93-07645A-5	Sequence 5, Appli
c 694	10.8	41.5	30	4	US-09-125-576B-3	Sequence 3, Appli	c 767	10.8	41.5	35	5	PCT-US93-07645-5	Sequence 5, Appli
c 695	10.8	41.5	31	1	US-07-971-819A-34	Sequence 34, Appl	c 768	10.8	41.5	36	1	PCT-US93-07673-1	Sequence 1, Appli
c 696	10.8	41.5	31	1	US-07-971-819A-40	Sequence 40, Appl	c 769	10.8	41.5	36	1	US-08-689-823-4	Sequence 4, Appli
c 697	10.8	41.5	31	1	US-07-971-819A-30	Sequence 30, Appl	c 770	10.8	41.5	36	1	US-09-109-063-58	Sequence 58, Appl
c 698	10.8	41.5	31	1	US-08-073-384C-18	Sequence 18, Appl	c 771	10.8	41.5	36	3	US-09-276-295-4	Sequence 4, Appli
c 699	10.8	41.5	31	1	US-08-254-359A-18	Sequence 18, Appl	c 772	10.8	41.5	36	3	US-08-664-962B-23	Sequence 23, Appl
c 700	10.8	41.5	31	1	US-08-475-231-34	Sequence 34, Appl	c 773	10.8	41.5	36	3	US-09-311-743-23	Sequence 23, Appl
c 701	10.8	41.5	31	1	US-08-475-231-40	Sequence 40, Appl	c 774	10.8	41.5	36	3	US-08-943-136-17	Sequence 17, Appl
c 702	10.8	41.5	31	1	US-08-483-043-18	Sequence 18, Appl	c 775	10.8	41.5	36	3	US-09-344-888A-16	Sequence 16, Appl
c 703	10.8	41.5	31	1	US-08-458-819-30	Sequence 30, Appl	c 776	10.8	41.5	36	3	US-08-973-518-17	Sequence 17, Appl
c 704	10.8	41.5	31	1	US-08-481-238-18	Sequence 18, Appl	c 777	10.8	41.5	36	4	US-09-448-310-58	Sequence 58, Appl
c 705	10.8	41.5	31	2	US-08-471-066B-18	Sequence 18, Appl	c 778	10.8	41.5	36	4	US-09-479-005A-1055	Sequence 1055, Ap
c 706	10.8	41.5	31	2	US-08-484-956-18	Sequence 18, Appl	c 779	10.8	41.5	36	4	US-09-479-005A-1056	Sequence 1056, Ap
c 707	10.8	41.5	31	2	US-08-757-653-18	Sequence 18, Appl	c 780	10.8	41.5	36	4	US-09-479-005A-1059	Sequence 1059, Ap
c 708	10.8	41.5	31	2	US-08-599-491-18	Sequence 18, Appl	c 781	10.8	41.5	36	4	US-09-479-005A-1055	Sequence 1055, Ap
c 709	10.8	41.5	31	2	US-08-756-386-18	Sequence 18, Appl	c 782	10.8	41.5	37	1	US-08-330-535A-27	Sequence 27, Appl
c 710	10.8	41.5	31	2	US-08-823-516-18	Sequence 18, Appl	c 783	10.8	41.5	37	1	US-08-688-145-2	Sequence 2, Appli
c 711	10.8	41.5	31	2	US-08-890-980-82	Sequence 80, Appl	c 784	10.8	41.5	37	1	US-08-688-145-2	Sequence 2, Appli
c 712	10.8	41.5	31	2	US-08-890-980-82	Sequence 82, Appl	c 785	10.8	41.5	37	2	US-08-838-844-27	Sequence 27, Appl
c 713	10.8	41.5	31	3	US-08-682-853A-18	Sequence 18, Appl	c 786	10.8	41.5	37	2	US-08-776-944-2	Sequence 2, Appli
c 714	10.8	41.5	31	3	US-08-890-979-71	Sequence 71, Appl	c 787	10.8	41.5	37	2	US-08-776-944-2	Sequence 2, Appli
c 715	10.8	41.5	31	3	US-08-890-979-73	Sequence 73, Appl	c 788	10.8	41.5	37	3	US-08-700-670A-34	Sequence 34, Appl
c 716	10.8	41.5	31	3	US-08-759-038-18	Sequence 18, Appl	c 789	10.8	41.5	37	4	US-09-375-975-33	Sequence 33, Appl
c 717	10.8	41.5	31	3	US-08-758-314-18	Sequence 18, Appl	c 790	10.8	41.5	38	2	US-08-292-620A-2198	Sequence 2198, Ap
c 718	10.8	41.5	31	3	US-09-234-163-7	Sequence 7, Appli	c 791	10.8	41.5	38	3	US-09-071-845-2198	Sequence 19, Appl
c 719	10.8	41.5	31	3	US-09-032-894-80	Sequence 8, Appl	c 792	10.8	41.5	38	4	US-09-337-307A-19	Sequence 19, Appl
c 720	10.8	41.5	31	3	US-09-198-839-6	Sequence 6, Appli	c 793	10.8	41.5	38	4	US-09-371-772B-9776	Sequence 9776, Ap
c 721	10.8	41.5	31	3	US-08-901-379-7	Sequence 7, Appli	c 794	10.8	41.5	38	4	US-09-371-772B-10654	Sequence 10654, A
c 722	10.8	41.5	31	3	US-09-031-626-80	Sequence 82, Appl	c 795	10.8	41.5	38	4	US-09-375-975-29	Sequence 29, Appl
c 723	10.8	41.5	31	3	US-09-031-626-82	Sequence 8, Appli	c 796	10.8	41.5	38	4	US-09-375-975-35	Sequence 35, Appl
c 724	10.8	41.5	31	3	US-09-031-626-82	Sequence 8, Appli	c 797	10.8	41.5	38	4	US-09-375-975-36	Sequence 36, Appl
c 725	10.8	41.5	31	3	US-09-562-834-6	Sequence 82, Appl	c 798	10.8	41.5	39	3	US-09-354-138-133	Sequence 133, App
c 726	10.8	41.5	31	3	US-09-350-309-18	Sequence 6, Appli	c 799	10.8	41.5	39	4	US-09-306-653-3	Sequence 3, Appli
c 727	10.8	41.5	31	3	US-08-520-946-18	Sequence 18, Appl	c 800	10.8	41.5	39	4	US-09-306-653-12	Sequence 12, Appl
c 728	10.8	41.5	31	4	US-09-077-028A-6	Sequence 6, Appli	c 801	10.8	41.5	39	4	US-09-306-653-13	Sequence 13, Appl
c 729	10.8	41.5	31	4	US-09-684-938-18	Sequence 18, Appl	c 802	10.8	41.5	39	4	US-09-621-275-10	Sequence 10, Appl
c 730	10.8	41.5	31	4	US-09-308-825A-18	Sequence 18, Appl	c 803	10.8	41.5	39	4	US-09-621-275-19	Sequence 19, Appl
c 731	10.8	41.5	31	4	US-09-995-396-6	Sequence 6, Appli	c 804	10.8	41.5	39	4	US-09-621-275-20	Sequence 20, Appl
c 732	10.8	41.5	31	4	US-09-655-378A-18	Sequence 18, Appl	c 805	10.8	41.5	41	3	US-08-691-045-41	Sequence 41, Appl
c 733	10.8	41.5	31	4	US-09-940-244-18	Sequence 18, Appl	c 806	10.8	41.5	41	3	US-08-813-507-54	Sequence 54, Appl
c 734	10.8	41.5	31	4	US-09-333-145-18	Sequence 18, Appl	c 807	10.8	41.5	41	3	US-09-464-453-54	Sequence 54, Appl
c 735	10.8	41.5	31	5	PCT-US91-07035-30	Sequence 18, Appl	c 808	10.8	41.5	42	1	US-08-464-136-74	Sequence 74, Appl
c 736	10.8	41.5	32	1	US-08-433-924-14	Sequence 14, Appl	c 809	10.8	41.5	42	2	US-08-349-131-74	Sequence 74, Appl
c 737	10.8	41.5	32	1	US-08-471-791-42	Sequence 42, Appl	c 810	10.8	41.5	42	3	US-08-470-297A-74	Sequence 74, Appl
c 738	10.8	41.5	32	3	US-08-722-719-17	Sequence 17, Appl	c 811	10.8	41.5	42	3	US-08-879-565-5	Sequence 5, Appli
c 739	10.8	41.5	32	4	US-09-334-951-17	Sequence 17, Appl	c 812	10.8	41.5	42	5	PCT-US91-07149-74	Sequence 74, Appl
c 740	10.8	41.5	32	4	US-09-334-923A-17	Sequence 17, Appl	c 813	10.8	41.5	43	2	US-08-418-897-74	Sequence 8, Appli
c 741	10.8	41.5	32	4	US-09-689-693-18	Sequence 18, Appl	c 814	10.8	41.5	43	2	US-08-418-897-24	Sequence 24, Appl
c 742	10.8	41.5	32	4	US-09-334-954A-17	Sequence 17, Appl	c 815	10.8	41.5	43	2	US-08-418-897-32	Sequence 28, Appl
c 743	10.8	41.5	32	5	PCT-US91-01746-42	Sequence 42, Appl	c 816	10.8	41.5	43	3	US-08-418-897-32	Sequence 32, Appl
c 744	10.8	41.5	33	1	US-08-138-608-7	Sequence 7, Appli	c 817	10.8	41.5	43	3	US-09-351-814-26	Sequence 26, Appl
c 745	10.8	41.5	33	1	US-08-094-534-20	Sequence 20, Appl	c 818	10.8	41.5	44	3	US-09-050-559C-9	Sequence 9, Appli
c 746	10.8	41.5	33	5	PCT-US94-08000-20	Sequence 20, Appl	c 819	10.8	41.5	44	4	US-09-313-221A-47	Sequence 47, Appl
c 747	10.8	41.5	34	2	US-08-422-333-19	Sequence 19, Appl	c 820	10.8	41.5	44	4	US-09-736-116-18	Sequence 18, Appl
c 748	10.8	41.5	34	3	US-09-270-140A-53	Sequence 53, Appl	c 821	10.8	41.5	45	3	US-08-863-813A-56	Sequence 56, Appl
c 749	10.8	41.5	34	3	US-09-556-877-198	Sequence 198, App	c 822	10.8	41.5	45	3	US-08-863-813A-59	Sequence 59, Appl
c 750	10.8	41.5	34	4	US-09-620-412C-198	Sequence 198, App	c 823	10.8	41.5	45	4	US-09-839-477-2	Sequence 2, Appli
c 751	10.8	41.5	34	4	US-09-598-419-198	Sequence 198, App	c 824	10.8	41.5	45	4	US-09-500-700-56	Sequence 56, Appl
c 752	10.8	41.5	34	4	US-09-721-908-62	Sequence 62, Appl	c 825	10.8	41.5	45	4	US-09-500-700-59	Sequence 59, Appl
c 753	10.8	41.5	34	4	US-09-451-739H-18	Sequence 18, Appl	c 826	10.8	41.5	46	4	US-08-944-410-57	Sequence 57, Appl
c 754	10.8	41.5	35	1	US-09-913-524-32	Sequence 32, Appl	c 827	10.8	41.5	46	6	5240845-12	Patent No. 5240845
c 755	10.8	41.5	35	1	US-08-075-533-18	Sequence 18, Appl	c 828	10.8	41.5	47	2	US-07-316-098A-18	Sequence 18, Appl
c 756	10.8	41.5	35	1	US-08-012-543-5	Sequence 5, Appli	c 829	10.8	41.5	47	4	US-09-671-317-733	Sequence 733, App
							c 830	10.8	41.5	47	4	US-09-422-978-781	Sequence 781, App

C 831	10.8	41.5	47	4	US-09-422-978-995	Sequence 995, App	C 904	10.6	40.8	25	4	US-09-484-317A-11	Sequence 11, Appl
C 832	10.8	41.5	47	4	US-09-422-978-3857	Sequence 3857, App	C 905	10.6	40.8	25	4	US-09-806-708B-6	Sequence 6, Appl
C 833	10.8	41.5	49	2	US-07-916-098A-17	Sequence 17, App	C 906	10.6	40.8	26	2	US-08-859-998-1257	Sequence 1257, Ap
C 834	10.8	41.5	50	1	US-08-259-612A-7	Sequence 7, Appl	C 907	10.6	40.8	26	3	US-09-225-928-1257	Sequence 1257, Ap
C 835	10.8	41.5	50	1	US-08-644-291-7	Sequence 7, Appl	C 908	10.6	40.8	26	4	US-09-225-201B-1257	Sequence 1257, Ap
C 836	10.8	41.5	50	5	PCT-US91-04744-10	Sequence 10, Appl	C 909	10.6	40.8	27	2	US-08-479-733A-1	Sequence 1, Appl
C 837	10.8	41.5	50	6	5258302-9	Patent No. 5258302	C 910	10.6	40.8	27	2	US-08-211-718-11	Sequence 11, Appl
C 838	10.6	40.8	18	1	US-08-181-271A-55	Sequence 55, Appl	C 911	10.6	40.8	27	3	US-08-487-427-1	Sequence 1, Appl
C 839	10.6	40.8	18	1	US-08-449-315-55	Sequence 55, Appl	C 912	10.6	40.8	27	3	US-08-479-727A-1	Sequence 1, Appl
C 840	10.6	40.8	18	1	US-08-444-803-55	Sequence 55, Appl	C 913	10.6	40.8	27	3	US-08-482-369A-1	Sequence 1, Appl
C 841	10.6	40.8	18	1	US-08-449-043-55	Sequence 55, Appl	C 914	10.6	40.8	27	3	US-09-009-217-15	Sequence 15, Appl
C 842	10.6	40.8	18	1	US-08-456-265A-55	Sequence 55, Appl	C 915	10.6	40.8	27	3	US-09-009-656-15	Sequence 15, Appl
C 843	10.6	40.8	18	1	US-08-458-416-55	Sequence 55, Appl	C 916	10.6	40.8	27	3	US-09-345-214-10	Sequence 10, Appl
C 844	10.6	40.8	18	1	US-08-455-244-55	Sequence 55, Appl	C 917	10.6	40.8	27	4	US-09-743-980-10	Sequence 10, Appl
C 845	10.6	40.8	18	1	US-08-454-876-55	Sequence 55, Appl	C 918	10.6	40.8	27	5	PCT-US95-07439-1	Sequence 1, Appl
C 846	10.6	40.8	18	2	US-08-457-364-55	Sequence 55, Appl	C 919	10.6	40.8	28	1	US-08-140-729A-16	Sequence 16, Appl
C 847	10.6	40.8	18	2	US-08-456-262-55	Sequence 55, Appl	C 920	10.6	40.8	28	2	US-08-546-666-16	Sequence 16, Appl
C 848	10.6	40.8	18	2	US-08-456-240-55	Sequence 55, Appl	C 921	10.6	40.8	28	2	US-08-916-745-16	Sequence 16, Appl
C 849	10.6	40.8	18	2	US-08-458-197C-14	Sequence 14, Appl	C 922	10.6	40.8	28	2	US-09-042-929-16	Sequence 16, Appl
C 850	10.6	40.8	18	2	US-08-455-736-55	Sequence 55, Appl	C 923	10.6	40.8	28	2	US-08-546-661-16	Sequence 16, Appl
C 851	10.6	40.8	18	2	US-08-971-217-55	Sequence 55, Appl	C 924	10.6	40.8	28	2	US-09-042-960-16	Sequence 16, Appl
C 852	10.6	40.8	18	2	US-08-996-306-39	Sequence 39, Appl	C 925	10.6	40.8	28	3	US-09-198-650-16	Sequence 16, Appl
C 853	10.6	40.8	18	3	US-09-350-600-55	Sequence 55, Appl	C 926	10.6	40.8	28	3	US-09-042-913-16	Sequence 16, Appl
C 854	10.6	40.8	18	3	US-09-338-907-39	Sequence 39, Appl	C 927	10.6	40.8	28	3	US-09-042-937-16	Sequence 16, Appl
C 855	10.6	40.8	18	3	US-09-338-907-360	Sequence 360, App	C 928	10.6	40.8	28	4	US-09-042-709A-16	Sequence 16, Appl
C 856	10.6	40.8	18	3	US-09-218-207-39	Sequence 39, Appl	C 929	10.6	40.8	28	4	US-09-260-629-5	Sequence 5, Appl
C 857	10.6	40.8	18	3	US-09-218-207-360	Sequence 360, App	C 930	10.6	40.8	28	4	US-09-227-614-16	Sequence 16, Appl
C 858	10.6	40.8	18	4	US-09-422-978-5490	Sequence 5490, App	C 931	10.6	40.8	29	1	US-08-466-033-129	Sequence 129, App
C 859	10.6	40.8	18	4	US-09-422-978-7849	Sequence 7849, App	C 932	10.6	40.8	29	1	US-08-444-733-129	Sequence 129, App
C 860	10.6	40.8	18	4	US-09-906-234-55	Sequence 55, Appl	C 933	10.6	40.8	29	2	US-08-464-134-129	Sequence 129, App
C 861	10.6	40.8	20	1	US-07-964-151-1	Sequence 1, Appl	C 934	10.6	40.8	29	2	US-08-461-361-129	Sequence 129, App
C 862	10.6	40.8	20	1	US-08-222-177A-287	Sequence 287, App	C 935	10.6	40.8	29	2	US-08-485-910-129	Sequence 129, App
C 863	10.6	40.8	20	1	US-08-484-192-74	Sequence 74, Appl	C 936	10.6	40.8	29	3	US-09-635-747-28	Sequence 28, Appl
C 864	10.6	40.8	20	1	US-08-484-192-127	Sequence 127, App	C 937	10.6	40.8	29	4	US-09-304-232-750	Sequence 750, Appl
C 865	10.6	40.8	20	2	US-08-505-377-9	Sequence 9, Appl	C 938	10.6	40.8	29	5	PCT-US95-06266-109	Sequence 109, App
C 866	10.6	40.8	20	2	US-08-748-104-6	Sequence 6, Appl	C 939	10.6	40.8	30	1	US-08-461-773-8	Sequence 8, Appl
C 867	10.6	40.8	20	3	US-08-899-786-8	Sequence 8, Appl	C 940	10.6	40.8	30	2	US-08-870-010A-3	Sequence 3, Appl
C 868	10.6	40.8	20	3	US-09-045-106-12	Sequence 12, Appl	C 941	10.6	40.8	30	2	US-08-921-382-4	Sequence 4, Appl
C 869	10.6	40.8	20	3	US-08-798-269-9	Sequence 9, Appl	C 942	10.6	40.8	30	2	US-08-859-998-290	Sequence 290, App
C 870	10.6	40.8	20	3	US-08-813-507-18	Sequence 18, Appl	C 943	10.6	40.8	30	3	US-09-102-371-3	Sequence 3, Appl
C 871	10.6	40.8	20	3	US-09-490-692-19	Sequence 19, Appl	C 944	10.6	40.8	30	3	US-09-225-928-290	Sequence 290, App
C 872	10.6	40.8	20	3	US-09-055-210-9	Sequence 9, Appl	C 945	10.6	40.8	30	3	US-09-638-436B-3	Sequence 3, Appl
C 873	10.6	40.8	20	3	US-09-464-453-18	Sequence 18, Appl	C 946	10.6	40.8	30	4	US-09-225-201B-290	Sequence 290, App
C 874	10.6	40.8	20	4	US-09-843-376-34	Sequence 34, Appl	C 947	10.6	40.8	30	4	US-09-386-380-4	Sequence 4, Appl
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C 877	10.6	40.8	21	4	US-09-493-784-6	Sequence 6, Appl	C 950	10.6	40.8	31	3	US-09-575-602-8	Sequence 8, Appl
C 878	10.6	40.8	21	4	US-09-689-065B-57	Sequence 57, Appl	C 951	10.6	40.8	31	3	US-09-625-570-8	Sequence 8, Appl
C 879	10.6	40.8	22	3	US-08-943-731-552	Sequence 552, App	C 952	10.6	40.8	32	3	US-08-996-441B-103	Sequence 103, App
C 880	10.6	40.8	22	4	US-09-274-163E-7	Sequence 7, Appl	C 953	10.6	40.8	32	3	US-08-993-722A-103	Sequence 103, App
C 881	10.6	40.8	22	4	US-09-701-069-13	Sequence 13, Appl	C 954	10.6	40.8	32	3	US-08-993-170A-103	Sequence 103, App
C 882	10.6	40.8	23	3	US-08-250-802-15	Sequence 15, Appl	C 955	10.6	40.8	32	3	US-08-993-775B-103	Sequence 103, App
C 883	10.6	40.8	23	4	US-09-602-586-18	Sequence 18, Appl	C 956	10.6	40.8	32	4	US-09-377-466B-40	Sequence 40, Appl
C 884	10.6	40.8	23	4	US-09-602-586-40	Sequence 40, Appl	C 957	10.6	40.8	32	4	US-09-427-770-103	Sequence 103, App
C 885	10.6	40.8	23	4	US-09-643-217-15	Sequence 15, Appl	C 958	10.6	40.8	32	4	US-09-427-769-103	Sequence 103, App
C 886	10.6	40.8	23	4	US-09-561-579A-18	Sequence 18, Appl	C 959	10.6	40.8	33	3	US-08-557-210A-14	Sequence 14, Appl
C 887	10.6	40.8	23	4	US-09-561-579A-40	Sequence 40, Appl	C 960	10.6	40.8	33	3	US-09-349-627-3	Sequence 3, Appl
C 888	10.6	40.8	23	4	US-09-825-244A-18	Sequence 18, Appl	C 961	10.6	40.8	33	3	US-09-232-468A-26	Sequence 26, Appl
C 889	10.6	40.8	23	5	PCT-US92-07916-15	Sequence 15, Appl	C 962	10.6	40.8	33	4	US-09-597-877-17	Sequence 17, Appl
C 890	10.6	40.8	24	1	US-08-029-404-3	Sequence 3, Appl	C 963	10.6	40.8	33	4	US-09-597-877-18	Sequence 18, Appl
C 891	10.6	40.8	24	1	US-08-290-933-2	Sequence 3, Appl	C 964	10.6	40.8	33	4	US-09-311-784A-58	Sequence 58, Appl
C 892	10.6	40.8	24	3	US-08-459-953A-3	Sequence 3, Appl	C 965	10.6	40.8	33	4	US-08-793-229-4	Sequence 4, Appl
C 893	10.6	40.8	24	4	US-09-475-947A-307	Sequence 307, App	C 966	10.6	40.8	34	2	US-08-793-229-4	Sequence 4, Appl
C 894	10.6	40.8	24	4	US-09-393-212-3	Sequence 3, Appl	C 967	10.6	40.8	34	2	US-08-521-871A-7	Sequence 7, Appl
C 895	10.6	40.8	25	1	US-08-343-379-11	Sequence 11, Appl	C 968	10.6	40.8	34	3	US-09-285-957-4	Sequence 4, Appl
C 896	10.6	40.8	25	4	US-09-479-122-11	Sequence 11, Appl	C 969	10.6	40.8	36	1	US-08-450-384-20	Sequence 20, Appl
C 897	10.6	40.8	25	4	US-09-484-997-11	Sequence 11, Appl	C 970	10.6	40.8	36	3	US-09-050-559C-23	Sequence 23, Appl
C 898	10.6	40.8	25	4	US-09-481-355-11	Sequence 11, Appl	C 971	10.6	40.8	36	3	US-09-101-629A-13	Sequence 13, Appl
C 899	10.6	40.8	25	4	US-09-481-282-11	Sequence 11, Appl	C 972	10.6	40.8	36	3	US-09-101-629A-14	Sequence 14, Appl
C 900	10.6	40.8	25	4	US-09-455-659A-11	Sequence 11, Appl	C 973	10.6	40.8	36	4	US-09-810-502-6	Sequence 6, Appl
C 901	10.6	40.8	25	4	US-09-484-996-11	Sequence 11, Appl	C 974	10.6	40.8	37	2	US-08-561-521-18	Sequence 18, Appl
C 902	10.6	40.8	25	4	US-09-827-998-1359	Sequence 1359, App	C 975	10.6	40.8	37	2	US-08-561-521-18	Sequence 18, Appl
C 903	10.6	40.8	25	4	US-09-479-123-11	Sequence 11, Appl	C 976	10.6	40.8	37	4	US-09-301-593-63	Sequence 63, Appl

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RESULT 3
US-10-353-589-1
; Sequence 1, Application US/10353589
; Patent No. 6642204
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/106
; CURRENT APPLICATION NUMBER: US/10/353,589
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,370,396
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer

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US-10-353-589-1

Query Match 100.0%; Score 26; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 4

US-10-029-907-17
; Sequence 17, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-029-907-17

Query Match 100.0%; Score 26; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 5

US-09-493-353-1
; Sequence 1, Application US/09493353
; Patent No. 6638714
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; APPLICANT: Linnin, J.M.
; APPLICANT: Gorman, K.M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT
; TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2094/1E286-US1
; CURRENT APPLICATION NUMBER: US/09/493,353
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,497
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-1

Query Match 96.2%; Score 25; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 CAGAAAGCGTCTAGCCATGGCGTTA 28

Db 1 CAGAAAGCGTCTAGCCATGGCGTTA 25

RESULT 6

US-08-240-547-5
; Sequence 5, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-5

Query Match 92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 7

US-08-449-050-17
; Sequence 17, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David
; APPLICANT: Myers, Thomas
; APPLICANT: Sigafoos, Christopher
; TITLE OF INVENTION: Reagents and Methods for Coupled High
; TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
; NUMBER OF SEQUENCES: 19
; TITLE OF INVENTION: Reactions
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley

US-08-332-616A-9

Query Match 92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
| | | | | | | | | | | | | |
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 9
US-08-317-220-9
Sequence 9, Application US/08317220
Patent No. 5654179
GENERAL INFORMATION:
APPLICANT: LIN, LILY
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-317-220-9

Query Match 92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
pb 1 GCAGAAAGCGTCTAGCCATGGCGT 24

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; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
; TITLE OF INVENTION: RNA STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/675,153
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-675-153-7

Query Match          92.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
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Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 11
US-08-738-928-4
; Sequence 4, Application US/08738928
; Patent No. 5837442
; GENERAL INFORMATION:
; APPLICANT: Tsang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
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; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-738-928-4

Query Match          92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||||||||||||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 12
US-08-841-252-7
; Sequence 7, Application US/08841252
; Patent No. 5919625
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
; TITLE OF INVENTION: STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,252
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,677,124
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-300
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-841-252-7

Query Match          92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 13
US-08-881-571-7
; Sequence 7, Application US/08891571
; Patent No. 5939262
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: linear
; US-08-881-571-7

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 14
US-08-881-571-7
; Sequence 9, Application US/09078290A
; Patent No. 6048696
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Leslie M.
; APPLICANT: Hawkins, Gregory A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH:
; TYPE:
; STRANDEDNESS:
; TOPOLOGY:
; MOLECULE TYPE:
; US-08-881-571-7

Query Match 92.3%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 15
US-09-282-054-7
; Sequence 7, Application US/09282054
; Patent No. 6214982
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH:
; TYPE:
; STRANDEDNESS:
; TOPOLOGY:
; MOLECULE TYPE:
; US-09-282-054-7

Query Match 92.3%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGT 25
    |||||
Db 1 CAGAAAGCGTCTAGCCATGGCGT 24

RESULT 16
US-09-282-054-7
; Sequence 7, Application US/09282054
; Patent No. 6214982
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH:
; TYPE:
; STRANDEDNESS:
; TOPOLOGY:
; MOLECULE TYPE:
; US-09-282-054-7

Query Match 92.3%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGAAAGCGTCTAGCCATGGCGT 25
    |||||
Db 1 CAGAAAGCGTCTAGCCATGGCGT 24
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/021,145
;; FILING DATE: 03-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: AMBI:033
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-282-054-7

Query Match 92.3%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 16
US-09-665-638-7
; Sequence 7, Application US/09665638
; Patent No. 6399307
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, Dwight
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/665,638
; FILING DATE: 19-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-665-638-7
Query Match-
Best Local Similarity 92.3%; Score 24; DB 3; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 17
US-10-007-389-4
; Sequence 4, Application US/10007389
; Patent No. 6727067
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-007-389-4

Query Match 92.3%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 18
US-08-240-547-6
; Sequence 6, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,097A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-934-097A-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 22
US-08-851-588-25
; Sequence 25, Application US/08851588
; Patent No. 6214545
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/851,588
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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;
; DESCRIPTION: /desc = "DNA"
US-08-851-588-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 23
US-09-677-218B-25
; Sequence 25, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,218B
; FILING DATE: 02-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/034,205
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-677-218B-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 24
US-09-677-192-25
; Sequence 25, Application US/09677192
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; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-677-192-25

Query Match      80.8%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 25
US-09-402-618B-25
; Sequence 25, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-402-618B-25

Query Match      80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 26
US-09-825-574-25
; Sequence 25, Application US/09825574
```

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; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing With Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
; US-09-825-574-25

Query Match      80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAGAAAGCGTCTAGCCATGG 21
Db      1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 27
US-09-676-768-25
; Sequence 25, Application US/09676768
; Patent No. 6780585
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
```


STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/676,768
FILING DATE: 02-Oct-2000
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,588
FILING DATE: 05-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-676-768-25

Query Match 80.8%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGG 21
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 28
US-08-397-220B-33/c
Sequence 33, Application US/08397220B
Patent No. 6284458
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01293
FILING DATE: 10-Sep-93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289

FILING DATE: 10-Sep-92
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-397-220B-33

Query Match 76.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGGC 22
Db 20 AGAAGCGTCTAGCCATGGC 1

RESULT 29
US-08-650-093C-33/c
Sequence 33, Application US/08650093C
Patent No. 6391542
GENERAL INFORMATION:
APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: LICATA & TYRRELL P.C.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes

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; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-650-093C-33
Query Match          76.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGCGTCTAGCCATGCG 22
Db 20 AGAAGCGTCTAGCCATGCG 1

RESULT 30
US-08-735-381-4/c
; Sequence 4, Application US/08735381
; Patent No. 5853993
; GENERAL INFORMATION:
; APPLICANT: Dellinger, Douglas J.
; APPLICANT: Dahm, SueAnn
; APPLICANT: Troll, Mark
; TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
; STREET: 1501 Page Mill Road, MS 4U-10
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,381
; FILING DATE: 21-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10950427-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-857-4125
; TELEFAX: 650-852-8063
; TELEX: 348-461
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-735-381-4

Query Match          76.9%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 31
US-09-183-619-3/c
; Sequence 3, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-201-674-4

Query Match          76.9%; Score 20; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 33
US-09-210-657-1
; Sequence 1, Application US/09210657
; Patent No. 6248526
; GENERAL INFORMATION:
; APPLICANT: Weimer, Thomas
; TITLE OF INVENTION: LABELED PRIMER FOR USE IN AND DETECTION OF TARGET
; FILE REFERENCE: 06478-1421
; CURRENT APPLICATION NUMBER: US/09/210,657
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-210-657-1

Query Match          73.1%; Score 19; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGTCTAGCCATGGCGTTA 26
Db 1 GCGTCTAGCCATGGCGTTA 19

RESULT 34
US-08-240-547-4
; Sequence 4, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-4

Query Match          73.1%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 12 GCAGAAAGCGTCTAGCCAT 30

RESULT 35
US-09-014-416-16
; Sequence 16, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-16

Query Match          73.1%; Score 19; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
Db 12 GCAGAAAGCGTCTAGCCAT 30

RESULT 36
US-08-438-639-44/c
; Sequence 44, Application US/08438639
; Patent No. 5712383
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,639
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,338
; FILING DATE: 23-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-438-639-44
Query Match 73.1%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCAT 19
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 37
US-07-813-338A-44/c
; Sequence 44, Application US/07813338A
; Patent No. 5747244
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,338A
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.

```

```

; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-813-338A-44
Query Match 73.1%; Score 19; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCAT 19
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 38
US-08-470-124-77/c
; Sequence 77, Application US/08470124
; Patent No. 5849481
; GENERAL INFORMATION:
; APPLICANT: Urdea, Michael S.
; APPLICANT: Horn, Thomas
; APPLICANT: Chang, Chu-An
; APPLICANT: Warner, Brian
; APPLICANT: Fultz, Timothy J.
; TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
; TITLE OF INVENTION: POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,588
; FILING DATE: 23 December 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ciotti, Thomas E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20104.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-470-124-77
Query Match 73.1%; Score 19; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
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Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 39

US-08-441-971-120/c
; Sequence 120, Application US/08441971
; Patent No. 6071693
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,971
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-971-120

Query Match 73.1%; Score 19; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
|
Db 19 GCAGAAAGCGTCTAGCCAT 1

RESULT 40

US-08-221-653-120/c
; Sequence 120, Application US/08221653
; Patent No. 6190864
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-221-653-120

Query Match 73.1%; Score 19; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCAT 19
|
Db 19 GCAGAAAGCGTCTAGCCAT 1

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Job time : 38.0899 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 121.918 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-6

Perfect score: 26

Sequence: 1 gcagaaagcgtctagccatgcgtta 26

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Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	100.0	26	15	US-10-419-022-6
3	26	100.0	26	15	US-10-147-679A-15
4	26	100.0	30	13	US-10-029-907-17
5	26	100.0	30	15	US-10-309-561-17
6	26	100.0	30	15	US-10-198-680A-2
7	26	100.0	30	15	US-10-320-978-1
8	26	100.0	30	15	US-10-353-563-1
9	26	100.0	30	15	US-10-353-589-1
10	26	100.0	30	15	US-10-320-979-1
11	26	100.0	30	15	US-10-353-894-1
12	26	100.0	30	15	US-10-198-259A-2

13	26	100.0	30	16	US-10-198-384A-2	Sequence 2, Appli
14	26	100.0	30	17	US-10-789-355-17	Sequence 17, Appl
15	26	100.0	30	18	US-10-686-835-17	Sequence 17, Appl
16	26	100.0	30	18	US-10-791-318-1	Sequence 1, Appli
17	24	92.3	24	13	US-10-120-013-7	Sequence 7, Appli
18	24	92.3	24	15	US-10-011-855-1	Sequence 1, Appli
19	24	92.3	24	15	US-10-037-990-1	Sequence 1, Appli
20	24	92.3	24	15	US-10-007-389-4	Sequence 4, Appli
21	24	92.3	24	15	US-10-322-138-1	Sequence 1, Appli
22	24	92.3	24	15	US-10-147-679A-5	Sequence 5, Appli
23	24	92.3	24	16	US-10-655-508-4	Sequence 4, Appli
24	24	92.3	24	16	US-10-688-272-17	Sequence 17, Appli
25	24	92.3	24	17	US-10-307-523B-3	Sequence 3, Appli
26	24	92.3	25	9	US-09-747-419-12	Sequence 12, Appli
27	24	92.3	25	15	US-10-259-275-12	Sequence 12, Appli
28	22	84.6	36	17	US-10-451-882-35	Sequence 35, Appli
29	21	80.8	21	9	US-09-825-574-25	Sequence 25, Appli
30	21	80.8	21	10	US-09-882-945A-25	Sequence 25, Appli
31	21	80.8	21	15	US-10-240-460-10	Sequence 10, Appli
32	21	80.8	25	15	US-10-182-126-7	Sequence 7, Appli
33	20	76.9	20	8	US-08-887-505-69	Sequence 69, Appli
34	19	73.1	19	10	US-09-935-338-227	Sequence 227, App
35	19	73.1	19	18	US-10-667-271-99	Sequence 99, Appli
36	19	73.1	19	18	US-10-667-271-101	Sequence 101, App
37	19	73.1	19	18	US-10-667-271-102	Sequence 102, App
38	19	73.1	19	18	US-10-667-271-104	Sequence 104, App
39	19	73.1	19	18	US-10-667-271-107	Sequence 107, App
40	19	73.1	19	18	US-10-667-271-113	Sequence 113, App
41	19	73.1	19	18	US-10-667-271-115	Sequence 115, App
42	19	73.1	19	18	US-10-667-271-116	Sequence 116, App
43	19	73.1	19	18	US-10-667-271-795	Sequence 795, App
44	19	73.1	19	18	US-10-667-271-797	Sequence 797, App
45	19	73.1	19	18	US-10-667-271-798	Sequence 798, App
46	19	73.1	19	18	US-10-667-271-800	Sequence 800, App
47	19	73.1	19	18	US-10-667-271-803	Sequence 803, App
48	19	73.1	19	18	US-10-667-271-809	Sequence 809, App
49	19	73.1	19	18	US-10-667-271-811	Sequence 811, App
50	19	73.1	22	16	US-10-607-897-38	Sequence 812, App
51	19	73.1	22	16	US-10-407-897-38	Sequence 38, Appli
52	19	73.1	22	17	US-10-333-449A-2	Sequence 2, Appli
53	19	73.1	24	17	US-10-451-882-34	Sequence 34, Appli
54	19	73.1	27	9	US-09-747-419-6	Sequence 6, Appli
55	19	73.1	27	15	US-10-259-275-6	Sequence 6, Appli
56	19	73.1	30	17	US-10-333-449A-1	Sequence 1, Appli
57	18	69.2	19	18	US-10-667-271-105	Sequence 105, App
58	18	69.2	19	18	US-10-667-271-111	Sequence 111, App
59	18	69.2	19	18	US-10-667-271-801	Sequence 801, App
60	18	69.2	19	18	US-10-667-271-807	Sequence 807, App
61	18	69.2	20	16	US-10-399-843-1	Sequence 1, Appli
62	18	69.2	25	9	US-09-833-675B-8	Sequence 8, Appli
63	18	69.2	32	16	US-10-688-272-20	Sequence 20, Appli
64	17	65.4	17	10	US-09-740-332-14	Sequence 14, Appli
65	17	65.4	17	10	US-09-740-332-15	Sequence 15, Appli
66	17	65.4	17	10	US-09-740-332-16	Sequence 16, Appli
67	17	65.4	17	10	US-09-740-332-4540	Sequence 4540, Ap
68	17	65.4	17	10	US-09-740-332-4541	Sequence 4541, Ap
69	17	65.4	17	10	US-09-740-332-4542	Sequence 4542, Ap
70	17	65.4	17	10	US-09-817-879-14	Sequence 14, Appli
71	17	65.4	17	10	US-09-817-879-15	Sequence 15, Appli
72	17	65.4	17	10	US-09-817-879-16	Sequence 16, Appli
73	17	65.4	17	10	US-09-817-879-4540	Sequence 4540, Ap
74	17	65.4	17	10	US-09-817-879-4541	Sequence 4541, Ap
75	17	65.4	17	10	US-09-817-879-4542	Sequence 4542, Ap
76	17	65.4	17	15	US-10-298-255-5	Sequence 5, Appli
77	17	65.4	17	17	US-10-669-841-2607	Sequence 2607, Ap
78	17	65.4	17	17	US-10-669-841-2608	Sequence 2608, Ap
79	17	65.4	17	17	US-10-669-841-2609	Sequence 2609, Ap
80	17	65.4	17	17	US-10-669-841-7133	Sequence 7133, Ap
81	17	65.4	17	17	US-10-669-841-7134	Sequence 7134, Ap
82	17	65.4	17	17	US-10-669-841-7135	Sequence 7135, Ap
83	17	65.4	19	18	US-10-667-271-100	Sequence 100, App
84	17	65.4	19	18	US-10-667-271-117	Sequence 117, App
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c 87	17	65.4	32	15	US-10-111-817-3	Sequence 3, Appli	c 160	52.3	24	18	US-10-660-122-43	Sequence 43, Appl
c 88	17	65.4	47	10	US-10-318-416B-2	Sequence 2, Appli	c 161	52.3	30	10	US-09-948-137A-7	Sequence 7, Appli
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c 90	16	61.5	17	10	US-09-740-332-13	Sequence 4339, Ap	c 163	52.3	38	15	US-10-262-272A-20	Sequence 20, Appl
c 91	16	61.5	17	10	US-09-817-879-13	Sequence 13, Appl	c 164	52.3	39	9	US-09-784-980-23	Sequence 23, Appl
c 92	16	61.5	17	10	US-09-817-879-13	Sequence 4539, Ap	c 165	52.3	39	15	US-10-229-412-23	Sequence 23, Appl
c 93	16	61.5	17	10	US-10-669-841-2606	Sequence 2606, Ap	c 166	51.5	29	15	US-10-263-103-1	Sequence 1, Appli
c 94	16	61.5	17	10	US-10-669-841-7132	Sequence 7132, Ap	c 167	51.5	29	15	US-10-263-103-5	Sequence 5, Appli
c 95	16	61.5	17	10	US-10-667-271-106	Sequence 106, App	c 168	51.5	29	15	US-10-263-103-9	Sequence 9, Appli
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c 97	16	61.5	19	18	US-10-667-271-127	Sequence 802, App	c 170	50.8	20	17	US-10-688-706-1301	Sequence 1301, Ap
c 98	16	61.5	19	18	US-10-667-271-823	Sequence 823, App	c 171	50.8	20	17	US-10-688-706-1658	Sequence 1658, Ap
c 99	16	61.5	22	16	US-10-407-897-3	Sequence 3, Appli	c 172	50.8	22	15	US-10-459-970-8	Sequence 8, Appli
c 100	16	61.5	26	9	US-09-294-121A-3	Sequence 3, Appli	c 173	50.8	25	17	US-10-717-597-1103	Sequence 1103, Ap
c 101	16	61.5	26	9	US-09-899-082A-3	Sequence 3, Appli	c 174	50.8	30	15	US-10-272-898-29	Sequence 29, Appl
c 102	16	61.5	26	9	US-09-899-082A-3	Sequence 3, Appli	c 175	50.8	30	15	US-10-354-774-29	Sequence 29, Appl
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c 105	16	61.5	26	15	US-10-070-415A-3	Sequence 3, Appli	c 178	50.8	30	17	US-10-729-039-29	Sequence 29, Appl
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c 107	16	61.5	26	16	US-10-822-711-3	Sequence 3, Appli	c 180	50.8	39	14	US-10-066-593-85	Sequence 85, Appl
c 108	16	61.5	32	15	US-10-111-817-5	Sequence 5, Appli	c 181	50.8	39	15	US-10-307-724-85	Sequence 85, Appl
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c 110	15.8	60.8	38	15	US-10-358-037-6	Sequence 6, Appli	c 183	50.8	44	17	US-10-706-229-3	Sequence 3, Appli
c 111	15	57.7	15	9	US-09-504-231A-2	Sequence 2, Appli	c 184	50.8	47	16	US-10-349-143-1436	Sequence 1436, Ap
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c 113	15	57.7	15	9	US-09-504-231A-1580	Sequence 1580, Ap	c 186	50.0	13	10	US-09-740-332-4596	Sequence 4596, Ap
c 114	15	57.7	15	9	US-09-504-231A-1581	Sequence 1581, Ap	c 187	50.0	13	10	US-09-740-332-4597	Sequence 4597, Ap
c 115	15	57.7	15	9	US-09-504-231A-1582	Sequence 1582, Ap	c 188	50.0	13	10	US-09-817-879-4568	Sequence 4568, Ap
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c 119	15	57.7	15	9	US-09-274-553D-1581	Sequence 1581, Ap	c 192	50.0	13	17	US-10-669-841-7161	Sequence 7161, Ap
c 120	15	57.7	15	9	US-09-274-553D-1582	Sequence 1582, Ap	c 193	50.0	13	17	US-10-669-841-7189	Sequence 7189, Ap
c 121	15	57.7	15	10	US-09-740-332-4557	Sequence 4557, Ap	c 194	50.0	13	17	US-10-669-841-7190	Sequence 7190, Ap
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c 123	15	57.7	15	10	US-09-740-332-4619	Sequence 4619, Ap	c 196	50.0	15	10	US-09-817-879-4570	Sequence 4570, Ap
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c 127	15	57.7	15	17	US-10-669-841-7150	Sequence 7150, Ap	c 200	50.0	17	17	US-10-669-841-7131	Sequence 7131, Ap
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c 129	15	57.7	15	17	US-10-669-841-7212	Sequence 7212, Ap	c 202	50.0	19	18	US-10-667-271-140	Sequence 140, App
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c 141	14.6	56.2	30	15	US-10-289-135A-100	Sequence 100, App	c 214	50.0	33	9	US-09-948-966-4	Sequence 4, Appli
c 142	14.2	54.6	25	17	US-10-775-169-4336	Sequence 4336, Ap	c 215	50.0	33	9	US-09-875-228-34	Sequence 34, Appl
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c 146	14	53.8	17	10	US-09-817-879-17	Sequence 17, Appl	c 219	50.0	47	16	US-10-462-645-4	Sequence 4, Appli
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236	12.6	48.5	25	15	US-10-098-2638-111917	Sequence 111917, Ap	309	12.2	46.9	37	16	US-10-648-984-1	Sequence 1, Appli
237	12.6	48.5	25	15	US-10-098-2638-111918	Sequence 111918, Ap	310	12.2	46.9	38	15	US-10-050-902-302	Sequence 302, App
238	12.6	48.5	30	15	US-10-261-078-16	Sequence 16, Appl	311	12.2	46.9	38	15	US-10-050-898-302	Sequence 302, App
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240	12.6	48.5	38	10	US-09-877-478-4209	Sequence 4209, Ap	313	12.2	46.9	38	16	US-10-617-876-81	Sequence 81, Appl
241	12.6	48.5	38	16	US-10-342-902-4209	Sequence 4209, Ap	314	12.2	46.9	39	15	US-10-094-749-3292	Sequence 3292, Ap
242	12.6	48.5	38	16	US-10-467-431-4	Sequence 4, Appli	315	12.2	46.9	39	15	US-10-104-047-3950	Sequence 3950, Ap
243	12.6	48.5	38	17	US-10-669-841-9100	Sequence 9100, Ap	316	12.2	46.9	39	16	US-10-108-2608-4896	Sequence 4896, Ap
244	12.6	48.5	38	17	US-10-466-695A-4	Sequence 4, Appli	317	12.2	46.9	39	16	US-10-609-775-21	Sequence 21, Appl
245	12.6	48.5	41	14	US-10-038-723-55	Sequence 55, Appl	318	12.2	46.9	44	16	US-10-282-122A-2412	Sequence 2412, Ap
246	12.4	47.7	25	9	US-09-791-171-106	Sequence 106, App	319	12.2	46.9	44	17	US-10-706-229-6	Sequence 6, Appli
247	12.4	47.7	25	10	US-09-943-443-106	Sequence 106, App	320	12.2	46.9	47	16	US-10-349-143-1691	Sequence 4, Appli
248	12.4	47.7	25	10	US-09-804-980-106	Sequence 106, App	321	12.2	46.9	48	14	US-10-023-066A-4	Sequence 4, Appli
249	12.4	47.7	25	14	US-10-215-112-5596	Sequence 5596, Ap	322	12.2	46.9	48	15	US-10-161-547-38	Sequence 38, Appl
250	12.4	47.7	25	14	US-10-115-112-6086	Sequence 1086, Ap	323	12.2	46.9	50	16	US-10-131-827-5585	Sequence 5585, Ap
251	12.4	47.7	25	17	US-10-620-246-106	Sequence 106, App	324	12	46.2	13	10	US-09-740-332-4598	Sequence 4598, Ap
252	12.4	47.7	27	17	US-10-469-552-13	Sequence 13, Appl	325	12	46.2	13	10	US-09-817-879-4598	Sequence 4598, Ap
253	12.4	47.7	30	15	US-10-142-283-104	Sequence 104, Appl	326	12	46.2	13	17	US-10-669-841-7191	Sequence 7191, Ap
254	12.4	47.7	30	15	US-10-289-135A-102	Sequence 102, App	327	12	46.2	16	10	US-09-825-805-3	Sequence 3, Appli
255	12.4	47.7	30	17	US-10-651-674-3	Sequence 3, Appli	328	12	46.2	17	9	US-09-866-108-7460	Sequence 7460, Ap
256	12.4	47.7	30	17	US-10-651-674-4	Sequence 4, Appli	329	12	46.2	17	9	US-09-866-108-7461	Sequence 7461, Ap
257	12.4	47.7	31	9	US-09-841-132-204	Sequence 204, App	330	12	46.2	17	9	US-09-866-108-7462	Sequence 7462, Ap
258	12.4	47.7	31	10	US-09-740-332-5474	Sequence 5474, Ap	331	12	46.2	17	9	US-09-866-108-7463	Sequence 7463, Ap
259	12.4	47.7	31	10	US-09-817-879-5474	Sequence 5474, Ap	332	12	46.2	17	9	US-09-866-108-7464	Sequence 7464, Ap
260	12.4	47.7	31	17	US-10-712-672-4662	Sequence 4662, Ap	333	12	46.2	17	9	US-09-866-108-7465	Sequence 7465, Ap
261	12.4	47.7	31	17	US-10-712-672-4845	Sequence 4845, Ap	334	12	46.2	17	10	US-09-740-332-18	Sequence 18, Appl
262	12.4	47.7	31	17	US-10-669-841-12019	Sequence 12019, A	335	12	46.2	17	10	US-09-817-879-18	Sequence 18, Appl
263	12.4	47.7	33	15	US-10-289-135A-109	Sequence 109, App	336	12	46.2	17	17	US-10-669-841-2611	Sequence 2611, Ap
264	12.4	47.7	34	14	US-10-283-349-14	Sequence 14, Appl	337	12	46.2	17	17	US-10-723-361-7461	Sequence 7461, Ap
265	12.4	47.7	35	10	US-09-986-033-1	Sequence 1, Appli	338	12	46.2	17	17	US-10-723-361-7461	Sequence 7461, Ap
266	12.4	47.7	38	10	US-09-848-754A-4463	Sequence 4463, Ap	339	12	46.2	17	17	US-10-723-361-7462	Sequence 7462, Ap
267	12.4	47.7	38	15	US-10-156-306-2061	Sequence 2061, Ap	340	12	46.2	17	17	US-10-723-361-7463	Sequence 7463, Ap
268	12.4	47.7	41	14	US-10-043-573-87	Sequence 87, Appl	341	12	46.2	17	17	US-10-723-361-7464	Sequence 7464, Ap
269	12.4	47.7	41	14	US-10-283-349-9	Sequence 9, Appli	342	12	46.2	17	17	US-10-723-361-7465	Sequence 7465, Ap
270	12.4	47.7	42	16	US-10-162-743-8	Sequence 8, Appli	343	12	46.2	19	18	US-10-667-271-103	Sequence 103, App
271	12.4	47.7	45	9	US-09-878-766A-6	Sequence 6, Appli	344	12	46.2	19	18	US-10-667-271-137	Sequence 137, App
272	12.4	47.7	45	16	US-10-650-369-6	Sequence 6, Appli	345	12	46.2	19	18	US-10-667-271-799	Sequence 799, App
273	12.4	47.7	47	14	US-10-136-841-17	Sequence 17, Appl	346	12	46.2	19	18	US-10-667-271-833	Sequence 833, App
274	12.4	47.7	47	15	US-10-170-097-1257	Sequence 1257, Ap	347	12	46.2	21	18	US-10-786-720-7515	Sequence 7515, Ap
275	12.4	47.7	47	16	US-10-272-531A-13	Sequence 17, Appl	348	12	46.2	21	18	US-10-786-720-7965	Sequence 9765, Ap
276	12.4	47.7	47	16	US-10-272-483A-17	Sequence 17, Appl	349	12	46.2	23	15	US-10-323-463-6	Sequence 6, Appli
277	12.4	47.7	47	16	US-10-333-429-128	Sequence 128, App	350	12	46.2	23	16	US-10-632-658-27	Sequence 27, Appl
278	12.4	47.7	48	15	US-10-309-690-56	Sequence 56, Appl	351	12	46.2	23	17	US-10-605-708A-23	Sequence 23, Appl
279	12.4	47.7	50	10	US-09-308-683-5	Sequence 5, Appli	352	12	46.2	24	9	US-09-962-318-9	Sequence 9, Appli
280	12.4	47.7	50	14	US-10-136-841-13	Sequence 13, Appl	353	12	46.2	24	9	US-09-962-318-15	Sequence 15, Appl
281	12.4	47.7	50	16	US-10-272-531A-13	Sequence 13, Appl	354	12	46.2	24	16	US-10-632-658-25	Sequence 25, Appl
282	12.4	47.7	50	16	US-10-272-483A-13	Sequence 13, Appl	355	12	46.2	25	9	US-09-866-108-12352	Sequence 12352, A
283	12.2	46.9	18	15	US-10-044-115A-1	Sequence 1, Appli	356	12	46.2	25	9	US-09-866-108-12353	Sequence 12353, A
284	12.2	46.9	20	15	US-10-053-662A-27	Sequence 27, Appl	357	12	46.2	25	9	US-09-866-108-12354	Sequence 12354, A
285	12.2	46.9	20	17	US-10-688-706-704	Sequence 704, App	358	12	46.2	25	9	US-09-866-108-12355	Sequence 12355, A
286	12.2	46.9	20	17	US-10-688-706-1762	Sequence 1762, Ap	359	12	46.2	25	9	US-09-866-108-12356	Sequence 12356, A
287	12.2	46.9	22	10	US-09-931-936-1949	Sequence 1949, Ap	360	12	46.2	25	9	US-09-866-108-12357	Sequence 12357, A
288	12.2	46.9	25	15	US-10-098-263B-44798	Sequence 44798, A	361	12	46.2	25	9	US-09-866-108-12358	Sequence 12358, A
289	12.2	46.9	25	15	US-10-098-263B-87902	Sequence 87902, A	362	12	46.2	25	9	US-09-866-108-12359	Sequence 12359, A
290	12.2	46.9	25	15	US-10-223-646-31	Sequence 31, Appl	363	12	46.2	25	9	US-09-866-108-12360	Sequence 12360, A
291	12.2	46.9	25	17	US-10-717-597-4120	Sequence 4120, Ap	364	12	46.2	25	9	US-09-866-108-12361	Sequence 12361, A
292	12.2	46.9	26	14	US-10-096-718-76	Sequence 76, Appl	365	12	46.2	25	9	US-09-866-108-12362	Sequence 12362, A
293	12.2	46.9	26	16	US-10-456-129-26	Sequence 26, Appl	366	12	46.2	25	9	US-09-866-108-12363	Sequence 12363, A
294	12.2	46.9	29	10	US-09-862-393-20	Sequence 20, Appl	367	12	46.2	25	9	US-09-866-108-12364	Sequence 12364, A
295	12.2	46.9	29	18	US-10-777-010-4	Sequence 4, Appli	368	12	46.2	25	9	US-09-866-108-12365	Sequence 12365, A
296	12.2	46.9	30	15	US-10-300-699-9	Sequence 9, Appli	369	12	46.2	25	14	US-10-215-112-3129	Sequence 3129, Ap
297	12.2	46.9	30	15	US-10-418-820-9	Sequence 9, Appli	370	12	46.2	25	14	US-10-215-112-10461	Sequence 10461, A
298	12.2	46.9	33	16	US-09-790-399-19	Sequence 19, Appl	371	12	46.2	25	15	US-10-098-263B-49153	Sequence 49153, A
299	12.2	46.9	33	16	US-10-343-766-2	Sequence 2, Appli	372	12	46.2	25	15	US-10-098-263B-115494	Sequence 115494, A
300	12.2	46.9	34	18	US-10-784-880-191	Sequence 191, App	373	12	46.2	25	17	US-10-318-416B-7	Sequence 7, Appli
301	12.2	46.9	35	15	US-10-094-749-3291	Sequence 3291, Ap	374	12	46.2	25	17	US-10-723-361-12352	Sequence 12352, A
302	12.2	46.9	35	15	US-10-104-047-3949	Sequence 3949, Ap	375	12	46.2	25	17	US-10-723-361-12353	Sequence 12353, A
303	12.2	46.9	35	16	US-10-108-260A-4895	Sequence 4895, Ap	376	12	46.2	25	17	US-10-723-361-12354	Sequence 12354, A
304	12.2	46.9	36	15	US-10-053-662A-25	Sequence 25, Appl	377	12	46.2	25	17	US-10-723-361-12355	Sequence 12355, A

378	12	46.2	25	17	US-10-723-361-12356	Sequence 12356, A	C 451	11.8	45.4	30	15	US-10-289-135A-110	Sequence 110, Appl
379	12	46.2	25	17	US-10-723-361-12357	Sequence 12357, A	452	11.8	45.4	31	10	US-09-730-423-3615	Sequence 3615, Ap
380	12	46.2	25	17	US-10-723-361-12358	Sequence 12358, A	453	11.8	45.4	31	10	US-09-945-237A-3615	Sequence 3615, Ap
381	12	46.2	25	17	US-10-723-361-12359	Sequence 12359, A	C 454	11.8	45.4	32	9	US-09-150-811-1	GENERAL INFORMA
382	12	46.2	25	17	US-10-723-361-12360	Sequence 12360, A	455	11.8	45.4	32	17	US-10-306-275B-22	Sequence 22, Appl
383	12	46.2	25	17	US-10-723-361-12361	Sequence 12361, A	456	11.8	45.4	32	16	US-10-603-229-5	Sequence 5, Appli
384	12	46.2	25	17	US-10-723-361-12362	Sequence 12362, A	457	11.8	45.4	34	14	US-10-109-812-23	Sequence 23, Appl
385	12	46.2	25	17	US-10-723-361-12363	Sequence 12363, A	458	11.8	45.4	35	17	US-10-306-275B-23	Sequence 23, Appl
386	12	46.2	25	17	US-10-723-361-12364	Sequence 12364, A	C 459	11.8	45.4	36	14	US-10-098-276A-19	Sequence 19, Appl
387	12	46.2	25	17	US-10-723-361-12365	Sequence 12365, A	460	11.8	45.4	36	14	US-10-156-932-74	Sequence 74, Appl
388	12	46.2	27	15	US-10-262-589-3	Sequence 3, Appli	C 461	11.8	45.4	38	9	US-09-364-847-41	Sequence 41, Appl
389	12	46.2	30	9	US-09-791-171-164	Sequence 164, App	462	11.8	45.4	38	10	US-09-780-533A-3926	Sequence 3926, Ap
390	12	46.2	30	10	US-09-943-443-164	Sequence 164, App	463	11.8	45.4	38	10	US-09-848-754A-4496	Sequence 4496, Ap
391	12	46.2	30	10	US-09-804-980-164	Sequence 164, App	464	11.8	45.4	38	15	US-10-156-306-5607	Sequence 5607, Ap
392	12	46.2	30	15	US-10-220-908-1	Sequence 1, Appli	465	11.8	45.4	38	15	US-10-156-306-5607	Sequence 5607, Ap
393	12	46.2	30	15	US-10-220-908-2	Sequence 2, Appli	466	11.8	45.4	38	17	US-10-287-949A-16134	Sequence 16134, A
394	12	46.2	30	17	US-10-620-246-164	Sequence 164, App	C 467	11.8	45.4	39	15	US-10-005-956-1438	Sequence 1438, Ap
395	12	46.2	32	9	US-09-469-522-12	Sequence 12, Appli	468	11.8	45.4	39	15	US-10-369-378-26	Sequence 26, Appl
396	12	46.2	33	9	US-09-888-938-4	Sequence 4, Appli	469	11.8	45.4	39	15	US-10-369-378-48	Sequence 48, Appl
397	12	46.2	33	11	US-09-852-238A-4	Sequence 4, Appli	470	11.8	45.4	39	15	US-10-199-937-161	Sequence 161, App
398	12	46.2	34	17	US-10-432-326-4	Sequence 1, Appli	471	11.8	45.4	40	9	US-09-777-157A-7	Sequence 7, Appli
399	12	46.2	35	10	US-09-465-925-1	Sequence 1, Appli	472	11.8	45.4	40	17	US-10-742-343-6	Sequence 6, Appli
400	12	46.2	35	10	US-09-848-754A-9610	Sequence 9610, Ap	C 473	11.8	45.4	42	9	US-09-350-259-27	Sequence 27, Appl
401	12	46.2	35	15	US-10-100-294A-68	Sequence 68, Appl	474	11.8	45.4	42	10	US-09-940-244-147	Sequence 147, App
402	12	46.2	37	9	US-09-999-183-21	Sequence 21, Appli	C 475	11.8	45.4	42	10	US-09-891-943-27	Sequence 27, Appl
403	12	46.2	37	15	US-10-354-955-9	Sequence 9, Appli	476	11.8	45.4	42	13	US-10-033-297-147	Sequence 147, App
404	12	46.2	37	16	US-10-351-938-22	Sequence 22, Appli	477	11.8	45.4	42	15	US-10-290-386-147	Sequence 147, App
405	12	46.2	38	9	US-09-784-990-27	Sequence 27, Appli	478	11.8	45.4	42	16	US-10-356-863-147	Sequence 147, App
406	12	46.2	38	15	US-10-229-412-27	Sequence 27, Appl	479	11.8	45.4	42	18	US-10-309-584-147	Sequence 147, App
407	12	46.2	38	15	US-10-156-433-62	Sequence 62, Appl	C 480	11.8	45.4	44	9	US-09-962-628B-2	Sequence 2, Appli
408	12	46.2	39	16	US-10-453-827-389	Sequence 389, App	481	11.8	45.4	45	15	US-10-256-551-52	Sequence 52, Appl
409	12	46.2	39	16	US-10-453-827-390	Sequence 390, App	C 482	11.8	45.4	47	16	US-10-349-143-2982	Sequence 2982, Ap
410	12	46.2	41	16	US-10-035-833A-1334	Sequence 1334, Ap	483	11.8	45.4	47	16	US-10-349-143-2982	Sequence 2982, Ap
411	12	46.2	41	16	US-10-035-833A-7542	Sequence 7542, Ap	C 484	11.8	45.4	47	16	US-10-349-143-3606	Sequence 3606, Ap
412	12	46.2	43	14	US-10-150-648B-22	Sequence 22, Appl	C 485	11.8	45.4	48	17	US-10-478-442-8	Sequence 8, Appli
413	12	46.2	49	16	US-10-632-658-28	Sequence 28, Appl	C 486	11.8	45.4	50	8	US-08-781-386A-2687	Sequence 2687, Ap
414	11.8	45.4	20	16	US-10-043-573-20	Sequence 20, Appl	C 487	11.8	45.4	50	9	US-09-896-888A-10	Sequence 10, Appl
415	11.8	45.4	20	16	US-10-289-762-2105	Sequence 2105, Ap	C 488	11.8	45.4	50	15	US-10-414-760-15	Sequence 15, Appl
416	11.8	45.4	20	16	US-10-289-762-3610	Sequence 3610, Ap	C 489	11.8	45.4	50	15	US-10-414-760-18	Sequence 18, Appl
417	11.8	45.4	20	17	US-10-688-706-1855	Sequence 1855, Ap	C 490	11.8	45.4	50	16	US-10-131-827-416	Sequence 416, Appl
418	11.8	45.4	20	17	US-10-688-706-1962	Sequence 1962, Ap	C 491	11.8	45.4	50	16	US-10-329-624-2687	Sequence 2687, Ap
419	11.8	45.4	22	13	US-10-117-641-25	Sequence 25, Appl	C 492	11.8	44.6	18	14	US-10-054-387-8	Sequence 8, Appli
420	11.8	45.4	22	15	US-10-235-113-25	Sequence 25, Appl	C 493	11.6	44.6	18	18	US-10-660-122-41	Sequence 41, Appl
421	11.8	45.4	22	15	US-10-393-602-16	Sequence 16, Appl	C 494	11.6	44.6	18	18	US-10-660-122-339	Sequence 339, App
422	11.8	45.4	25	9	US-09-866-108-11899	Sequence 11899, A	C 495	11.6	44.6	19	9	US-09-969-373-4216	Sequence 4216, Ap
423	11.8	45.4	25	9	US-09-866-108-11900	Sequence 11900, A	496	11.6	44.6	19	16	US-10-333-429-385	Sequence 385, App
424	11.8	45.4	25	9	US-09-866-108-11901	Sequence 11901, A	C 497	11.6	44.6	19	17	US-10-665-951-1114	Sequence 1114, App
425	11.8	45.4	25	9	US-09-791-171-106	Sequence 106, App	C 498	11.6	44.6	19	17	US-10-665-951-1114	Sequence 1114, App
426	11.8	45.4	25	10	US-09-943-443-106	Sequence 106, App	C 499	11.6	44.6	20	14	US-10-092-771-36	Sequence 36, Appl
427	11.8	45.4	25	10	US-09-804-980-106	Sequence 106, App	C 500	11.6	44.6	20	15	US-10-177-573-78	Sequence 78, Appl
428	11.8	45.4	25	14	US-10-098-263B-3826	Sequence 9132, Ap	C 501	11.6	44.6	20	15	US-10-177-573-102	Sequence 102, App
429	11.8	45.4	25	14	US-10-098-263B-3826	Sequence 9132, Ap	C 502	11.6	44.6	22	15	US-10-384-361-8	Sequence 8, Appli
430	11.8	45.4	25	15	US-10-098-263B-3826	Sequence 9132, Ap	C 503	11.6	44.6	22	17	US-10-312-731B-9	Sequence 9, Appli
431	11.8	45.4	25	15	US-10-098-263B-3826	Sequence 9132, Ap	504	11.6	44.6	24	10	US-09-750-410-56	Sequence 56, Appl
432	11.8	45.4	25	15	US-10-098-263B-3826	Sequence 9132, Ap	C 505	11.6	44.6	24	10	US-09-940-185-1295	Sequence 1295, Ap
433	11.8	45.4	25	15	US-10-098-263B-3826	Sequence 9132, Ap	C 506	11.6	44.6	24	16	US-10-431-599-29	Sequence 29, Appl
434	11.8	45.4	25	17	US-10-723-361-11899	Sequence 11899, A	C 507	11.6	44.6	25	14	US-10-215-112-3648	Sequence 3648, App
435	11.8	45.4	25	17	US-10-723-361-11900	Sequence 11900, A	C 508	11.6	44.6	25	15	US-10-098-263B-452	Sequence 452, App
436	11.8	45.4	25	17	US-10-723-361-11901	Sequence 11901, A	C 509	11.6	44.6	25	15	US-10-098-263B-110740	Sequence 110740, A
437	11.8	45.4	26	10	US-09-373-361-11901	Sequence 9, Appli	510	11.6	44.6	25	15	US-10-098-263B-122140	Sequence 122140, A
438	11.8	45.4	26	14	US-10-086-718-69	Sequence 69, Appl	C 511	11.6	44.6	25	15	US-10-032-585-5032	Sequence 5032, Ap
439	11.8	45.4	26	14	US-10-096-718-69	Sequence 69, Appl	C 512	11.6	44.6	25	17	US-10-101-454-5	Sequence 5, Appli
440	11.8	45.4	26	15	US-10-174-209-57	Sequence 57, Appl	C 513	11.6	44.6	26	16	US-10-616-390-3	Sequence 3, Appli
441	11.8	45.4	26	15	US-10-065-1133A-37	Sequence 37, Appl	514	11.6	44.6	26	16	US-10-361-002-74	Sequence 74, Appl
442	11.8	45.4	26	16	US-10-434-811A-37	Sequence 37, Appl	515	11.6	44.6	26	17	US-10-361-004-74	Sequence 74, Appl
443	11.8	45.4	26	17	US-10-734-373-37	Sequence 37, Appl	516	11.6	44.6	27	17	US-10-362-924-21	Sequence 21, Appl
444	11.8	45.4	27	15	US-10-327-069-9	Sequence 9, Appli	517	11.6	44.6	27	17	US-10-343-561-95	Sequence 95, Appl
445	11.8	45.4	29	9	US-09-810-861B-1	Sequence 1, Appli	518	11.6	44.6	27	17	US-10-138-473-167	Sequence 167, App
446	11.8	45.4	29	14	US-10-090-827-20	Sequence 20, Appl	C 519	11.6	44.6	28	15	US-10-251-385-248	Sequence 248, App
447	11.8	45.4	29	16	US-10-321-039-649	Sequence 649, App	C 520	11.6	44.6	30	15	US-10-339-674-3421	Sequence 3421, Ap
448	11.8	45.4	29	17	US-10-641-001-14	Sequence 14, Appl	C 521	11.6	44.6	30	15	US-10-339-674-3422	Sequence 3422, Ap
449	11.8	45.4	30	14	US-10-085-906-259	Sequence 259, App	522	11.6	44.6	30	16	US-10-257-960-1	Sequence 1, Appli
450	11.8	45.4	30	14	US-10-085-906-259	Sequence 259, App	523	11.6	44.6	30	16	US-10-257-960-1	Sequence 1, Appli

670	11.4	43.8	40	18	US-10-469-851-255	Sequence 255, App	c 743	11.2	43.1	25	15	US-10-098-263B-65714	Sequence 65714, A
671	11.4	43.8	41	16	US-10-035-833A-118	Sequence 118, App	744	11.2	43.1	25	15	US-10-098-263B-65714	Sequence 65714, A
672	11.4	43.8	41	16	US-10-035-833A-186	Sequence 186, App	745	11.2	43.1	25	15	US-10-098-263B-60688	Sequence 60688, A
673	11.4	43.8	41	16	US-10-035-833A-573	Sequence 573, App	746	11.2	43.1	25	15	US-10-098-263B-95129	Sequence 95129, A
674	11.4	43.8	41	16	US-10-035-833A-5457	Sequence 5457, App	747	11.2	43.1	25	15	US-10-098-263B-96129	Sequence 96129, A
675	11.4	43.8	41	16	US-10-035-833A-5525	Sequence 5525, App	c 748	11.2	43.1	25	15	US-10-098-263B-108488	Sequence 108488, A
676	11.4	43.8	41	16	US-10-035-833A-5525	Sequence 5525, App	c 749	11.2	43.1	25	15	US-10-098-263B-115732	Sequence 115732, A
677	11.4	43.8	42	13	US-10-090-983-11	Sequence 11, App	750	11.2	43.1	25	15	US-10-098-263B-116716	Sequence 116716, A
678	11.4	43.8	47	15	US-10-117-087-7	Sequence 7, Appli	751	11.2	43.1	25	15	US-10-098-263B-130089	Sequence 130089, A
679	11.4	43.8	47	15	US-10-349-143-618	Sequence 618, App	752	11.2	43.1	25	15	US-10-098-263B-130090	Sequence 130090, A
680	11.4	43.8	47	16	US-10-349-143-1451	Sequence 1451, App	c 753	11.2	43.1	25	17	US-10-717-597-2438	Sequence 2438, App
681	11.4	43.8	47	16	US-10-349-143-3789	Sequence 3789, App	c 754	11.2	43.1	25	17	US-10-620-246-104	Sequence 104, App
682	11.4	43.8	48	9	US-09-761-534A-19	Sequence 19, Appl	c 755	11.2	43.1	26	15	US-10-228-629A-5	Sequence 5, Appli
683	11.4	43.8	49	15	US-10-300-011-5	Sequence 5, Appli	c 756	11.2	43.1	26	17	US-10-746-167-29	Sequence 29, Appl
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685	11.4	43.8	50	16	US-10-131-827-3650	Sequence 3650, App	758	11.2	43.1	27	15	US-10-317-444-35	Sequence 35, Appl
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691	11.2	43.1	17	16	US-10-287-949A-9165	Sequence 9165, App	c 764	11.2	43.1	28	15	US-10-648-984-23	Sequence 23, Appl
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694	11.2	43.1	20	10	US-09-887-145-31	Sequence 31, Appl	c 767	11.2	43.1	30	15	US-10-214-417A-105	Sequence 105, App
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732	11.2	43.1	25	14	US-10-215-112-8920	Sequence 8920, App	805	11.2	43.1	33	10	US-09-826-509-41	Sequence 41, Appl
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C 817	11.2	43.1	35	17	US-10-673-119-168	Sequence 168, App	890	11.2	43.1	50	10	US-09-905-056-138	Sequence 138, App
C 818	11.2	43.1	35	18	US-10-671-207-168	Sequence 168, App	891	11.2	43.1	50	10	US-09-909-064-138	Sequence 138, App
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C 825	11.2	43.1	37	15	US-10-272-756-70	Sequence 70, Appl	898	11.2	43.1	50	10	US-09-905-075-138	Sequence 138, App
C 826	11.2	43.1	37	15	US-10-273-228-70	Sequence 70, Appl	899	11.2	43.1	50	10	US-09-902-759-138	Sequence 138, App
C 827	11.2	43.1	38	9	US-09-426-548-189	Sequence 189, App	900	11.2	43.1	50	10	US-09-902-634-138	Sequence 138, App
C 828	11.2	43.1	38	15	US-10-156-433-59	Sequence 59, Appl	901	11.2	43.1	50	10	US-09-902-713-138	Sequence 138, App
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C 833	11.2	43.1	40	18	US-10-469-851-347	Sequence 347, App	906	11.2	43.1	50	10	US-09-903-823-138	Sequence 138, App
C 834	11.2	43.1	41	9	US-09-770-940-31	Sequence 31, Appl	907	11.2	43.1	50	10	US-09-907-652-138	Sequence 138, App
C 835	11.2	43.1	41	15	US-10-165-528-31	Sequence 31, Appl	908	11.2	43.1	50	10	US-09-902-572A-138	Sequence 138, App
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C 841	11.2	43.1	41	16	US-10-035-833A-3913	Sequence 3913, App	914	11.2	43.1	50	10	US-09-905-449-138	Sequence 138, App
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C 850	11.2	43.1	46	10	US-09-931-346-265	Sequence 265, App	923	11.2	43.1	50	10	US-09-904-877A-138	Sequence 138, App
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853	11.2	43.1	47	15	US-10-170-097-1125	Sequence 1125, App	926	11.2	43.1	50	10	US-09-907-728-138	Sequence 138, App
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C 855	11.2	43.1	47	16	US-10-349-143-1196	Sequence 1196, App	928	11.2	43.1	50	10	US-09-904-938A-138	Sequence 138, App
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C 857	11.2	43.1	47	16	US-10-349-143-2388	Sequence 2388, App	930	11.2	43.1	50	11	US-09-908-576-138	Sequence 138, App
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866	11.2	43.1	50	10	US-09-903-640-138	Sequence 138, App	939	11.2	43.1	50	16	US-10-131-827-5446	Sequence 5446, App
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871	11.2	43.1	50	10	US-09-907-942-138	Sequence 138, App	944	11.2	43.1	50	17	US-10-215-371-138	Sequence 138, App
872	11.2	43.1	50	10	US-09-904-859-138	Sequence 138, App	945	11.2	43.1	50	17	US-10-771-187-138	Sequence 138, App
873	11.2	43.1	50	10	US-09-909-204-138	Sequence 138, App	946	11	42.3	14	14	US-10-096-718-62	Sequence 62, Appl
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878	11.2	43.1	50	10	US-09-903-786-138	Sequence 138, App	951	11	42.3	16	10	US-09-825-805-4	Sequence 4, Appl
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882	11.2	43.1	50	10	US-09-904-956-138	Sequence 138, App	955	11	42.3	17	10	US-09-740-332-4537	Sequence 4537, App
883	11.2	43.1	50	10	US-09-902-736-138	Sequence 138, App	956	11	42.3	17	10	US-09-817-879-4537	Sequence 4537, App
884	11.2	43.1	50	10	US-09-907-794-138	Sequence 138, App	957	11	42.3	17	17	US-10-669-841-7130	Sequence 7130, App
885	11.2	43.1	50	10	US-09-903-943-138	Sequence 138, App	958	11	42.3	17	17	US-10-723-361-7459	Sequence 7459, App
886	11.2	43.1	50	10	US-09-904-462-138	Sequence 138, App	959	11	42.3	17	17	US-10-723-361-7466	Sequence 7466, App
887	11.2	43.1	50	10	US-09-907-925-138	Sequence 138, App	960	11	42.3	19	15	US-10-226-992-7	Sequence 7, Appl
888	11.2	43.1	50	10	US-09-902-692-138	Sequence 138, App	961	11	42.3	19	15	US-10-226-992-7	Sequence 7, Appl

; CURRENT APPLICATION NUMBER: US/10/198,680A
; CURRENT FILING DATE: 2002-07-18

```
; OTHER INFORMATION: Forward primer
US-10-353-563-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 9
US-10-353-589-1
; Sequence 1, Application US/10353589
; Publication No. US20030187018A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/106
; CURRENT APPLICATION NUMBER: US/10/353,589
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,370,396
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-353-589-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 10
US-10-320-979-1
; Sequence 1, Application US/10320979
; Publication No. US20030191067A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM INTERNATIONAL GmbH
; TITLE OF INVENTION: HEPATITIS C INHIBITOR TRI-PEPTIDES
; FILE REFERENCE: 13/107
; CURRENT APPLICATION NUMBER: US/10/320,979
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 2,369,970
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-320-979-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 11
US-10-353-894-1
; Sequence 1, Application US/10353894
; Publication No. US20030224977A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: MARCROCYCLIC PEPTIDES ACTIVE AGAINST THE HEPATITIS C VIRUS
; FILE REFERENCE: 13/092
; CURRENT APPLICATION NUMBER: US/10/353,894
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 2,369,711
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-353-894-1
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 12
US-10-198-259A-2
; Sequence 2, Application US/10198259A
; Publication No. US20030236251A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Viral Polymerase Inhibitors
; FILE REFERENCE: 13/089
; CURRENT APPLICATION NUMBER: US/10/198,259A
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,669
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/338,324
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-198-259A-2
Query Match      100.0%; Score 26; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 13
US-10-198-384A-2
; Sequence 2, Application US/10198384A
; Publication No. US20040024190A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Viral Polymerase inhibitors
; FILE REFERENCE: 13/090
```


; CURRENT APPLICATION NUMBER: US/10/198,384A
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/338,061
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/307,674
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-198-384A-2

Query Match 100.0%; Score 26; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 14
US-10-789-355-17
; Sequence 17, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-789-355-17

Query Match 100.0%; Score 26; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 15
US-10-686-835-17
; Sequence 17, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukulj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT APPLICATION NUMBER: US/10/686,835
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: HCV
US-10-686-835-17

Query Match 100.0%; Score 26; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 16
US-10-791-318-1
; Sequence 1, Application US/10791318
; Publication No. US20040224900A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Bailey, Murray D.
; APPLICANT: Llinas-Brunet, Montse
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptide Analogs
; FILE REFERENCE: 13/112
; CURRENT APPLICATION NUMBER: US/10/791,318
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US 60/452,187
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward primer
US-10-791-318-1

Query Match 100.0%; Score 26; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
|||
Db 3 GCAGAAAGCGTCTAGCCATGGCGTTA 28

RESULT 17
US-10-120-013-7
; Sequence 7, Application US/10120013
; Publication No. US20020192689A1
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, Dwight
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

```
;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/120,013
; FILING DATE: 10-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMB1:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-120-013-7
Query Match          92.3%; Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 18
US-10-011-855-1
; Sequence 1, Application US/10011855
; Publication No. US20030104582A1
; GENERAL INFORMATION:
; APPLICANT: BAUMANN, RUSSELL
; APPLICANT: HAMDAN, HASNAH
; APPLICANT: LEWINSKI, MICHAEL
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS FOR DETECTING HEPATITIS C
; FILE REFERENCE: 034827/0702
; CURRENT APPLICATION NUMBER: US/10/011,855
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-011-855-1
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 19
US-10-037-990-1
; Sequence 1, Application US/10037990
; Publication No. US20030124654A1
```

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;
;
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vijay
; APPLICANT: Kondiboyina, Venkat Ramana
; TITLE OF INVENTION: Method and Device for the Rapid Clinical Diagnosis of Hepatitis C
; FILE REFERENCE: RELIA P-106
; CURRENT APPLICATION NUMBER: US/10/037,990
; CURRENT FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-037-990-1
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 20
US-10-007-389-4
; Sequence 4, Application US/10007389
; Publication No. US20030165855A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-007-389-4
Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 21
US-10-322-138-1
; Sequence 1, Application US/10322138
; Publication No. US20030175765A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
; APPLICANT: Haberhausen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OQ
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
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; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-508-4

Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 22
US-10-147-679A-5
; Sequence 5, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide primer (HCV forward)
US-10-147-679A-5

Query Match          92.3%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 23
US-10-655-508-4
; Sequence 4, Application US/10655508
; Publication No. US20040063155A1
; GENERAL INFORMATION:
; APPLICANT: Ruseman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Rainer
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperease
; CURRENT APPLICATION NUMBER: US/10/655,508
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/10/007,389
; PRIOR FILING DATE: CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-508-4

Query Match          92.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 24
US-10-688-272-17
; Sequence 17, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: GeneMatrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 17
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward primer of 5'NCR of HCV
US-10-688-272-17

Query Match          92.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATGGCGT 24
    |||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 25
US-10-307-523B-3
; Sequence 3, Application US/10307523B
; Publication No. US20040106099A1
; GENERAL INFORMATION:
; APPLICANT: LEE, TZONG H
; TITLE OF INVENTION: METHOD FOR DETECTING HEPATITIS C VIRUS
; FILE REFERENCE: APV 31601
; CURRENT APPLICATION NUMBER: US/10/307,523B
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: TW 091134394
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-307-523B-3

Query Match          92.3%; Score 24; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-825-574-25

Query Match 80.8%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 30

US-09-882-945A-25
; Sequence 25, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-25

Query Match 80.8%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 31

US-10-240-460-10
; Sequence 10, Application US/10240460
; Publication No. US20030207292A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030207292Alomi, Tsugunori
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: METHOD FOR AMPLIFYING NUCLEIC ACID BY USING

; TITLE OF INVENTION: DOUBLE-STRANDED NUCLEIC ACID AS TEMPLATE
; FILE REFERENCE: 201487/1110
; CURRENT APPLICATION NUMBER: US/10/240,460
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/JP01/02771
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-111939
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-240-460-10

Query Match 80.8%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAGAAAGCGTCTAGCCATGG 21
|||||
Db 1 GCAGAAAGCGTCTAGCCATGG 21

RESULT 32

US-10-182-126-7
; Sequence 7, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmed
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIAT
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-7

Query Match 80.8%; Score 21; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AAGCGTCTAGCCATGGCGTTA 26
|||||
Db 1 AAGCGTCTAGCCATGGCGTTA 21

RESULT 33

US-08-887-505-69/c
; Sequence 69, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John
APPLICANT: Wolfe, Jia L.
APPLICANT: Roberts, Peter C.
APPLICANT: Hamlin, Jr., Henry A.
APPLICANT: Roberts, No. US20020081577A11 A.
APPLICANT: Walther, Debra M.
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 172
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,505
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-040CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-887-505-69

Query Match 76.9%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAAAGCGTCTAGCCATG 20
Db 20 GCAGAAAGCGTCTAGCCATG 1

RESULT 34

US-09-935-338-227
Sequence 227, Application US/09935338
Publication No. US20030073081A1
GENERAL INFORMATION:
APPLICANT: MUKAI, Hiroyuki
APPLICANT: SAGAWA, Hiroaki
APPLICANT: UEMORI, Takashi
APPLICANT: YAMAMOTO, Junko
APPLICANT: TOMONO, Jun
APPLICANT: KOBAYASHI, Ei-ji
APPLICANT: ENOKI, Tatsuji
APPLICANT: TAKEDA, Osamu
APPLICANT: MIYAKE, Kazue
APPLICANT: SATO, Yoshiaki
APPLICANT: MORIYAMA, Mari-ko
APPLICANT: SAWARAGI, Haruhisa
APPLICANT: HAGIYA, Michio

APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: A method for amplification of nucleic acids
FILE REFERENCE: MUKAI-1
CURRENT APPLICATION NUMBER: US/09/935,338
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: JP11-076966
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: JP11-370035
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP2000-251981
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: JP2000-284419
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: JP2000-288750
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: JP2001-104191
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: PCT/JP00/01534
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patent In version 3.2
SEQ ID NO 227
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Designed chimeric oligonucleotide primer designated as HCV-P3 to amplify a portion of HCV. "nucleotides 17 to 19 are
OTHER INFORMATION: ribonucleotides-other nucleotides are deoxyribonucleotides"
US-09-935-338-227

Query Match 73.1%; Score 19; DB 10; Length 19;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCGTCTAGCCATGGCGTTA 26
Db 1 GCGTCTAGCCATGGCGTUA 19

RESULT 35

US-10-667-271-99
Sequence 99, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (WBHE02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378

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; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-99

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGCGTCTAGCCATGGCGT 24
Db 1 AAGCGUCUAGCCGCGGCU 19

RESULT 36
US-10-667-271-101
; Sequence 101, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-101

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-10-087-631b-6.max.rnpb
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Qy 5 AAGCGTCTAGCCATGGCG 23
Db 1 AAGCGUCUAGCCGCGGCU 19

RESULT 37
US-10-667-271-102
; Sequence 102, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-102

Query Match          73.1%; Score 19; DB 18; Length 19;
Best Local Similarity 73.7%; Pred. No. 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGTCTAGCCATGGCGTTA 26
Db 1 GCGUCUAGCCGCGGCUA 19

RESULT 38
US-10-667-271-104
; Sequence 104, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
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;; CURRENT APPLICATION NUMBER: US/10/667,271
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR APPLICATION NUMBER: US 10/444,853
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2003-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2003-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 104
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-104

Query Match 73.1%; Score 19; DB 18; Length 19;

Best Local Similarity 73.1%; Pred. No. 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCGTCTAGCCATGGCGTT 25
|||||:|||||:|||||:
DB 1 AGCGUCUAGCGGCGUU 19

RESULT 39
US-10-667-271-107
;; Sequence 107, Application US/10667271
;; Publication No. US20040209831A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics
;; APPLICANT: McSwiggen, James
;; APPLICANT: Macejak, Dennis
;; APPLICANT: Beigelman, Leonid
;; APPLICANT: Morrissey, David
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
;; FILE REFERENCE: 400/129 (MBH02-763B)
;; CURRENT APPLICATION NUMBER: US/10/667,271
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 105
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 107
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-107

Query Match 73.1%; Score 19; DB 18; Length 19;

Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAAGCGTCTAGCCATGGC 22
|||||:|||||:|||||:
DB 1 GAAAGCGUCUAGCCGCGC 19

RESULT 40

US-10-667-271-113
;; Sequence 113, Application US/10667271
;; Publication No. US20040209831A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics
;; APPLICANT: McSwiggen, James
;; APPLICANT: Macejak, Dennis
;; APPLICANT: Beigelman, Leonid
;; APPLICANT: Morrissey, David
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
;; FILE REFERENCE: 400/129 (MBH02-763B)
;; CURRENT APPLICATION NUMBER: US/10/667,271
;; CURRENT FILING DATE: 2003-09-16
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT / US03/05043
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT / US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: USSN 60/401,104
;; PRIOR FILING DATE: 2002-08-05
;; PRIOR APPLICATION NUMBER: USSN 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: USSN 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: USSN 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: USSN 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: USSN 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: USSN 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1705
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 113
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-113

Query Match 73.1%; Score 19; DB 18; Length 19;

Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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| | | | | : | | | | : |
Db 1 CAGAAAGCGUCUAGCCAUG 19

Search completed: November 24, 2004, 03:42:43
Job time : 131.018 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 17:02:50 ; Search time 1363.58 Seconds
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624.507 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgcagccagattactgac 21

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Gapop 10.0 , Gapext 1.0

Searched: 44308572 seqs, 20275418765 residues

Total number of hits satisfying chosen parameters: 36539538

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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 124: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:
 125: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	46	US-10-087-631B-1
2	21	100.0	21	53	US-10-419-022-1
3	15.4	73.3	25	41	US-09-953-570A-49187
4	15.4	73.3	25	41	US-09-953-570A-49194
5	15.2	72.4	25	60	US-10-719-900-152753
6	15.2	72.4	25	60	US-10-719-956-219125
7	15.2	72.4	25	108	US-60-427-808-152753
8	15.2	72.4	25	108	US-60-427-808-219125
9	15	71.4	25	116	US-60-507-511-165285
10	14.8	70.5	25	116	US-60-507-481-158095
11	14.8	70.5	25	116	US-60-507-481-158096
12	14.4	68.6	25	42	US-09-956-604D-44625
13	14.4	68.6	25	42	US-09-956-604D-61437
14	14.4	68.6	50	124	US-60-585-352-61322
15	14.2	67.6	22	58	US-10-708-204-1327
16	14.2	67.6	25	41	US-09-953-570-116813
17	14.2	67.6	25	41	US-09-953-570A-90293
18	14.2	67.6	25	42	US-09-956-584A-596217
19	14.2	67.6	25	42	US-09-956-584A-596219
20	14.2	67.6	25	42	US-09-956-584A-596221
21	14.2	67.6	25	42	US-09-956-604D-42268
22	14.2	67.6	25	60	US-10-719-900-116595
23	14.2	67.6	25	60	US-10-719-900-122509
24	14.2	67.6	25	60	US-10-719-900-276673
25	14.2	67.6	25	64	US-10-933-982-98903
26	14.2	67.6	25	88	US-60-427-808-116595
27	14.2	67.6	25	108	US-60-427-808-122509
28	14.2	67.6	25	108	US-60-427-808-276673
29	14.2	67.6	50	124	US-60-585-352-43851
30	14.2	67.6	50	124	US-60-585-352-55437
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35	13.8	65.7	19	59	US-10-714-333A-765169
36	13.8	65.7	25	41	US-09-953-570A-91613
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38	13.8	65.7	25	42	US-09-956-584-124056
39	13.8	65.7	25	42	US-09-956-584-124063
40	13.8	65.7	25	60	US-10-719-900-480794
41	13.8	65.7	25	60	US-10-719-956-163542
42	13.8	65.7	25	64	US-10-933-982-104592
43	13.8	65.7	25	64	US-10-933-982-159094
44	13.8	65.7	25	64	US-10-933-982-175454
45	13.8	65.7	25	88	US-60-234-017-96996
46	13.8	65.7	25	88	US-60-234-017-96996
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48	13.8	65.7	25	108	US-60-427-808-480794
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51	13.8	65.7	25	116	US-60-507-481-164697
52	13.8	65.7	25	116	US-60-507-511-93185
53	13.8	65.7	25	41	US-09-953-570A-100602

55	13.6	64.8	25	41	US-09-954-427A-193341
56	13.6	64.8	25	41	US-09-954-427A-316725
57	13.6	64.8	25	52	US-10-355-577-598713
58	13.6	64.8	25	60	US-10-719-900-68584
59	13.6	64.8	25	60	US-10-719-900-152754
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62	13.6	64.8	25	60	US-10-719-900-641712
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65	13.6	64.8	25	60	US-10-719-956-219126
66	13.6	64.8	25	60	US-10-719-956-223074
67	13.6	64.8	25	64	US-10-933-982-174604
68	13.6	64.8	25	101	US-60-353-987-598713
69	13.6	64.8	25	108	US-60-427-808-68584
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71	13.6	64.8	25	108	US-60-427-808-172887
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79	13.6	64.8	25	116	US-60-507-511-172111
80	13.6	64.8	25	53	US-09-605-701-21002
81	13.6	64.8	39	53	US-10-401-229-21002
82	13.6	64.8	50	2	PCT-US03-18714-18545
83	13.6	64.8	50	124	US-60-585-352-45410
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85	13.4	63.8	19	59	US-10-714-333A-97981
86	13.4	63.8	19	59	US-10-714-333A-1334055
87	13.4	63.8	25	41	US-09-953-115-23932
88	13.4	63.8	25	42	US-09-956-584A-46142
89	13.4	63.8	25	42	US-09-956-584A-46154
90	13.4	63.8	25	42	US-09-956-584A-46154
91	13.4	63.8	25	57	US-10-681-773-91491
92	13.4	63.8	25	57	US-10-681-773-113094
93	13.4	63.8	25	60	US-10-719-900-839161
94	13.4	63.8	25	64	US-10-933-982-115457
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96	13.4	63.8	25	107	US-60-417-190-449
97	13.4	63.8	25	107	US-60-417-190-450
98	13.4	63.8	25	108	US-60-427-808-839161
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107	13.2	62.9	22	53	US-10-418-837-24
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115	13.2	62.9	25	42	US-09-956-584A-200293
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118	13.2	62.9	25	42	US-09-956-584A-502816
119	13.2	62.9	25	42	US-09-956-584A-596214
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121	13.2	62.9	25	57	US-10-681-773-18090
122	13.2	62.9	25	57	US-10-681-773-53108
123	13.2	62.9	25	57	US-10-719-900-70179
124	13.2	62.9	25	60	US-10-719-900-154870
125	13.2	62.9	25	60	US-10-719-900-155740
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149	13.2	62.9	25	107	US-60-417-190-5180	Sequence 5180, Ap	c 222	13	61.9	25	60	Sequence 147352,	Sequence 147352, A
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152	13.2	62.9	25	108	US-60-427-808-155740	Sequence 155740,	c 225	13	61.9	25	64	Sequence 170048,	Sequence 170048, A
153	13.2	62.9	25	108	US-60-427-808-202789	Sequence 202789,	c 226	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
154	13.2	62.9	25	108	US-60-427-808-315609	Sequence 315609,	c 227	13	61.9	25	64	Sequence 344745,	Sequence 344745, A
155	13.2	62.9	25	108	US-60-427-808-339476	Sequence 339476,	c 228	13	61.9	25	64	Sequence 32512, A	Sequence 32512, A
156	13.2	62.9	25	108	US-60-427-808-374194	Sequence 374194,	c 229	13	61.9	25	64	Sequence 32513, A	Sequence 32513, A
157	13.2	62.9	25	108	US-60-427-808-374195	Sequence 374195,	c 230	13	61.9	25	64	Sequence 32514, A	Sequence 32514, A
158	13.2	62.9	25	108	US-60-427-808-377255	Sequence 377255,	c 231	13	61.9	25	64	Sequence 74515, A	Sequence 74515, A
159	13.2	62.9	25	108	US-60-427-808-430290	Sequence 430290,	c 232	13	61.9	25	64	Sequence 104213,	Sequence 104213, A
160	13.2	62.9	25	108	US-60-427-808-630374	Sequence 630374,	c 233	13	61.9	25	64	Sequence 109823,	Sequence 109823, A
161	13.2	62.9	25	108	US-60-427-808-811694	Sequence 811694,	c 234	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
162	13.2	62.9	25	108	US-60-427-808-829245	Sequence 829245,	c 235	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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164	13.2	62.9	25	108	US-60-427-836-50694	Sequence 50694, A	c 237	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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167	13.2	62.9	25	108	US-60-427-836-388714	Sequence 388714,	c 240	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
168	13.2	62.9	25	108	US-60-427-836-680545	Sequence 680545,	c 241	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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173	13.2	62.9	25	116	US-60-507-481-179056	Sequence 179056,	c 246	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
174	13.2	62.9	25	116	US-60-507-511-34367	Sequence 34367, A	c 247	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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177	13.2	62.9	25	120	US-60-545-213-229423	Sequence 229423,	c 250	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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179	13.2	62.9	32	50	US-10-250-997-25	Sequence 25, Appl	c 252	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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181	13.2	62.9	35	2	PCT-US04-26344-117	Sequence 117, Appl	c 254	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
182	13.2	62.9	35	57	US-10-641-455A-117	Sequence 117, Appl	c 255	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
183	13.2	62.9	48	2	PCT-US03-02085-57	Sequence 57, Appl	c 256	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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186	13.2	62.9	50	124	US-60-585-352-89750	Sequence 89750, A	c 259	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
187	13	61.9	16	50	US-10-287-787-15500	Sequence 15500, A	c 260	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
188	13	61.9	16	50	US-10-287-787-26920	Sequence 26920, A	c 261	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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195	13	61.9	18	48	US-10-197-290-29	Sequence 29, Appl	c 268	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
196	13	61.9	18	52	US-10-388-263-182	Sequence 182, Appl	c 269	13	61.9	25	64	Sequence 176445,	Sequence 176445, A
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c 275	12.8	61.0	19	59	US-10-714-333A-342124	Sequence 342124,	348	12.8	61.0	25	88	US-60-234-049-1133939	Sequence 133939,
276	12.8	61.0	19	59	US-10-714-333A-468849	Sequence 468849,	349	12.8	61.0	25	108	US-60-427-808-168516	Sequence 168516,
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279	12.8	61.0	19	59	US-10-714-333A-1151256	Sequence 1151256,	c 352	12.8	61.0	25	108	US-60-427-808-177539	Sequence 177539,
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c 282	12.8	61.0	24	2	PCI-US02-40227A-8	Sequence 8, Appli	c 355	12.8	61.0	25	108	US-60-427-808-401285	Sequence 401285,
c 283	12.8	61.0	24	51	US-09-940-185-787	Sequence 787, App	c 356	12.8	61.0	25	108	US-60-427-808-401286	Sequence 401286,
c 284	12.8	61.0	24	51	US-10-320-231A-8	Sequence 8, Appli	c 357	12.8	61.0	25	108	US-60-427-808-513324	Sequence 513324,
c 285	12.8	61.0	24	63	US-10-819-039-20	Sequence 20, Appl	358	12.8	61.0	25	108	US-60-427-808-522969	Sequence 522969,
c 286	12.8	61.0	24	63	US-10-867-506-8	Sequence 8, Appli	359	12.8	61.0	25	108	US-60-427-808-559261	Sequence 559261,
c 287	12.8	61.0	25	40	US-09-940-185-4752	Sequence 4752, Ap	c 360	12.8	61.0	25	108	US-60-427-808-706664	Sequence 706664,
c 288	12.8	61.0	25	41	US-09-953-570A-28434	Sequence 28434, A	c 361	12.8	61.0	25	108	US-60-427-808-838207	Sequence 838207,
c 289	12.8	61.0	25	41	US-09-953-570A-77409	Sequence 77409, A	c 362	12.8	61.0	25	108	US-60-427-808-857738	Sequence 857738,
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c 291	12.8	61.0	25	41	US-09-954-427-34193	Sequence 34193, A	c 364	12.8	61.0	25	108	US-60-427-808-905085	Sequence 905085,
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c 293	12.8	61.0	25	41	US-09-954-427A-48691	Sequence 48691, A	c 366	12.8	61.0	25	108	US-60-427-836-509311	Sequence 509311,
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c 296	12.8	61.0	25	41	US-09-954-429-18604	Sequence 18604, A	c 369	12.8	61.0	25	116	US-60-507-481-77247	Sequence 77247, A
c 297	12.8	61.0	25	41	US-09-954-429B-18604	Sequence 18604, A	c 370	12.8	61.0	25	116	US-60-507-481-96989	Sequence 96989, A
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c 299	12.8	61.0	25	42	US-09-956-584A-24300	Sequence 24300, A	c 372	12.8	61.0	25	116	US-60-507-481-180069	Sequence 180069,
c 300	12.8	61.0	25	42	US-09-956-584A-211684	Sequence 211684,	c 373	12.8	61.0	25	116	US-60-507-511-45091	Sequence 45091, A
c 301	12.8	61.0	25	42	US-09-956-584A-248616	Sequence 248616,	c 374	12.8	61.0	25	116	US-60-507-511-55105	Sequence 55105, A
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c 303	12.8	61.0	25	42	US-09-956-584A-248630	Sequence 248630,	c 376	12.8	61.0	25	116	US-60-507-511-121605	Sequence 121605,
c 304	12.8	61.0	25	42	US-09-956-604-139744	Sequence 139744,	c 377	12.8	61.0	25	120	US-60-545-213-12015	Sequence 12015,
c 305	12.8	61.0	25	42	US-09-956-604-139745	Sequence 139745,	c 378	12.8	61.0	25	120	US-60-545-213-298921	Sequence 298921,
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c 307	12.8	61.0	25	42	US-09-956-604B-139744	Sequence 139744,	c 380	12.8	61.0	25	33	US-10-891-260-3420	Sequence 3420, Ap
c 308	12.8	61.0	25	42	US-09-956-604B-139745	Sequence 139745,	c 381	12.8	61.0	39	101	US-60-353-790-1988	Sequence 1988, Ap
c 309	12.8	61.0	25	42	US-09-956-604B-59826	Sequence 59826, A	c 382	12.8	61.0	39	101	US-60-353-790-1988	Sequence 1988, Ap
c 310	12.8	61.0	25	42	US-09-956-604D-120818	Sequence 120818,	c 383	12.8	61.0	50	93	US-60-585-353-60091	Sequence 60091, A
c 311	12.8	61.0	25	42	US-09-956-604D-136040	Sequence 136040,	c 384	12.8	61.0	50	124	US-60-585-353-63349	Sequence 63349, A
c 312	12.8	61.0	25	42	US-09-956-604D-136040	Sequence 136040,	c 385	12.8	61.0	50	124	US-60-585-353-67967	Sequence 67967, A
c 313	12.8	61.0	25	60	US-10-719-900-168516	Sequence 168516,	c 386	12.8	61.0	50	124	US-60-585-353-68574	Sequence 68574, A
c 314	12.8	61.0	25	60	US-10-719-900-169722	Sequence 169722,	c 387	12.8	61.0	50	124	US-60-585-353-82268	Sequence 82268, A
c 315	12.8	61.0	25	60	US-10-719-900-173391	Sequence 173391,	c 388	12.8	61.0	50	124	US-10-714-333A-1194033	Sequence 1194033,
c 316	12.8	61.0	25	60	US-10-719-900-177539	Sequence 177539,	c 389	12.6	60.0	19	59	US-10-289-762-3669	Sequence 3669, Ap
c 317	12.8	61.0	25	60	US-10-719-900-248519	Sequence 248519,	c 390	12.6	60.0	20	50	US-10-770-726-13622	Sequence 13622, A
c 318	12.8	61.0	25	60	US-10-719-900-360624	Sequence 360624,	c 391	12.6	60.0	21	61	US-10-770-726-14630	Sequence 14630, A
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c 322	12.8	61.0	25	60	US-10-719-900-522969	Sequence 522969,	c 395	12.6	60.0	25	20	US-09-396-196G-95290	Sequence 95290, A
c 323	12.8	61.0	25	60	US-10-719-900-559261	Sequence 559261,	c 396	12.6	60.0	25	20	US-09-396-196G-103159	Sequence 103159,
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c 325	12.8	61.0	25	60	US-10-719-900-838207	Sequence 838207,	c 398	12.6	60.0	25	32	US-09-754-853A-418	Sequence 418, App
c 326	12.8	61.0	25	60	US-10-719-900-857738	Sequence 857738,	c 399	12.6	60.0	25	41	US-09-953-115A-14594	Sequence 14594, A
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c 331	12.8	61.0	25	60	US-10-719-956-584226	Sequence 584226,	c 404	12.6	60.0	25	41	US-09-953-570A-107848	Sequence 107848,
c 332	12.8	61.0	25	60	US-10-933-982-102015	Sequence 102015,	c 405	12.6	60.0	25	41	US-09-954-427-29655	Sequence 29655, A
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c 335	12.8	61.0	25	64	US-10-933-982-68452	Sequence 68452, A	c 408	12.6	60.0	25	42	US-09-956-584-183108	Sequence 183108,
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c 344	12.8	61.0	25	68	US-10-933-982-222479	Sequence 222479,	c 417	12.6	60.0	25	42	US-09-956-584A-417549	Sequence 417549,
c 345	12.8	61.0	25	88	US-60-233-166-34193	Sequence 34193, A	c 418	12.6	60.0	25	42	US-09-956-604-8348	Sequence 8348, Ap
c 346	12.8	61.0	25	88	US-60-233-166-79773	Sequence 79773, A	c 419	12.6	60.0	25	42		

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C 421	12.6	60.0	25	42	US-09-956-604B-8348	Sequence 8348, Ap	494	12.6	60.0	25	108	US-60-427-808-880950	Sequence 880950,
C 422	12.6	60.0	25	42	US-09-956-604D-49799	Sequence 49799, A	495	12.6	60.0	25	108	US-60-427-808-929175	Sequence 929175,
C 423	12.6	60.0	25	42	US-09-956-604D-71928	Sequence 71928, A	496	12.6	60.0	25	108	US-60-427-836-89990	Sequence 89990, A
C 424	12.6	60.0	25	42	US-09-956-604D-140704	Sequence 140704, A	497	12.6	60.0	25	108	US-60-427-836-142557	Sequence 142557,
C 425	12.6	60.0	25	52	US-10-355-577-270500	Sequence 270500,	c 498	12.6	60.0	25	108	US-60-427-836-145988	Sequence 145988,
C 426	12.6	60.0	25	52	US-10-355-577-422372	Sequence 422372,	c 499	12.6	60.0	25	108	US-60-427-836-173166	Sequence 173166,
C 427	12.6	60.0	25	52	US-10-355-577-437303	Sequence 437303,	c 500	12.6	60.0	25	108	US-60-427-836-234400	Sequence 234400,
C 428	12.6	60.0	25	52	US-10-355-577-594010	Sequence 594010,	c 501	12.6	60.0	25	108	US-60-427-836-234401	Sequence 234401,
C 429	12.6	60.0	25	52	US-10-355-577-889379	Sequence 889379,	c 502	12.6	60.0	25	108	US-60-427-836-329028	Sequence 329028,
C 430	12.6	60.0	25	52	US-10-355-577-952475	Sequence 952475,	c 503	12.6	60.0	25	108	US-60-427-836-340925	Sequence 340925,
C 431	12.6	60.0	25	52	US-10-355-577-952476	Sequence 952476,	c 504	12.6	60.0	25	108	US-60-427-836-583417	Sequence 583417,
C 432	12.6	60.0	25	60	US-10-719-900-116596	Sequence 116596,	c 505	12.6	60.0	25	108	US-60-427-836-645692	Sequence 645692,
C 433	12.6	60.0	25	60	US-10-719-900-122510	Sequence 122510,	c 506	12.6	60.0	25	116	US-60-507-511-7144	Sequence 7144, Ap
C 434	12.6	60.0	25	60	US-10-719-900-126366	Sequence 126366,	c 507	12.6	60.0	25	116	US-60-507-511-90302	Sequence 90302, A
C 435	12.6	60.0	25	60	US-10-719-900-172673	Sequence 172673,	c 508	12.6	60.0	25	116	US-60-507-511-185079	Sequence 185079,
C 436	12.6	60.0	25	60	US-10-719-900-172674	Sequence 172674,	c 509	12.6	60.0	25	120	US-60-545-213-34143	Sequence 34143, A
C 437	12.6	60.0	25	60	US-10-719-900-282264	Sequence 282264,	c 510	12.6	60.0	25	120	US-60-545-213-34168	Sequence 34168, A
C 438	12.6	60.0	25	60	US-10-719-900-324816	Sequence 324816,	c 511	12.6	60.0	25	120	US-60-545-213-34169	Sequence 34169, A
C 439	12.6	60.0	25	60	US-10-719-900-340214	Sequence 340214,	c 512	12.6	60.0	25	120	US-60-545-213-126960	Sequence 126960,
C 440	12.6	60.0	25	60	US-10-719-900-444357	Sequence 444357,	c 513	12.6	60.0	25	120	US-60-545-213-171908	Sequence 171908,
C 441	12.6	60.0	25	60	US-10-719-900-550499	Sequence 550499,	c 514	12.6	60.0	25	120	US-60-545-213-171909	Sequence 171909,
C 442	12.6	60.0	25	60	US-10-719-900-762930	Sequence 762930,	c 515	12.6	60.0	25	120	US-60-545-213-263148	Sequence 263148,
C 443	12.6	60.0	25	60	US-10-719-900-775364	Sequence 775364,	c 516	12.6	60.0	33	63	US-10-891-260-7208	Sequence 7208, Ap
C 444	12.6	60.0	25	60	US-10-719-900-880950	Sequence 880950,	c 517	12.6	60.0	34	36	US-09-869-334-29	Sequence 29, Appl
C 445	12.6	60.0	25	60	US-10-719-900-929175	Sequence 929175,	c 518	12.6	60.0	34	36	US-09-869-334B-29	Sequence 29, Appl
C 446	12.6	60.0	25	60	US-10-719-956-89990	Sequence 89990, A	c 519	12.6	60.0	36	31	US-09-870-161-15043	Sequence 15043, A
C 447	12.6	60.0	25	60	US-10-719-956-142557	Sequence 142557,	c 520	12.6	60.0	36	36	US-09-870-161-15043	Sequence 15043, A
C 448	12.6	60.0	25	60	US-10-719-956-145988	Sequence 145988,	c 521	12.6	60.0	36	36	US-10-138-674-15043	Sequence 15043, A
C 449	12.6	60.0	25	60	US-10-719-956-173166	Sequence 173166,	c 522	12.6	60.0	36	47	US-10-138-674-15043	Sequence 15043, A
C 450	12.6	60.0	25	60	US-10-719-956-234400	Sequence 234400,	c 523	12.6	60.0	36	47	US-10-138-674-15043	Sequence 15043, A
C 451	12.6	60.0	25	60	US-10-719-956-329028	Sequence 329028,	c 524	12.6	60.0	36	47	US-10-138-674-15043	Sequence 15043, A
C 452	12.6	60.0	25	60	US-10-719-956-329028	Sequence 329028,	c 525	12.6	60.0	36	50	US-10-287-949A-15043	Sequence 15043, A
C 453	12.6	60.0	25	60	US-10-719-956-340925	Sequence 340925,	c 526	12.6	60.0	50	124	US-60-585-352-4889	Sequence 4889, Ap
C 454	12.6	60.0	25	60	US-10-719-956-583417	Sequence 583417,	c 527	12.6	60.0	50	124	US-60-585-352-57268	Sequence 57268, A
C 455	12.6	60.0	25	60	US-10-719-956-645692	Sequence 645692,	c 528	12.6	60.0	50	124	US-60-585-352-58213	Sequence 58213, A
C 456	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	c 529	12.6	60.0	50	124	US-60-585-352-63027	Sequence 63027, A
C 457	12.6	60.0	25	62	US-10-809-189-95290	Sequence 95290, A	c 530	12.6	60.0	50	124	US-60-585-352-63351	Sequence 63351, A
C 458	12.6	60.0	25	62	US-10-809-189-22389	Sequence 22389, A	c 531	12.6	60.0	50	124	US-60-585-352-103149	Sequence 103149,
C 459	12.6	60.0	25	63	US-10-859-198-22391	Sequence 22391, A	c 532	12.4	59.0	19	59	US-10-714-333A-97999	Sequence 97999, A
C 460	12.6	60.0	25	63	US-10-859-198-22391	Sequence 22391, A	c 533	12.4	59.0	19	59	US-10-714-333A-687118	Sequence 687118,
C 461	12.6	60.0	25	63	US-10-859-198-22393	Sequence 22393, A	c 534	12.4	59.0	19	59	US-10-714-333A-899294	Sequence 899294,
C 462	12.6	60.0	25	63	US-10-859-198-212779	Sequence 212779, A	c 535	12.4	59.0	19	59	US-10-714-333A-1307409	Sequence 1307409,
C 463	12.6	60.0	25	64	US-10-933-982-20755	Sequence 20755, A	c 536	12.4	59.0	19	59	US-10-714-333A-1428136	Sequence 1428136,
C 464	12.6	60.0	25	64	US-10-933-982-67868	Sequence 67868, A	c 537	12.4	59.0	21	31	US-09-318-970-29	Sequence 29, Appl
C 465	12.6	60.0	25	64	US-10-933-982-87996	Sequence 87996, A	c 538	12.4	59.0	21	31	US-09-715-849-184	Sequence 184, Appl
C 466	12.6	60.0	25	64	US-10-933-982-98901	Sequence 98901, A	c 539	12.4	59.0	23	54	US-10-499-886-8	Sequence 8, Appl
C 467	12.6	60.0	25	88	US-60-232-638-115899	Sequence 115899,	c 540	12.4	59.0	25	20	US-09-396-196F-4324	Sequence 4324, Ap
C 468	12.6	60.0	25	88	US-60-233-166-2291622	Sequence 2291622,	c 541	12.4	59.0	25	20	US-09-396-196F-59293	Sequence 59293, A
C 469	12.6	60.0	25	88	US-60-233-166-2291622	Sequence 2291622,	c 542	12.4	59.0	25	20	US-09-396-196F-93995	Sequence 93995, A
C 470	12.6	60.0	25	88	US-60-233-620-118507	Sequence 118507,	c 543	12.4	59.0	25	20	US-09-396-196F-93996	Sequence 93996, A
C 471	12.6	60.0	25	88	US-60-234-017-72587	Sequence 72587, A	c 544	12.4	59.0	25	20	US-09-396-196G-4324	Sequence 4324, Ap
C 472	12.6	60.0	25	88	US-60-234-017-72587	Sequence 72587, A	c 545	12.4	59.0	25	20	US-09-396-196G-59293	Sequence 59293, A
C 473	12.6	60.0	25	88	US-60-234-017-228634	Sequence 228634,	c 546	12.4	59.0	25	20	US-09-396-196G-93995	Sequence 93995, A
C 474	12.6	60.0	25	88	US-60-234-049-41998	Sequence 41998, A	c 547	12.4	59.0	25	20	US-09-396-196G-93996	Sequence 93996, A
C 475	12.6	60.0	25	101	US-60-353-987-270500	Sequence 270500,	c 548	12.4	59.0	25	29	US-09-660-222-22532	Sequence 22532, A
C 476	12.6	60.0	25	101	US-60-353-987-422372	Sequence 422372,	c 549	12.4	59.0	25	41	US-09-953-115A-6081	Sequence 6081, Ap
C 477	12.6	60.0	25	101	US-60-353-987-437303	Sequence 437303,	c 550	12.4	59.0	25	41	US-09-953-115A-11672	Sequence 11672, A
C 478	12.6	60.0	25	101	US-60-353-987-594010	Sequence 594010,	c 551	12.4	59.0	25	41	US-09-953-570A-27512	Sequence 27512, A
C 479	12.6	60.0	25	101	US-60-353-987-889379	Sequence 889379,	c 552	12.4	59.0	25	41	US-09-953-570A-76315	Sequence 76315, A
C 480	12.6	60.0	25	101	US-60-353-987-952475	Sequence 952475,	c 553	12.4	59.0	25	41	US-09-953-570A-83706	Sequence 83706, A
C 481	12.6	60.0	25	107	US-60-417-190-107293	Sequence 107293,	c 554	12.4	59.0	25	41	US-09-953-570A-83719	Sequence 83719, A
C 482	12.6	60.0	25	108	US-60-427-808-116596	Sequence 116596,	c 555	12.4	59.0	25	41	US-09-953-570A-106360	Sequence 106360,
C 483	12.6	60.0	25	108	US-60-427-808-122510	Sequence 122510,	c 556	12.4	59.0	25	41	US-09-954-427-175728	Sequence 175728,
C 484	12.6	60.0	25	108	US-60-427-808-126366	Sequence 126366,	c 557	12.4	59.0	25	41	US-09-954-427-175739	Sequence 175739, A
C 485	12.6	60.0	25	108	US-60-427-808-172673	Sequence 172673,	c 558	12.4	59.0	25	41	US-09-954-427A-12359	Sequence 12359, A
C 486	12.6	60.0	25	108	US-60-427-808-276674	Sequence 276674,	c 559	12.4	59.0	25	41	US-09-954-427A-12360	Sequence 12360, A
C 487	12.6	60.0	25	108	US-60-427-808-282264	Sequence 282264,	c 560	12.4	59.0	25	41	US-09-954-427A-44144	Sequence 44144, A
C 488	12.6	60.0	25	108	US-60-427-808-324816	Sequence 324816,	c 561	12.4	59.0	25	41	US-09-954-427A-98825	Sequence 98825, A
C 489	12.6	60.0	25	108	US-60-427-808-340214	Sequence 340214,	c 562	12.4	59.0	25	41	US-09-954-427A-98825	Sequence 98825, A
C 490	12.6	60.0	25	108	US-60-427-808-44357	Sequence 44357,	c 563	12.4	59.0	25	41	US-09-954-427A-369418	Sequence 369418, A
C 491	12.6	60.0	25	108	US-60-427-808-550499	Sequence 550499,	c 564	12.4	59.0	25	42	US-09-956-584-203927	Sequence 203927,
C 492	12.6	60.0	25	108	US-60-427-808-762930	Sequence 762930,	c 565	12.4	59.0	25	42	US-09-956-584A-3824	Sequence 3824, Ap

C 566	12.4	59.0	25	42	US-09-956-584A-3827	Sequence 3827, Ap	639	12.4	59.0	25	107	US-60-417-190-107295	Sequence 107295,
C 567	12.4	59.0	25	42	US-09-956-584A-3829	Sequence 3829, Ap	640	12.4	59.0	25	107	US-60-417-190-107296	Sequence 107296,
C 568	12.4	59.0	25	42	US-09-956-584A-3830	Sequence 3830, Ap	641	12.4	59.0	25	107	US-60-417-190-107297	Sequence 107297,
C 569	12.4	59.0	25	42	US-09-956-584A-23425	Sequence 23425, A	642	12.4	59.0	25	108	US-60-427-808-161435	Sequence 161435,
C 570	12.4	59.0	25	42	US-09-956-584A-23430	Sequence 23430, A	643	12.4	59.0	25	108	US-60-427-808-233524	Sequence 233524,
C 571	12.4	59.0	25	42	US-09-956-584A-23432	Sequence 23432, A	644	12.4	59.0	25	108	US-60-427-808-344380	Sequence 344380,
C 572	12.4	59.0	25	42	US-09-956-584A-27522	Sequence 27522, A	645	12.4	59.0	25	108	US-60-427-808-359916	Sequence 359916,
C 573	12.4	59.0	25	42	US-09-956-584A-85828	Sequence 85828, A	646	12.4	59.0	25	108	US-60-427-808-562857	Sequence 562857,
C 574	12.4	59.0	25	42	US-09-956-584A-254810	Sequence 254810, A	647	12.4	59.0	25	108	US-60-427-808-562867	Sequence 562867,
C 575	12.4	59.0	25	42	US-09-956-584A-254812	Sequence 254812, A	648	12.4	59.0	25	108	US-60-427-808-747133	Sequence 747133,
C 576	12.4	59.0	25	42	US-09-956-584A-271694	Sequence 271694, A	649	12.4	59.0	25	108	US-60-427-836-155490	Sequence 155490,
C 577	12.4	59.0	25	42	US-09-956-584A-319739	Sequence 319739, A	650	12.4	59.0	25	108	US-60-427-836-308010	Sequence 308010,
C 578	12.4	59.0	25	42	US-09-956-584A-319742	Sequence 319742, A	651	12.4	59.0	25	108	US-60-427-836-332284	Sequence 332284,
C 579	12.4	59.0	25	42	US-09-956-584A-319745	Sequence 319745, A	652	12.4	59.0	25	108	US-60-427-836-348030	Sequence 348030,
C 580	12.4	59.0	25	42	US-09-956-584A-319749	Sequence 319749, A	653	12.4	59.0	25	113	US-60-470-475-29307	Sequence 29307, A
C 581	12.4	59.0	25	42	US-09-956-604A-62461	Sequence 62461, A	654	12.4	59.0	25	113	US-60-470-475-33290	Sequence 33290, A
C 582	12.4	59.0	25	42	US-09-956-604A-84729	Sequence 84729, A	655	12.4	59.0	25	113	US-60-470-475-77421	Sequence 77421, A
C 583	12.4	59.0	25	42	US-09-956-604A-85117	Sequence 85117, A	656	12.4	59.0	25	113	US-60-470-475-93922	Sequence 93922, A
C 584	12.4	59.0	25	42	US-09-956-604A-85118	Sequence 85118, A	657	12.4	59.0	25	113	US-60-470-475-93922	Sequence 93922, A
C 585	12.4	59.0	25	42	US-09-956-604A-111820	Sequence 111820, A	658	12.4	59.0	25	113	US-60-470-475-118963	Sequence 118963,
C 586	12.4	59.0	25	42	US-09-956-604A-62461	Sequence 62461, A	659	12.4	59.0	25	116	US-60-507-481-47893	Sequence 47893, A
C 587	12.4	59.0	25	42	US-09-956-604A-84729	Sequence 84729, A	660	12.4	59.0	25	116	US-60-507-481-55930	Sequence 55930, A
C 588	12.4	59.0	25	42	US-09-956-604A-85117	Sequence 85117, A	661	12.4	59.0	25	116	US-60-507-481-76438	Sequence 76438, A
C 589	12.4	59.0	25	42	US-09-956-604A-85118	Sequence 85118, A	662	12.4	59.0	25	116	US-60-507-481-158546	Sequence 158546,
C 590	12.4	59.0	25	42	US-09-956-604A-111820	Sequence 111820, A	663	12.4	59.0	25	116	US-60-507-481-167178	Sequence 167178,
C 591	12.4	59.0	25	42	US-09-956-604B-62461	Sequence 62461, A	664	12.4	59.0	25	116	US-60-507-511-189916	Sequence 189916,
C 592	12.4	59.0	25	42	US-09-956-604B-84729	Sequence 84729, A	665	12.4	59.0	25	120	US-60-545-213-89482	Sequence 89482, A
C 593	12.4	59.0	25	42	US-09-956-604B-85117	Sequence 85117, A	666	12.4	59.0	25	120	US-60-545-213-89483	Sequence 89483, A
C 594	12.4	59.0	25	42	US-09-956-604B-85118	Sequence 85118, A	667	12.4	59.0	25	120	US-60-545-213-89489	Sequence 89489, A
C 595	12.4	59.0	25	42	US-09-956-604B-111820	Sequence 111820, A	668	12.4	59.0	25	120	US-60-545-213-89491	Sequence 89491, A
C 596	12.4	59.0	25	42	US-09-956-604B-49811	Sequence 49811, A	669	12.4	59.0	25	120	US-60-545-213-89499	Sequence 89499, A
C 597	12.4	59.0	25	46	US-10-098-263B-96896	Sequence 96896, A	670	12.4	59.0	25	120	US-60-545-213-160082	Sequence 160082,
C 598	12.4	59.0	25	46	US-10-098-263B-105617	Sequence 105617, A	671	12.4	59.0	25	120	US-60-545-213-267824	Sequence 267824,
C 599	12.4	59.0	25	52	US-10-355-577-170459	Sequence 170459, A	672	12.4	59.0	32	7	US-08-215-116A-15	Sequence 15, Appl
C 600	12.4	59.0	25	52	US-10-355-577-844405	Sequence 844405, A	673	12.4	59.0	32	7	US-08-215-116A-38	Sequence 38, Appl
C 601	12.4	59.0	25	57	US-10-681-773-29307	Sequence 29307, A	674	12.4	59.0	32	9	US-08-472-988A-15	Sequence 15, Appl
C 602	12.4	59.0	25	57	US-10-681-773-32290	Sequence 32290, A	675	12.4	59.0	32	9	US-08-472-988A-38	Sequence 38, Appl
C 603	12.4	59.0	25	57	US-10-681-773-77421	Sequence 77421, A	676	12.4	59.0	32	9	US-08-472-988B-15	Sequence 15, Appl
C 604	12.4	59.0	25	57	US-10-681-773-77422	Sequence 77422, A	677	12.4	59.0	32	9	US-08-472-988B-38	Sequence 38, Appl
C 605	12.4	59.0	25	57	US-10-681-773-93922	Sequence 93922, A	678	12.4	59.0	32	9	US-08-472-988C-38	Sequence 38, Appl
C 606	12.4	59.0	25	57	US-10-681-773-119863	Sequence 119863, A	679	12.4	59.0	32	9	US-08-472-988C-38	Sequence 38, Appl
C 607	12.4	59.0	25	60	US-10-719-900-161435	Sequence 161435, A	680	12.4	59.0	32	9	US-08-472-988D-15	Sequence 15, Appl
C 608	12.4	59.0	25	60	US-10-719-900-323524	Sequence 323524, A	681	12.4	59.0	32	9	US-08-472-988D-38	Sequence 38, Appl
C 609	12.4	59.0	25	60	US-10-719-900-344380	Sequence 344380, A	682	12.4	59.0	32	9	US-08-485-552A-15	Sequence 15, Appl
C 610	12.4	59.0	25	60	US-10-719-900-359916	Sequence 359916, A	683	12.4	59.0	32	9	US-08-485-552A-38	Sequence 38, Appl
C 611	12.4	59.0	25	60	US-10-719-900-562857	Sequence 562857, A	684	12.4	59.0	32	10	US-08-528-756-15	Sequence 15, Appl
C 612	12.4	59.0	25	60	US-10-719-900-664053	Sequence 664053, A	685	12.4	59.0	32	10	US-08-528-756-38	Sequence 38, Appl
C 613	12.4	59.0	25	60	US-10-719-900-747133	Sequence 747133, A	686	12.4	59.0	32	10	US-08-528-756A-49	Sequence 49, Appl
C 614	12.4	59.0	25	60	US-10-719-956-155490	Sequence 155490, A	687	12.4	59.0	32	10	US-08-528-756A-81	Sequence 81, Appl
C 615	12.4	59.0	25	60	US-10-719-956-308010	Sequence 308010, A	688	12.4	59.0	32	10	US-08-528-756B-49	Sequence 49, Appl
C 616	12.4	59.0	25	60	US-10-719-956-332284	Sequence 332284, A	689	12.4	59.0	32	10	US-08-528-756B-81	Sequence 81, Appl
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C 618	12.4	59.0	25	62	US-10-809-189-4324	Sequence 4324, Ap	691	12.4	59.0	42	2	PCT-US03-18714-14925	Sequence 14925, A
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C 620	12.4	59.0	25	62	US-10-809-189-93995	Sequence 93995, A	693	12.4	59.0	42	28	US-09-647-309A-133	Sequence 133, App
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C 770	12.2	58.1	25	41	US-09-954-427A-29695	Sequence 29695, A	C 843	12.2	58.1	25	42	US-09-956-604D-126177	Sequence 126177,
C 771	12.2	58.1	25	41	US-09-954-427A-64553	Sequence 64553, A	C 844	12.2	58.1	25	46	US-10-084-839-3753	Sequence 3753, Ap
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RESULT 1
US-10-087-631B-1
; Sequence 1, Application US/10087631B
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE OF INVENTION: CONTROL
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-087-631B-1

Query Match      100.0%; Score 21; DB 46; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
Db 1 AGCGCATGCCAGATTACTGGC 21

RESULT 2
US-10-419-022-1
; Sequence 1, Application US/10419022
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE OF INVENTION: CONTROL
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exempl
; OTHER INFORMATION: principle
US-10-419-022-1

Query Match      100.0%; Score 21; DB 53; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

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RESULT 3
US-09-953-570A-49187
; Sequence 49187, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49194
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; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49194

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

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RESULT 4
US-09-953-570A-49194
; Sequence 49194, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49194
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49194

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 2 GCGCATGCCAGATTACT 18
Db 2 GAGCATGCCAGATTACT 18

RESULT 5
US-10-719-900-152753
; Sequence 152753, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152753

Query Match      72.4%; Score 15.2; DB 60; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 1 AGAGCATGCCTGATTGCTGG 20
```

```
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49187

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 2 GCGCATGCCAGATTACT 18
Db 8 GAGCATGCCAGATTACT 24

RESULT 4
US-09-953-570A-49194
; Sequence 49194, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49194
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-49194

Query Match      73.3%; Score 15.4; DB 41; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.3e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 2 GCGCATGCCAGATTACT 18
Db 2 GAGCATGCCAGATTACT 18

RESULT 5
US-10-719-900-152753
; Sequence 152753, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152753

Query Match      72.4%; Score 15.2; DB 60; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 1 AGAGCATGCCTGATTGCTGG 20
```

RESULT 6

US-10-719-956-219125
; Sequence 219125, Application US/10719956
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

; PRIOR FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219125
; TYPE: DNA
; LENGTH: 25

; ORGANISM: Rattus norvegicus

US-10-719-956-219125

Query Match

Best Local Similarity 72.4%; Score 15.2; DB 60; Length 25;

Mismatches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20

DB 3 AGAGCATGCCAGTTTGCTGG 22

RESULT 7

US-60-427-808-152753
; Sequence 152753, Application US/60427808
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528

; CURRENT APPLICATION NUMBER: US/60/427,808

; CURRENT FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152753
; TYPE: DNA
; LENGTH: 25

; ORGANISM: Mus musculus

US-60-427-808-152753

Query Match

Best Local Similarity 72.4%; Score 15.2; DB 108; Length 25;

Mismatches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20

DB 1 AGAGCATGCCAGTTTGCTGG 20

RESULT 8

US-60-427-836-219125

; Sequence 219125, Application US/60427836
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527

; CURRENT APPLICATION NUMBER: US/60/427,836

; CURRENT FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219125
; TYPE: DNA
; LENGTH: 25

; ORGANISM: Rattus norvegicus

US-60-427-836-219125

Query Match

Best Local Similarity 72.4%; Score 15.2; DB 108; Length 25;

Mismatches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20

DB 3 AGAGCATGCCAGTTTGCTGG 22

RESULT 9

US-60-507-511-165285/c

; Sequence 165285, Application US/60507511
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: AM 101081

; CURRENT APPLICATION NUMBER: US/60/507,511

; CURRENT FILING DATE: 2003-10-02

; NUMBER OF SEQ ID NOS: 203623

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 165285

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-507-511-165285

Query Match

Best Local Similarity 71.4%; Score 15; DB 116; Length 25;

Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACT 18

DB 23 GCATGCCAGATTACT 9

RESULT 10

US-60-507-481-158095

; Sequence 158095, Application US/60507481
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; FILE REFERENCE: AM101084

; CURRENT APPLICATION NUMBER: US/60/507,481

; CURRENT FILING DATE: 2003-10-02

; NUMBER OF SEQ ID NOS: 210107

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 158095

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Canis familiaris

US-60-507-481-158095

Query Match

Best Local Similarity 70.5%; Score 14.8; DB 116; Length 25;

Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCATGCCAGATTACTG 19

DB 2 GAGCGTCCAGATTACTG 19

RESULT 11

US-60-507-481-158096

; Sequence 158096, Application US/60507481
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; FILE REFERENCE: AM101084

; CURRENT APPLICATION NUMBER: US/60/507,481

; CURRENT FILING DATE: 2003-10-02

; NUMBER OF SEQ ID NOS: 210107

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 158095

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Canis familiaris

US-60-507-481-158095

FILE REFERENCE: AM101084
CURRENT APPLICATION NUMBER: US/60/507,481
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 210107
SOFTWARE: PatentIn version 3.2
SEQ ID NO 158096
LENGTH: 25
TYPE: DNA
ORGANISM: Canis familiaris
US-60-507-481-158096

Query Match 70.5%; Score 14.8; DB 116; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GAGCGTGCAGATTACTG 19
| | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-09-956-604D-44625/c
Sequence 44625, Application US/09956604D
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604D
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
SEQ ID NO 44625
LENGTH: 25
TYPE: DNA
ORGANISM: E. coli
US-09-956-604D-44625

Query Match 68.6%; Score 14.4; DB 42; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ATGCCAGTTTACTGTC 5
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-956-604D-61437/c
Sequence 61437, Application US/09956604D
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604D
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
SEQ ID NO 61437
LENGTH: 25
TYPE: DNA
ORGANISM: E. coli
US-09-956-604D-61437

Query Match 68.6%; Score 14.4; DB 42; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGTC 21
| | | | | | | | | | | | | | | | | | | | | |

Db 16 ATGCCAGATAACTGGC 1
| | | | | | | | | | | | | | | | | | | | | |
RESULT 14
US-60-585-352-61322
Sequence 61322, Application US/60585352
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690
CURRENT APPLICATION NUMBER: US/60/585,352
CURRENT FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: TBD
PRIOR FILING DATE: TBD
NUMBER OF SEQ ID NOS: 116211
SOFTWARE: PatentIn version 3.2
SEQ ID NO 61322
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-60-585-352-61322

Query Match 68.6%; Score 14.4; DB 124; Length 50;
Best Local Similarity 83.3%; Pred. No. 8.8e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 23 GCAGCCAAATTATTGGC 40
| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-10-708-204-1327/c
Sequence 1327, Application US/10708204
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1327
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-1327

Query Match 67.6%; Score 14.2; DB 58; Length 22;
Best Local Similarity 84.2%; Pred. No. 1e+04; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 21 GCACATCCAGATGACTGG 3
| | | | | | | | | | | | | | | | | | | | | |

RESULT 16
US-09-953-570-116813/c
Sequence 116813, Application US/09953570
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110.1
CURRENT APPLICATION NUMBER: US/09/953,570
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/232,638
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 116813.
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
US-09-953-570A-116813

Query Match      67.6%; Score 14.2; DB 41; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACTGCG 21
    ||||| ||||| ||||| |||||
Db 24 CGCATGCCAGATTACTAGC 6

RESULT 17
US-09-953-570A-90293/c
; Sequence 90293, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-90293

Query Match      67.6%; Score 14.2; DB 41; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACTGCG 21
    ||||| ||||| ||||| |||||
Db 25 CGCATGCCAGATTACTGAC 7

RESULT 18
US-09-956-584A-596217
; Sequence 596217, Application US/09956584A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Genetic Analysis of Mouse
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 596217
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584A-596217

Query Match      67.6%; Score 14.2; DB 42; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTG 19
    ||||| ||||| ||||| |||||
Db 7 AGCACATTCAGATCACTG 25

RESULT 21
US-09-956-604D-42268/c
; Sequence 42268, Application US/09956604D
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604D
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
; SEQ ID NO 42268
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-09-956-604D-42268
```

Query Match 67.6%; Score 14.2; DB 42; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||
Db 19 GCGGATGCCGTTACTGG 1

RESULT 22
US-10-719-900-116595/c
; Sequence 116595, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116595
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-116595

Query Match 67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGG 20
||| ||||| ||||| |||
Db 23 GCACATGCCAGATTACTGG 5

RESULT 23
US-10-719-900-122509
; Sequence 122509, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 122509
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-122509

Query Match 67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGCATGCCAGATTACTGG 21
||| ||||| ||||| |||
Db 6 GCGCAGCCAGATAACCGC 24

RESULT 24
US-10-719-900-276673
; Sequence 276673, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276673
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-276673

Query Match 67.6%; Score 14.2; DB 60; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTG 19
||| ||||| ||||| |||
Db 4 AGATCATGCCATATTACTG 22

RESULT 25
US-10-933-982-98903
; Sequence 98903, Application US/10933982
; GENERAL INFORMATION:
; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 98903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-98903

Query Match 67.6%; Score 14.2; DB 64; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
||| ||||| ||||| |||
Db 4 CGCATGCCAGATTACTGGC 22

RESULT 26
US-60-232-638-116814/c
; Sequence 116814, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116814
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YNL237W
US-60-232-638-116814

Query Match 67.6%; Score 14.2; DB 88; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
||| ||||| ||||| |||
Db 24 CGCATGCAAGATTAAATAGC 6


```
; CURRENT APPLICATION NUMBER: US/60/585,352
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: TBD
; PRIOR FILING DATE: TBD
; NUMBER OF SEQ ID NOS: 116211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55437
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-60-585-352-55437

Query Match      67.6%; Score 14.2; DB 124; Length 50;
Best Local Similarity 76.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGGC 21
Db 31 AACCCRTGCTGGATTACTGGC 11

RESULT 33
US-09-953-570A-50875/c
; Sequence 50875, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-50875

Query Match      66.7%; Score 14; DB 41; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATT 15
Db 22 GCGCATGCCAGATT 9

RESULT 34
US-10-714-333A-748734/c
; Sequence 748734, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 748734
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-714-333A-748734

Query Match      65.7%; Score 13.8; DB 59; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
Db 17 GCATGCCACTACTGG 1

RESULT 35
US-10-714-333A-765169
; Sequence 765169, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 765169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-765169

Query Match      65.7%; Score 13.8; DB 59; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.6e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTAC 17
Db 3 AGCGCAUGUCAGAAUAC 19

RESULT 36
US-09-953-570A-91613
; Sequence 91613, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 91613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-953-570A-91613

Query Match      65.7%; Score 13.8; DB 41; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGATGCCAGATTACTG 19
Db 1 GCGATGCCAGATTCTCG 17
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RESULT 37
US-09-956-584-124055
; Sequence 124055, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124055
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124055
Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 3 CAAGCAAGATTACTGCG 19

RESULT 38
US-09-956-584-124056
; Sequence 124056, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124056
Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 3 CAAGCAAGATTACTGCG 19

RESULT 39
US-09-956-584-124063
; Sequence 124063, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124063
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-956-584-124063
Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 5 CAAGCAAGATTACTGCG 21
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; ORGANISM: Mus musculus
US-09-956-584-124063
Query Match      65.7%; Score 13.8; DB 42; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGCG 21
Db 4 CAAGCAAGATTACTGCG 20

RESULT 40
US-10-719-900-480794
; Sequence 480794, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 480794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-480794
Query Match      65.7%; Score 13.8; DB 60; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGCG 20
Db 7 GCATGCCAGATTACTGCG 23

Search completed: November 24, 2004, 03:15:11
Job time : 1381.58 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 17:30:18 ; Search time 26.2697 Seconds
(without alignments)
338.188 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgatgccagattactggc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 892029 seqs, 211525902 residues

Total number of hits satisfying chosen parameters: 1282072

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pending Patents NA, New: *

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
c	1	15	71.4	25	6	US-10-956-157-281467		Sequence 281467,
	2	14.8	70.5	25	6	US-10-956-160-158095		Sequence 158095,
	3	14.8	70.5	25	6	US-10-956-160-158096		Sequence 158096,
	4	13.8	65.7	25	6	US-10-956-157-209367		Sequence 209367,
	5	13.8	65.7	25	6	US-10-956-160-164697		Sequence 164697,
c	6	13.6	64.8	25	6	US-10-956-157-288293		Sequence 288293,
	7	13.6	64.8	25	6	US-10-956-160-119577		Sequence 119577,
c	8	13.2	62.9	25	6	US-10-956-157-150549		Sequence 150549,
	9	13.2	62.9	25	6	US-10-956-160-44697		Sequence 44697, A
	10	13.2	62.9	25	6	US-10-956-160-179056		Sequence 179056,
	11	13	61.9	25	6	US-10-956-160-109185		Sequence 109185,
	12	12.8	61.0	25	6	US-10-956-157-85795		Sequence 85795, A
	13	12.8	61.0	25	6	US-10-956-157-85796		Sequence 85796, A
	14	12.8	61.0	25	6	US-10-956-157-85797		Sequence 85797, A
	15	12.8	61.0	25	6	US-10-956-157-85802		Sequence 85802, A
	16	12.8	61.0	25	6	US-10-956-157-85805		Sequence 85805, A
	17	12.8	61.0	25	6	US-10-956-157-161273		Sequence 161273,
	18	12.8	61.0	25	6	US-10-956-157-171287		Sequence 171287,
c	19	12.8	61.0	25	6	US-10-956-157-210009		Sequence 210009,
	20	12.8	61.0	25	6	US-10-956-157-237787		Sequence 237787,
	21	12.8	61.0	25	6	US-10-956-160-16692		Sequence 16692, A
c	22	12.8	61.0	25	6	US-10-956-160-77247		Sequence 77247, A
	23	12.8	61.0	25	6	US-10-956-160-96989		Sequence 96989, A
c	24	12.8	61.0	25	6	US-10-956-160-159211		Sequence 159211,
	25	12.8	61.0	25	6	US-10-956-160-180069		Sequence 180069,

26	12.6	60.0	25	6	US-10-956-157-123326		Sequence 123326,
27	12.6	60.0	25	6	US-10-956-157-206484		Sequence 206484,
c	28	12.6	60.0	25	US-10-956-157-301261		Sequence 301261,
c	29	12.4	59.0	25	US-10-956-157-306098		Sequence 306098,
c	30	12.4	59.0	25	US-10-956-160-47893		Sequence 47893, A
c	31	12.4	59.0	25	US-10-956-160-55930		Sequence 55930, A
c	32	12.4	59.0	25	US-10-956-160-76438		Sequence 76438, A
c	33	12.4	59.0	25	US-10-956-160-158546		Sequence 158546,
c	34	12.4	59.0	25	US-10-956-160-167178		Sequence 167178,
c	35	12.4	59.0	28	US-10-489-273-35		Sequence 35, Appl
36	12.2	58.1	19	6	US-10-758-155-2666		Sequence 2666, Ap
37	12.2	58.1	19	6	US-10-758-155-2667		Sequence 2667, Ap
38	12.2	58.1	19	6	US-10-758-155-2732		Sequence 2732, Ap
39	12.2	58.1	19	6	US-10-758-155-2733		Sequence 2733, Ap
40	12.2	58.1	19	6	US-10-758-155-2738		Sequence 2738, Ap
41	12.2	58.1	19	6	US-10-758-155-2739		Sequence 2739, Ap
42	12.2	58.1	19	6	US-10-844-076-2666		Sequence 2666, Ap
43	12.2	58.1	19	6	US-10-844-076-2667		Sequence 2667, Ap
44	12.2	58.1	19	6	US-10-844-076-2732		Sequence 2732, Ap
45	12.2	58.1	19	6	US-10-844-076-2733		Sequence 2733, Ap
46	12.2	58.1	19	6	US-10-844-076-2738		Sequence 2738, Ap
47	12.2	58.1	19	6	US-10-844-076-2739		Sequence 2739, Ap
48	12.2	58.1	23	6	US-10-758-155-2576		Sequence 2576, Ap
49	12.2	58.1	23	6	US-10-758-155-2577		Sequence 2577, Ap
50	12.2	58.1	23	6	US-10-758-155-2582		Sequence 2582, Ap
51	12.2	58.1	23	6	US-10-758-155-2583		Sequence 2583, Ap
52	12.2	58.1	23	6	US-10-758-155-2588		Sequence 2588, Ap
53	12.2	58.1	23	6	US-10-758-155-2589		Sequence 2589, Ap
54	12.2	58.1	23	6	US-10-758-155-2630		Sequence 2630, Ap
55	12.2	58.1	23	6	US-10-758-155-2631		Sequence 2631, Ap
56	12.2	58.1	23	6	US-10-758-155-2636		Sequence 2636, Ap
57	12.2	58.1	23	6	US-10-758-155-2637		Sequence 2637, Ap
58	12.2	58.1	23	6	US-10-758-155-2643		Sequence 2643, Ap
59	12.2	58.1	23	6	US-10-758-155-2643		Sequence 2643, Ap
60	12.2	58.1	23	6	US-10-758-155-2648		Sequence 2648, Ap
61	12.2	58.1	23	6	US-10-758-155-2649		Sequence 2649, Ap
62	12.2	58.1	23	6	US-10-844-076-2576		Sequence 2576, Ap
63	12.2	58.1	23	6	US-10-844-076-2577		Sequence 2577, Ap
64	12.2	58.1	23	6	US-10-844-076-2582		Sequence 2582, Ap
65	12.2	58.1	23	6	US-10-844-076-2583		Sequence 2583, Ap
66	12.2	58.1	23	6	US-10-844-076-2588		Sequence 2588, Ap
67	12.2	58.1	23	6	US-10-844-076-2589		Sequence 2589, Ap
68	12.2	58.1	23	6	US-10-844-076-2630		Sequence 2630, Ap
69	12.2	58.1	23	6	US-10-844-076-2631		Sequence 2631, Ap
70	12.2	58.1	23	6	US-10-844-076-2636		Sequence 2636, Ap
71	12.2	58.1	23	6	US-10-844-076-2637		Sequence 2637, Ap
72	12.2	58.1	23	6	US-10-844-076-2642		Sequence 2642, Ap
73	12.2	58.1	23	6	US-10-844-076-2643		Sequence 2643, Ap
74	12.2	58.1	23	6	US-10-844-076-2648		Sequence 2648, Ap
75	12.2	58.1	23	6	US-10-844-076-2649		Sequence 2649, Ap
c	76	12.2	58.1	25	US-10-956-157-216754		Sequence 216754,
c	77	12.2	58.1	25	US-10-956-160-84311		Sequence 84311, A
c	78	12.2	58.1	25	US-10-956-160-146866		Sequence 146866,
c	79	12.2	58.1	25	US-10-956-160-151959		Sequence 151959,
c	80	12.2	58.1	25	US-10-956-160-158894		Sequence 158894,
c	81	12.2	58.1	25	US-10-956-160-183781		Sequence 183781,
c	82	12.2	58.1	44	US-10-861-930-13		Sequence 13, Appl
c	83	12	57.1	25	US-10-956-157-137663		Sequence 137663,
c	84	12	57.1	25	US-10-956-157-139568		Sequence 139568,
c	85	12	57.1	25	US-10-956-157-146425		Sequence 146425,
c	86	12	57.1	25	US-10-956-157-146578		Sequence 146578,
c	87	12	57.1	25	US-10-956-157-200742		Sequence 200742,
c	88	12	57.1	25	US-10-956-157-202625		Sequence 202625,
c	89	12	57.1	25	US-10-956-157-203787		Sequence 203787,
c	90	12	57.1	25	US-10-956-157-221776		Sequence 221776,
c	91	12	57.1	25	US-10-956-157-234899		Sequence 234899,
c	92	12	57.1	25	US-10-956-157-253573		Sequence 253573,
c	93	12	57.1	25	US-10-956-157-262123		Sequence 262123,
c	94	12	57.1	25	US-10-956-157-276584		Sequence 276584,
c	95	12	57.1	25	US-10-956-157-287655		Sequence 287655,
c	96	12	57.1	25	US-10-956-157-287752		Sequence 287752,
c	97	12	57.1	25	US-10-956-157-294027		Sequence 294027,
c	98	12	57.1	25	US-10-956-157-295281		Sequence 295281,

c 99	12	57.1	25	6	US-10-956-157-295380	Sequence 295380,	172	11.6	55.2	25	6	US-10-956-160-44145	Sequence 44145, A
c 100	12	57.1	25	6	US-10-956-160-14295	Sequence 14295, A	c 173	11.6	55.2	25	6	US-10-956-160-45807	Sequence 45807, A
c 101	12	57.1	25	6	US-10-956-160-23663	Sequence 23663, A	c 174	11.6	55.2	25	6	US-10-956-160-51729	Sequence 51729, A
c 102	12	57.1	25	6	US-10-956-160-27651	Sequence 27651, A	c 175	11.6	55.2	25	6	US-10-956-160-74424	Sequence 74424, A
c 103	12	57.1	25	6	US-10-956-160-46429	Sequence 46429, A	c 176	11.6	55.2	25	6	US-10-956-160-77410	Sequence 77410, A
c 104	12	57.1	25	6	US-10-956-160-49344	Sequence 49344, A	c 177	11.6	55.2	25	6	US-10-956-160-77411	Sequence 77411, A
c 105	12	57.1	25	6	US-10-956-160-145971	Sequence 145971,	c 178	11.6	55.2	25	6	US-10-956-160-77484	Sequence 77484, A
c 106	12	57.1	25	6	US-10-511-278-11	Sequence 11, Appl	c 179	11.6	55.2	25	6	US-10-956-160-99187	Sequence 99187, A
c 107	12	57.1	29	6	US-10-915-740A-1060	Sequence 1060, Ap	c 180	11.6	55.2	25	6	US-10-956-160-99188	Sequence 99188, A
c 108	11.8	56.2	25	6	US-10-956-157-131869	Sequence 131869,	c 181	11.6	55.2	25	6	US-10-956-160-99189	Sequence 99189, A
c 109	11.8	56.2	25	6	US-10-956-157-139316	Sequence 139316,	c 182	11.6	55.2	25	6	US-10-956-160-99190	Sequence 99190, A
c 110	11.8	56.2	25	6	US-10-956-157-139317	Sequence 139317,	c 183	11.6	55.2	25	6	US-10-956-160-109584	Sequence 109584, A
c 111	11.8	56.2	25	6	US-10-956-157-143397	Sequence 143397,	c 184	11.6	55.2	25	6	US-10-956-160-114168	Sequence 114168, A
c 112	11.8	56.2	25	6	US-10-956-157-148550	Sequence 148550,	c 185	11.6	55.2	25	6	US-10-956-160-132693	Sequence 132693, A
c 113	11.8	56.2	25	6	US-10-956-157-152698	Sequence 152698,	c 186	11.6	55.2	25	6	US-10-956-160-137239	Sequence 137239, A
c 114	11.8	56.2	25	6	US-10-956-157-153801	Sequence 153801,	c 187	11.6	55.2	25	6	US-10-956-160-137240	Sequence 137240, A
c 115	11.8	56.2	25	6	US-10-956-157-172027	Sequence 172027,	c 188	11.6	55.2	25	6	US-10-956-160-137241	Sequence 137241, A
c 116	11.8	56.2	25	6	US-10-956-157-176331	Sequence 176331,	c 189	11.6	55.2	25	6	US-10-956-160-143201	Sequence 143201, A
c 117	11.8	56.2	25	6	US-10-956-157-187594	Sequence 187594,	c 190	11.6	55.2	25	6	US-10-956-160-163933	Sequence 163933, A
c 118	11.8	56.2	25	6	US-10-956-157-194089	Sequence 194089,	c 191	11.6	55.2	25	6	US-10-956-160-168075	Sequence 168075, A
c 119	11.8	56.2	25	6	US-10-956-157-199823	Sequence 199823,	c 192	11.6	55.2	39	6	US-10-794-381-4	Sequence 4, Appl
c 120	11.8	56.2	25	6	US-10-956-157-209554	Sequence 209554,	c 193	11.6	55.2	39	6	US-10-794-381-6	Sequence 6, Appl
c 121	11.8	56.2	25	6	US-10-956-157-215284	Sequence 215284,	c 194	11.4	54.3	23	6	US-10-758-155-2626	Sequence 2626, Ap
c 122	11.8	56.2	25	6	US-10-956-157-228761	Sequence 228761,	c 195	11.4	54.3	23	6	US-10-758-155-2627	Sequence 2627, Ap
c 123	11.8	56.2	25	6	US-10-956-157-228733	Sequence 228733,	c 196	11.4	54.3	23	6	US-10-758-155-2629	Sequence 2629, Ap
c 124	11.8	56.2	25	6	US-10-956-157-260706	Sequence 260706,	c 197	11.4	54.3	23	6	US-10-758-155-2632	Sequence 2632, Ap
c 125	11.8	56.2	25	6	US-10-956-157-282908	Sequence 282908,	c 198	11.4	54.3	23	6	US-10-758-155-2633	Sequence 2633, Ap
c 126	11.8	56.2	25	6	US-10-956-157-285821	Sequence 285821,	c 199	11.4	54.3	23	6	US-10-758-155-2635	Sequence 2635, Ap
c 127	11.8	56.2	25	6	US-10-956-157-303700	Sequence 303700,	c 200	11.4	54.3	23	6	US-10-758-155-2638	Sequence 2638, Ap
c 128	11.8	56.2	25	6	US-10-956-160-13834	Sequence 13834, A	c 201	11.4	54.3	23	6	US-10-758-155-2639	Sequence 2639, Ap
c 129	11.8	56.2	25	6	US-10-956-160-21601	Sequence 21601, A	c 202	11.4	54.3	23	6	US-10-758-155-2641	Sequence 2641, Ap
c 130	11.8	56.2	25	6	US-10-956-160-27492	Sequence 27492, A	c 203	11.4	54.3	23	6	US-10-844-076-2626	Sequence 2626, Ap
c 131	11.8	56.2	25	6	US-10-956-160-36475	Sequence 36475, A	c 204	11.4	54.3	23	6	US-10-844-076-2627	Sequence 2627, Ap
c 132	11.8	56.2	25	6	US-10-956-160-69812	Sequence 69812, A	c 205	11.4	54.3	23	6	US-10-844-076-2629	Sequence 2629, Ap
c 133	11.8	56.2	25	6	US-10-956-160-81536	Sequence 81536, A	c 206	11.4	54.3	23	6	US-10-844-076-2632	Sequence 2632, Ap
c 134	11.8	56.2	25	6	US-10-956-160-88024	Sequence 88024, A	c 207	11.4	54.3	23	6	US-10-844-076-2633	Sequence 2633, Ap
c 135	11.8	56.2	25	6	US-10-956-160-95371	Sequence 95371, A	c 208	11.4	54.3	23	6	US-10-844-076-2635	Sequence 2635, Ap
c 136	11.8	56.2	25	6	US-10-956-160-114349	Sequence 114349,	c 209	11.4	54.3	23	6	US-10-844-076-2638	Sequence 2638, Ap
c 137	11.8	56.2	25	6	US-10-956-160-172910	Sequence 172910,	c 210	11.4	54.3	23	6	US-10-844-076-2639	Sequence 2639, Ap
c 138	11.8	56.2	25	6	US-10-956-160-178450	Sequence 178450,	c 211	11.4	54.3	23	6	US-10-844-076-2641	Sequence 2641, Ap
c 139	11.8	56.2	25	6	US-10-956-160-188185	Sequence 188185,	c 212	11.4	54.3	25	6	US-10-956-157-117342	Sequence 117342, A
c 140	11.8	56.2	25	6	US-10-956-160-186221	Sequence 186221,	c 213	11.4	54.3	25	6	US-10-956-157-117358	Sequence 117358, A
c 141	11.8	56.2	25	6	US-10-956-160-198152	Sequence 198152,	c 214	11.4	54.3	25	6	US-10-956-157-122450	Sequence 122450, A
c 142	11.8	56.2	25	6	US-10-956-160-198198	Sequence 198198,	c 215	11.4	54.3	25	6	US-10-956-157-139796	Sequence 139796, A
c 143	11.8	56.2	25	6	US-10-956-160-199131	Sequence 199131,	c 216	11.4	54.3	25	6	US-10-956-157-143574	Sequence 143574, A
c 144	11.6	55.2	20	6	US-10-831-286A-31266	Sequence 31266, A	c 217	11.4	54.3	25	6	US-10-956-157-147277	Sequence 147277, A
c 145	11.6	55.2	20	6	US-10-831-286A-41161	Sequence 41161, A	c 218	11.4	54.3	25	6	US-10-956-157-147360	Sequence 147360, A
c 146	11.6	55.2	20	6	US-10-831-286A-41771	Sequence 41771, A	c 219	11.4	54.3	25	6	US-10-956-157-160076	Sequence 160076, A
c 147	11.6	55.2	22	6	US-10-982-908-9	Sequence 9, Appl	c 220	11.4	54.3	25	6	US-10-956-157-161592	Sequence 161592, A
c 148	11.6	55.2	25	6	US-10-956-157-96913	Sequence 96913, A	c 221	11.4	54.3	25	6	US-10-956-157-162125	Sequence 162125, A
c 149	11.6	55.2	25	6	US-10-956-157-96921	Sequence 96921, A	c 222	11.4	54.3	25	6	US-10-956-157-162212	Sequence 162212, A
c 150	11.6	55.2	25	6	US-10-956-157-96922	Sequence 96922, A	c 223	11.4	54.3	25	6	US-10-956-157-162275	Sequence 162275, A
c 151	11.6	55.2	25	6	US-10-956-157-96924	Sequence 96924, A	c 224	11.4	54.3	25	6	US-10-956-157-162757	Sequence 162757, A
c 152	11.6	55.2	25	6	US-10-956-157-96927	Sequence 96927, A	c 225	11.4	54.3	25	6	US-10-956-157-173874	Sequence 173874, A
c 153	11.6	55.2	25	6	US-10-956-157-119257	Sequence 119257,	c 226	11.4	54.3	25	6	US-10-956-157-181911	Sequence 181911, A
c 154	11.6	55.2	25	6	US-10-956-157-135305	Sequence 135305,	c 227	11.4	54.3	25	6	US-10-956-157-199554	Sequence 199554, A
c 155	11.6	55.2	25	6	US-10-956-157-154958	Sequence 154958,	c 228	11.4	54.3	25	6	US-10-956-157-217732	Sequence 217732, A
c 156	11.6	55.2	25	6	US-10-956-157-161796	Sequence 161796,	c 229	11.4	54.3	25	6	US-10-956-157-224402	Sequence 224402, A
c 157	11.6	55.2	25	6	US-10-956-157-162594	Sequence 162594,	c 230	11.4	54.3	25	6	US-10-956-157-226730	Sequence 226730, A
c 158	11.6	55.2	25	6	US-10-956-157-162697	Sequence 162697,	c 231	11.4	54.3	25	6	US-10-956-157-235221	Sequence 235221, A
c 159	11.6	55.2	25	6	US-10-956-157-175369	Sequence 175369,	c 232	11.4	54.3	25	6	US-10-956-157-240801	Sequence 240801, A
c 160	11.6	55.2	25	6	US-10-956-157-184921	Sequence 184921,	c 233	11.4	54.3	25	6	US-10-956-157-270645	Sequence 270645, A
c 161	11.6	55.2	25	6	US-10-956-157-205338	Sequence 205338,	c 234	11.4	54.3	25	6	US-10-956-157-276531	Sequence 276531, A
c 162	11.6	55.2	25	6	US-10-956-157-230773	Sequence 230773,	c 235	11.4	54.3	25	6	US-10-956-157-289404	Sequence 289404, A
c 163	11.6	55.2	25	6	US-10-956-157-244385	Sequence 244385,	c 236	11.4	54.3	25	6	US-10-956-157-304429	Sequence 304429, A
c 164	11.6	55.2	25	6	US-10-956-157-294343	Sequence 294343,	c 237	11.4	54.3	25	6	US-10-956-160-30509	Sequence 30509, A
c 165	11.6	55.2	25	6	US-10-956-157-294493	Sequence 294493,	c 238	11.4	54.3	25	6	US-10-956-160-49063	Sequence 49063, A
c 166	11.6	55.2	25	6	US-10-956-157-302855	Sequence 302855,	c 239	11.4	54.3	25	6	US-10-956-160-50221	Sequence 50221, A
c 167	11.6	55.2	25	6	US-10-956-157-305232	Sequence 305232,	c 240	11.4	54.3	25	6	US-10-956-160-56053	Sequence 56053, A
c 168	11.6	55.2	25	6	US-10-956-157-305233	Sequence 305233,	c 241	11.4	54.3	25	6	US-10-956-160-93359	Sequence 93359, A
c 169	11.6	55.2	25	6	US-10-956-157-315420	Sequence 315420,	c 242	11.4	54.3	25	6	US-10-956-160-103344	Sequence 103344, A
c 170	11.6	55.2	25	6	US-10-956-160-31988	Sequence 31988, A	c 243	11.4	54.3	25	6	US-10-956-160-118549	Sequence 118549, A
c 171	11.6	55.2	25	6	US-10-956-160-40448	Sequence 40448, A	c 244	11.4	54.3	25	6	US-10-956-160-118898	Sequence 118898, A

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c 246	11.4	54.3	25	6	US-10-956-160-124102	Sequence 124102,	c 319	11.2	53.3	25	6	US-10-956-160-122293	Sequence 122293,
c 247	11.4	54.3	25	6	US-10-956-160-141151	Sequence 141151,	c 320	11.2	53.3	25	6	US-10-956-160-146207	Sequence 146207,
248	11.4	54.3	25	6	US-10-956-160-153468	Sequence 153468,	c 321	11.2	53.3	25	6	US-10-956-160-153672	Sequence 153672,
249	11.4	54.3	25	6	US-10-956-160-162898	Sequence 162898,	c 322	11.2	53.3	25	6	US-10-956-160-158902	Sequence 158902,
250	11.4	54.3	25	6	US-10-956-160-180912	Sequence 180912,	c 323	11.2	53.3	25	6	US-10-956-160-163418	Sequence 163418,
251	11.4	54.3	25	6	US-10-956-160-206545	Sequence 206545,	c 324	11.2	53.3	25	6	US-10-956-160-172926	Sequence 172926,
c 252	11.4	54.3	44	5	US-09-749-280C-1766	Sequence 1766, Ap	c 325	11.2	53.3	25	6	US-10-956-160-178493	Sequence 178493,
253	11.2	53.3	17	6	US-10-722-939-582	Sequence 582, App	c 326	11.2	53.3	25	6	US-10-956-160-182311	Sequence 182311,
254	11.2	53.3	19	6	US-10-758-155-2672	Sequence 2672, Ap	c 327	11.2	53.3	25	6	US-10-956-160-201269	Sequence 201269,
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257	11.2	53.3	19	6	US-10-758-155-2727	Sequence 2727, Ap	c 330	11.2	53.3	31	1	PCT-US04-36459-29	Sequence 29, Appl
258	11.2	53.3	19	6	US-10-844-076-2672	Sequence 2672, Ap	c 331	11.2	53.3	34	5	US-09-749-280C-1321	Sequence 49, Appl
259	11.2	53.3	19	6	US-10-844-076-2673	Sequence 2673, Ap	c 332	11.2	53.3	50	5	US-09-749-280C-7567	Sequence 1321, Ap
260	11.2	53.3	19	6	US-10-844-076-2726	Sequence 2726, Ap	c 333	11.2	53.3	50	5	US-10-831-286A-1263	Sequence 7567, Ap
261	11.2	53.3	19	6	US-10-844-076-2727	Sequence 2727, Ap	c 334	11	52.4	20	6	US-10-831-286A-1263	Sequence 669, App
c 262	11.2	53.3	20	1	PCT-US04-31673-178	Sequence 178, App	c 335	11	52.4	20	6	US-10-831-286A-1263	Sequence 1263, Ap
c 263	11.2	53.3	20	1	PCT-US04-31673-260	Sequence 260, App	c 336	11	52.4	20	6	US-10-831-286A-1263	Sequence 1263, Ap
c 264	11.2	53.3	20	6	US-10-983-197-20	Sequence 20, Appl	c 337	11	52.4	20	6	US-10-831-286A-1263	Sequence 1263, Ap
265	11.2	53.3	20	6	US-10-983-197-97	Sequence 97, Appl	c 338	11	52.4	21	6	US-10-974-036-57	Sequence 19297, A
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267	11.2	53.3	23	6	US-10-758-155-2625	Sequence 2625, Ap	c 340	11	52.4	25	5	US-09-999-829B-240	Sequence 240, App
268	11.2	53.3	23	6	US-10-844-076-2624	Sequence 2624, Ap	c 341	11	52.4	25	6	US-10-949-845-9	Sequence 9, Appl
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c 270	11.2	53.3	25	6	US-10-956-157-12070	Sequence 12070, A	c 343	11	52.4	25	6	US-10-956-157-137600	Sequence 137600,
c 271	11.2	53.3	25	6	US-10-956-157-12074	Sequence 12074, A	c 344	11	52.4	25	6	US-10-956-157-138153	Sequence 138153,
c 272	11.2	53.3	25	6	US-10-956-157-23846	Sequence 23846, A	c 345	11	52.4	25	6	US-10-956-157-145300	Sequence 145300,
c 273	11.2	53.3	25	6	US-10-956-157-23847	Sequence 23847, A	c 346	11	52.4	25	6	US-10-956-157-146111	Sequence 146111,
c 274	11.2	53.3	25	6	US-10-956-157-23848	Sequence 23848, A	c 347	11	52.4	25	6	US-10-956-157-147417	Sequence 147417,
c 275	11.2	53.3	25	6	US-10-956-157-23850	Sequence 23850, A	c 348	11	52.4	25	6	US-10-956-157-151571	Sequence 151571,
c 276	11.2	53.3	25	6	US-10-956-157-23853	Sequence 23853, A	c 349	11	52.4	25	6	US-10-956-157-152484	Sequence 152484,
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c 279	11.2	53.3	25	6	US-10-956-157-26136	Sequence 26136, A	c 352	11	52.4	25	6	US-10-956-157-155829	Sequence 155829,
c 280	11.2	53.3	25	6	US-10-956-157-47065	Sequence 47065, A	c 353	11	52.4	25	6	US-10-956-157-174958	Sequence 174958,
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c 283	11.2	53.3	25	6	US-10-956-157-96925	Sequence 96925, A	c 356	11	52.4	25	6	US-10-956-157-193285	Sequence 193285,
c 284	11.2	53.3	25	6	US-10-956-157-148052	Sequence 148052, A	c 357	11	52.4	25	6	US-10-956-157-200982	Sequence 200982,
c 285	11.2	53.3	25	6	US-10-956-157-148625	Sequence 148625, A	c 358	11	52.4	25	6	US-10-956-157-201074	Sequence 201074,
c 286	11.2	53.3	25	6	US-10-956-157-160202	Sequence 160202, A	c 359	11	52.4	25	6	US-10-956-157-203344	Sequence 203344,
c 287	11.2	53.3	25	6	US-10-956-157-162383	Sequence 162383, A	c 360	11	52.4	25	6	US-10-956-157-205007	Sequence 205007,
c 288	11.2	53.3	25	6	US-10-956-157-163977	Sequence 163977, A	c 361	11	52.4	25	6	US-10-956-157-207341	Sequence 207341,
c 289	11.2	53.3	25	6	US-10-956-157-168316	Sequence 168316, A	c 362	11	52.4	25	6	US-10-956-157-208841	Sequence 208841,
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c 291	11.2	53.3	25	6	US-10-956-157-192006	Sequence 192006, A	c 364	11	52.4	25	6	US-10-956-157-214773	Sequence 214773,
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c 293	11.2	53.3	25	6	US-10-956-157-200732	Sequence 200732, A	c 366	11	52.4	25	6	US-10-956-157-257984	Sequence 257984,
c 294	11.2	53.3	25	6	US-10-956-157-201272	Sequence 201272, A	c 367	11	52.4	25	6	US-10-956-157-262762	Sequence 262762,
c 295	11.2	53.3	25	6	US-10-956-157-201626	Sequence 201626, A	c 368	11	52.4	25	6	US-10-956-157-269827	Sequence 269827,
c 296	11.2	53.3	25	6	US-10-956-157-203928	Sequence 203928, A	c 369	11	52.4	25	6	US-10-956-157-270897	Sequence 270897,
c 297	11.2	53.3	25	6	US-10-956-157-216988	Sequence 216988, A	c 370	11	52.4	25	6	US-10-956-157-277319	Sequence 277319,
c 298	11.2	53.3	25	6	US-10-956-157-225156	Sequence 225156, A	c 371	11	52.4	25	6	US-10-956-157-280569	Sequence 280569,
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c 300	11.2	53.3	25	6	US-10-956-157-253324	Sequence 253324, A	c 373	11	52.4	25	6	US-10-956-157-284400	Sequence 284400,
c 301	11.2	53.3	25	6	US-10-956-157-253325	Sequence 253325, A	c 374	11	52.4	25	6	US-10-956-157-297394	Sequence 297394,
c 302	11.2	53.3	25	6	US-10-956-157-258788	Sequence 258788, A	c 375	11	52.4	25	6	US-10-956-157-303699	Sequence 303699,
c 303	11.2	53.3	25	6	US-10-956-157-274693	Sequence 274693, A	c 376	11	52.4	25	6	US-10-956-157-308988	Sequence 308988,
c 304	11.2	53.3	25	6	US-10-956-157-279272	Sequence 279272, A	c 377	11	52.4	25	6	US-10-956-160-15623	Sequence 15623, A
c 305	11.2	53.3	25	6	US-10-956-157-295387	Sequence 295387, A	c 378	11	52.4	25	6	US-10-956-160-30099	Sequence 30099, A
c 306	11.2	53.3	25	6	US-10-956-157-311027	Sequence 311027, A	c 379	11	52.4	25	6	US-10-956-160-32887	Sequence 32887, A
c 307	11.2	53.3	25	6	US-10-956-157-312846	Sequence 312846, A	c 380	11	52.4	25	6	US-10-956-160-50447	Sequence 50447, A
c 308	11.2	53.3	25	6	US-10-956-160-18137	Sequence 18137, A	c 381	11	52.4	25	6	US-10-956-160-51728	Sequence 51728, A
c 309	11.2	53.3	25	6	US-10-956-160-21192	Sequence 21192, A	c 382	11	52.4	25	6	US-10-956-160-84133	Sequence 84133, A
c 310	11.2	53.3	25	6	US-10-956-160-65734	Sequence 65734, A	c 383	11	52.4	25	6	US-10-956-160-93380	Sequence 93380, A
c 311	11.2	53.3	25	6	US-10-956-160-79165	Sequence 79165, A	c 384	11	52.4	25	6	US-10-956-160-94808	Sequence 94808, A
c 312	11.2	53.3	25	6	US-10-956-160-81718	Sequence 81718, A	c 385	11	52.4	25	6	US-10-956-160-96740	Sequence 96740, A
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c 314	11.2	53.3	25	6	US-10-956-160-90277	Sequence 90277, A	c 387	11	52.4	25	6	US-10-956-160-97798	Sequence 97798, A
c 315	11.2	53.3	25	6	US-10-956-160-94263	Sequence 94263, A	c 388	11	52.4	25	6	US-10-956-160-98480	Sequence 98480, A
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c 317	11.2	53.3	25	6	US-10-956-160-114535	Sequence 114535, A	c 390	11	52.4	25	6	US-10-956-160-98605	Sequence 98605, A

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C 393	11	52.4	25	6	US-10-956-160-98608	Sequence 98608, A	466	10.8	51.4	25	6	US-10-956-157-196259	Sequence 196259,
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C 398	11	52.4	25	6	US-10-956-160-117634	Sequence 117634, A	471	10.8	51.4	25	6	US-10-956-157-217634	Sequence 217634,
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C 401	11	52.4	25	6	US-10-956-160-122819	Sequence 122819, A	474	10.8	51.4	25	6	US-10-956-157-240209	Sequence 240209,
C 402	11	52.4	25	6	US-10-956-160-126186	Sequence 126186, A	475	10.8	51.4	25	6	US-10-956-157-241988	Sequence 241988,
C 403	11	52.4	25	6	US-10-956-160-154980	Sequence 154980, A	476	10.8	51.4	25	6	US-10-956-157-250072	Sequence 250072,
C 404	11	52.4	25	6	US-10-956-160-159142	Sequence 159142, A	477	10.8	51.4	25	6	US-10-956-157-253502	Sequence 253502,
C 405	11	52.4	25	6	US-10-956-160-160524	Sequence 160524, A	478	10.8	51.4	25	6	US-10-956-157-256536	Sequence 256536,
C 406	11	52.4	25	6	US-10-956-160-162313	Sequence 162313, A	479	10.8	51.4	25	6	US-10-956-157-258672	Sequence 258672,
C 407	11	52.4	25	6	US-10-956-160-176908	Sequence 176908, A	480	10.8	51.4	25	6	US-10-956-157-270531	Sequence 270531,
C 408	11	52.4	25	6	US-10-956-160-183950	Sequence 183950, A	481	10.8	51.4	25	6	US-10-956-157-272169	Sequence 272169,
C 409	11	52.4	25	6	US-10-956-160-193871	Sequence 193871, A	482	10.8	51.4	25	6	US-10-956-157-272170	Sequence 272170,
C 410	11	52.4	25	6	US-10-956-160-196415	Sequence 196415, A	483	10.8	51.4	25	6	US-10-956-157-272170	Sequence 272170,
C 411	11	52.4	25	6	US-10-956-160-199284	Sequence 199284, A	484	10.8	51.4	25	6	US-10-956-157-303152	Sequence 303152,
C 412	11	52.4	25	6	US-10-977-537-9	Sequence 9, Appl	485	10.8	51.4	25	6	US-10-956-157-303961	Sequence 303961,
C 413	11	52.4	30	6	US-10-831-286A-25841	Sequence 25841, A	486	10.8	51.4	25	6	US-10-956-157-304967	Sequence 304967,
C 414	11	52.4	38	6	US-10-951-303-4562	Sequence 4562, Ap	487	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 415	11	52.4	46	6	US-10-949-845-11	Sequence 11, Appl	488	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 416	11	52.4	46	6	US-10-977-537-11	Sequence 11, Appl	489	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 417	11	52.4	50	5	US-09-978-191B-344	Sequence 344, App	490	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 418	11	52.4	50	5	US-09-999-829B-344	Sequence 344, App	491	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 419	11	52.4	50	5	US-09-749-280C-5306	Sequence 5306, Ap	492	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 420	11	52.4	50	5	US-09-749-280C-5341	Sequence 5341, Ap	493	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 421	11	52.4	50	5	US-09-749-280C-5342	Sequence 5342, Ap	494	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 422	10.8	51.4	20	6	US-10-866-013-23	Sequence 23, Appl	495	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 423	10.8	51.4	20	6	US-10-831-286A-26110	Sequence 26110, A	496	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 424	10.8	51.4	20	6	US-10-831-286A-26751	Sequence 26751, A	497	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 425	10.8	51.4	20	6	US-10-831-286A-26839	Sequence 26839, A	498	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 426	10.8	51.4	20	6	US-10-831-286A-26849	Sequence 26849, A	499	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 427	10.8	51.4	20	6	US-10-831-286A-27400	Sequence 27400, A	500	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 428	10.8	51.4	20	6	US-10-831-286A-43362	Sequence 43362, A	501	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 429	10.8	51.4	21	6	US-10-475-021A-10	Sequence 10, Appl	502	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 430	10.8	51.4	25	6	US-10-956-157-12053	Sequence 12053, A	503	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 431	10.8	51.4	25	6	US-10-956-157-36136	Sequence 36136, A	504	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 432	10.8	51.4	25	6	US-10-956-157-36137	Sequence 36137, A	505	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 433	10.8	51.4	25	6	US-10-956-157-36140	Sequence 36140, A	506	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 434	10.8	51.4	25	6	US-10-956-157-36145	Sequence 36145, A	507	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 435	10.8	51.4	25	6	US-10-956-157-36149	Sequence 36149, A	508	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 436	10.8	51.4	25	6	US-10-956-157-48971	Sequence 48971, A	509	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 437	10.8	51.4	25	6	US-10-956-157-57473	Sequence 57473, A	510	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 438	10.8	51.4	25	6	US-10-956-157-85669	Sequence 85669, A	511	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 439	10.8	51.4	25	6	US-10-956-157-85670	Sequence 85670, A	512	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 440	10.8	51.4	25	6	US-10-956-157-85671	Sequence 85671, A	513	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 441	10.8	51.4	25	6	US-10-956-157-118986	Sequence 118986, A	514	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 442	10.8	51.4	25	6	US-10-956-157-118987	Sequence 118987, A	515	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 443	10.8	51.4	25	6	US-10-956-157-118989	Sequence 118989, A	516	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 444	10.8	51.4	25	6	US-10-956-157-118993	Sequence 118993, A	517	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 445	10.8	51.4	25	6	US-10-956-157-123975	Sequence 123975, A	518	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 446	10.8	51.4	25	6	US-10-956-157-127194	Sequence 127194, A	519	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 447	10.8	51.4	25	6	US-10-956-157-129604	Sequence 129604, A	520	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 448	10.8	51.4	25	6	US-10-956-157-131238	Sequence 131238, A	521	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 449	10.8	51.4	25	6	US-10-956-157-133166	Sequence 133166, A	522	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 450	10.8	51.4	25	6	US-10-956-157-135681	Sequence 135681, A	523	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 451	10.8	51.4	25	6	US-10-956-157-136376	Sequence 136376, A	524	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 452	10.8	51.4	25	6	US-10-956-157-145876	Sequence 145876, A	525	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 453	10.8	51.4	25	6	US-10-956-157-150696	Sequence 150696, A	526	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 454	10.8	51.4	25	6	US-10-956-157-151852	Sequence 151852, A	527	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 455	10.8	51.4	25	6	US-10-956-157-154184	Sequence 154184, A	528	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 456	10.8	51.4	25	6	US-10-956-157-154499	Sequence 154499, A	529	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 457	10.8	51.4	25	6	US-10-956-157-159152	Sequence 159152, A	530	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 458	10.8	51.4	25	6	US-10-956-157-161595	Sequence 161595, A	531	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 459	10.8	51.4	25	6	US-10-956-157-165543	Sequence 165543, A	532	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 460	10.8	51.4	25	6	US-10-956-157-166073	Sequence 166073, A	533	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 461	10.8	51.4	25	6	US-10-956-157-175084	Sequence 175084, A	534	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 462	10.8	51.4	25	6	US-10-956-157-185652	Sequence 185652, A	535	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,
C 463	10.8	51.4	25	6	US-10-956-157-192676	Sequence 192676, A	536	10.8	51.4	25	6	US-10-956-157-314148	Sequence 314148,

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538	10.6	50.5	19	6	US-10-758-155-2264	Sequence 2264, Ap	c 611	10.6	50.5	21	6	US-10-758-155-2508	Sequence 2508, Ap
539	10.6	50.5	19	6	US-10-758-155-2265	Sequence 2265, Ap	c 612	10.6	50.5	21	6	US-10-758-155-2509	Sequence 2509, Ap
540	10.6	50.5	19	6	US-10-758-155-2662	Sequence 2662, Ap	613	10.6	50.5	21	6	US-10-844-076-2275	Sequence 2275, Ap
541	10.6	50.5	19	6	US-10-758-155-2663	Sequence 2663, Ap	c 614	10.6	50.5	21	6	US-10-844-076-2278	Sequence 2278, Ap
542	10.6	50.5	19	6	US-10-758-155-2664	Sequence 2664, Ap	615	10.6	50.5	21	6	US-10-844-076-2373	Sequence 2373, Ap
543	10.6	50.5	19	6	US-10-758-155-2665	Sequence 2665, Ap	616	10.6	50.5	21	6	US-10-844-076-2374	Sequence 2374, Ap
544	10.6	50.5	19	6	US-10-758-155-2728	Sequence 2728, Ap	c 617	10.6	50.5	21	6	US-10-844-076-2385	Sequence 2385, Ap
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546	10.6	50.5	19	6	US-10-758-155-2730	Sequence 2730, Ap	619	10.6	50.5	21	6	US-10-844-076-2449	Sequence 2449, Ap
547	10.6	50.5	19	6	US-10-758-155-2731	Sequence 2731, Ap	c 620	10.6	50.5	21	6	US-10-844-076-2451	Sequence 2451, Ap
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553	10.6	50.5	19	6	US-10-844-076-2264	Sequence 2264, Ap	c 626	10.6	50.5	21	6	US-10-844-076-2501	Sequence 2501, Ap
554	10.6	50.5	19	6	US-10-844-076-2265	Sequence 2265, Ap	c 627	10.6	50.5	21	6	US-10-844-076-2504	Sequence 2504, Ap
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557	10.6	50.5	19	6	US-10-844-076-2664	Sequence 2664, Ap	c 630	10.6	50.5	21	6	US-10-844-076-2509	Sequence 2509, Ap
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560	10.6	50.5	19	6	US-10-844-076-2729	Sequence 2729, Ap	633	10.6	50.5	23	6	US-10-758-155-2573	Sequence 2573, Ap
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562	10.6	50.5	19	6	US-10-844-076-2731	Sequence 2731, Ap	635	10.6	50.5	23	6	US-10-758-155-2575	Sequence 2575, Ap
563	10.6	50.5	19	6	US-10-844-076-2734	Sequence 2734, Ap	636	10.6	50.5	23	6	US-10-758-155-2578	Sequence 2578, Ap
564	10.6	50.5	19	6	US-10-844-076-2735	Sequence 2735, Ap	637	10.6	50.5	23	6	US-10-758-155-2579	Sequence 2579, Ap
565	10.6	50.5	19	6	US-10-844-076-2736	Sequence 2736, Ap	638	10.6	50.5	23	6	US-10-758-155-2580	Sequence 2580, Ap
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567	10.6	50.5	19	6	US-10-883-218-142	Sequence 142, App	640	10.6	50.5	23	6	US-10-758-155-2584	Sequence 2584, Ap
568	10.6	50.5	19	6	US-10-883-218-144	Sequence 544, App	641	10.6	50.5	23	6	US-10-758-155-2585	Sequence 2585, Ap
569	10.6	50.5	19	8	PCT-US04-36522-459-6349	Sequence 6349, App	642	10.6	50.5	23	6	US-10-758-155-2586	Sequence 2586, Ap
570	10.6	50.5	20	1	PCT-US04-36520-150	Sequence 150, App	643	10.6	50.5	23	6	US-10-758-155-2587	Sequence 2587, Ap
571	10.6	50.5	20	1	PCT-US04-36520-250	Sequence 250, App	644	10.6	50.5	23	6	US-10-758-155-2628	Sequence 2628, Ap
572	10.6	50.5	20	6	US-10-832-622B-458	Sequence 458, App	645	10.6	50.5	23	6	US-10-758-155-2634	Sequence 2634, Ap
573	10.6	50.5	20	6	US-10-832-622B-799	Sequence 799, App	646	10.6	50.5	23	6	US-10-758-155-2640	Sequence 2640, Ap
574	10.6	50.5	20	6	US-10-831-286A-1718	Sequence 1718, Ap	647	10.6	50.5	23	6	US-10-758-155-2644	Sequence 2644, Ap
575	10.6	50.5	20	6	US-10-831-286A-1809	Sequence 1809, Ap	648	10.6	50.5	23	6	US-10-758-155-2645	Sequence 2645, Ap
576	10.6	50.5	20	6	US-10-831-286A-2841	Sequence 2841, Ap	649	10.6	50.5	23	6	US-10-758-155-2646	Sequence 2646, Ap
577	10.6	50.5	20	6	US-10-831-286A-3225	Sequence 3226, Ap	650	10.6	50.5	23	6	US-10-758-155-2647	Sequence 2647, Ap
578	10.6	50.5	20	6	US-10-831-286A-9089	Sequence 9089, Ap	651	10.6	50.5	23	6	US-10-844-076-2572	Sequence 2572, Ap
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584	10.6	50.5	20	6	US-10-831-286A-19685	Sequence 19685, A	657	10.6	50.5	23	6	US-10-844-076-2580	Sequence 2580, Ap
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587	10.6	50.5	20	6	US-10-831-286A-25726	Sequence 25726, A	660	10.6	50.5	23	6	US-10-844-076-2585	Sequence 2585, Ap
588	10.6	50.5	20	6	US-10-831-286A-28548	Sequence 28548, A	661	10.6	50.5	23	6	US-10-844-076-2586	Sequence 2586, Ap
589	10.6	50.5	20	6	US-10-831-286A-28949	Sequence 28949, A	662	10.6	50.5	23	6	US-10-844-076-2587	Sequence 2587, Ap
590	10.6	50.5	20	6	US-10-831-286A-33684	Sequence 33684, A	663	10.6	50.5	23	6	US-10-844-076-2628	Sequence 2628, Ap
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593	10.6	50.5	20	6	US-10-980-002-150	Sequence 150, App	666	10.6	50.5	23	6	US-10-844-076-2644	Sequence 2644, Ap
594	10.6	50.5	20	6	US-10-980-002-250	Sequence 250, App	667	10.6	50.5	23	6	US-10-844-076-2645	Sequence 2645, Ap
595	10.6	50.5	21	6	US-10-758-155-2275	Sequence 2275, Ap	668	10.6	50.5	23	6	US-10-844-076-2646	Sequence 2646, Ap
596	10.6	50.5	21	6	US-10-758-155-2278	Sequence 2278, Ap	669	10.6	50.5	23	6	US-10-844-076-2647	Sequence 2647, Ap
597	10.6	50.5	21	6	US-10-758-155-2373	Sequence 2373, Ap	c 670	10.6	50.5	25	6	US-10-956-157-12877	Sequence 12877, A
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602	10.6	50.5	21	6	US-10-758-155-2451	Sequence 2451, Ap	c 675	10.6	50.5	25	6	US-10-956-157-28657	Sequence 28657, A
603	10.6	50.5	21	6	US-10-758-155-2453	Sequence 2453, Ap	c 676	10.6	50.5	25	6	US-10-956-157-28663	Sequence 28663, A
604	10.6	50.5	21	6	US-10-758-155-2455	Sequence 2455, Ap	677	10.6	50.5	25	6	US-10-956-157-47923	Sequence 47923, A
605	10.6	50.5	21	6	US-10-758-155-2496	Sequence 2496, Ap	678	10.6	50.5	25	6	US-10-956-157-47924	Sequence 47924, A
606	10.6	50.5	21	6	US-10-758-155-2497	Sequence 2497, Ap	679	10.6	50.5	25	6	US-10-956-157-47926	Sequence 47926, A
607	10.6	50.5	21	6	US-10-758-155-2500	Sequence 2500, Ap	680	10.6	50.5	25	6	US-10-956-157-47930	Sequence 47930, A
608	10.6	50.5	21	6	US-10-758-155-2501	Sequence 2501, Ap	681	10.6	50.5	25	6	US-10-956-157-47934	Sequence 47934, A
609	10.6	50.5	21	6	US-10-758-155-2504	Sequence 2504, Ap	682	10.6	50.5	25	6	US-10-956-157-70289	Sequence 70289, A

683	10.6	50.5	25	6	US-10-956-157-87785	Sequence 87785, A	756	10.6	50.5	25	6	US-10-956-160-39990	Sequence 39990, A
684	10.6	50.5	25	6	US-10-956-157-87786	Sequence 87786, A	c 757	10.6	50.5	25	6	US-10-956-160-44931	Sequence 44931, A
685	10.6	50.5	25	6	US-10-956-157-110900	Sequence 110900, A	c 758	10.6	50.5	25	6	US-10-956-160-48439	Sequence 48439, A
686	10.6	50.5	25	6	US-10-956-157-123848	Sequence 123848, A	c 759	10.6	50.5	25	6	US-10-956-160-48473	Sequence 48473, A
687	10.6	50.5	25	6	US-10-956-157-124026	Sequence 124026, A	c 760	10.6	50.5	25	6	US-10-956-160-49958	Sequence 49958, A
688	10.6	50.5	25	6	US-10-956-157-132216	Sequence 132216, A	c 761	10.6	50.5	25	6	US-10-956-160-53597	Sequence 53597, A
689	10.6	50.5	25	6	US-10-956-157-137378	Sequence 137378, A	c 762	10.6	50.5	25	6	US-10-956-160-53597	Sequence 53597, A
690	10.6	50.5	25	6	US-10-956-157-137607	Sequence 137607, A	c 763	10.6	50.5	25	6	US-10-956-160-57518	Sequence 57518, A
691	10.6	50.5	25	6	US-10-956-157-143108	Sequence 143108, A	c 764	10.6	50.5	25	6	US-10-956-160-57914	Sequence 57914, A
692	10.6	50.5	25	6	US-10-956-157-145092	Sequence 145092, A	c 765	10.6	50.5	25	6	US-10-956-160-61413	Sequence 61413, A
693	10.6	50.5	25	6	US-10-956-157-154915	Sequence 154915, A	c 766	10.6	50.5	25	6	US-10-956-160-62726	Sequence 62726, A
694	10.6	50.5	25	6	US-10-956-157-158730	Sequence 158730, A	c 767	10.6	50.5	25	6	US-10-956-160-65934	Sequence 65934, A
695	10.6	50.5	25	6	US-10-956-157-159262	Sequence 159262, A	c 768	10.6	50.5	25	6	US-10-956-160-68626	Sequence 68626, A
696	10.6	50.5	25	6	US-10-956-157-160511	Sequence 160511, A	c 769	10.6	50.5	25	6	US-10-956-160-68627	Sequence 68627, A
697	10.6	50.5	25	6	US-10-956-157-162472	Sequence 162472, A	c 770	10.6	50.5	25	6	US-10-956-160-68628	Sequence 68628, A
698	10.6	50.5	25	6	US-10-956-157-166249	Sequence 166249, A	c 771	10.6	50.5	25	6	US-10-956-160-72202	Sequence 72202, A
699	10.6	50.5	25	6	US-10-956-157-168650	Sequence 168650, A	c 772	10.6	50.5	25	6	US-10-956-160-81656	Sequence 81656, A
700	10.6	50.5	25	6	US-10-956-157-170232	Sequence 170232, A	c 773	10.6	50.5	25	6	US-10-956-160-86129	Sequence 86129, A
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703	10.6	50.5	25	6	US-10-956-157-175857	Sequence 175857, A	c 776	10.6	50.5	25	6	US-10-956-160-95702	Sequence 95702, A
704	10.6	50.5	25	6	US-10-956-157-177494	Sequence 177494, A	c 777	10.6	50.5	25	6	US-10-956-160-100228	Sequence 100228, A
705	10.6	50.5	25	6	US-10-956-157-178675	Sequence 178675, A	c 778	10.6	50.5	25	6	US-10-956-160-101026	Sequence 101026, A
706	10.6	50.5	25	6	US-10-956-157-178796	Sequence 178796, A	c 779	10.6	50.5	25	6	US-10-956-160-101229	Sequence 101229, A
707	10.6	50.5	25	6	US-10-956-157-188344	Sequence 188344, A	c 780	10.6	50.5	25	6	US-10-956-160-102057	Sequence 102057, A
708	10.6	50.5	25	6	US-10-956-157-192392	Sequence 192392, A	c 781	10.6	50.5	25	6	US-10-956-160-106949	Sequence 106949, A
709	10.6	50.5	25	6	US-10-956-157-193555	Sequence 193555, A	c 782	10.6	50.5	25	6	US-10-956-160-119693	Sequence 119693, A
710	10.6	50.5	25	6	US-10-956-157-196952	Sequence 196952, A	c 783	10.6	50.5	25	6	US-10-956-160-127931	Sequence 127931, A
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712	10.6	50.5	25	6	US-10-956-157-197606	Sequence 197606, A	c 785	10.6	50.5	25	6	US-10-956-160-133352	Sequence 133352, A
713	10.6	50.5	25	6	US-10-956-157-199492	Sequence 199492, A	c 786	10.6	50.5	25	6	US-10-956-160-137086	Sequence 137086, A
714	10.6	50.5	25	6	US-10-956-157-199497	Sequence 199497, A	c 787	10.6	50.5	25	6	US-10-956-160-138103	Sequence 138103, A
715	10.6	50.5	25	6	US-10-956-157-200173	Sequence 200173, A	c 788	10.6	50.5	25	6	US-10-956-160-138350	Sequence 138350, A
716	10.6	50.5	25	6	US-10-956-157-201523	Sequence 201523, A	c 789	10.6	50.5	25	6	US-10-956-160-138558	Sequence 138558, A
717	10.6	50.5	25	6	US-10-956-157-202585	Sequence 202585, A	c 790	10.6	50.5	25	6	US-10-956-160-140100	Sequence 140100, A
718	10.6	50.5	25	6	US-10-956-157-203535	Sequence 203535, A	c 791	10.6	50.5	25	6	US-10-956-160-141731	Sequence 141731, A
719	10.6	50.5	25	6	US-10-956-157-206281	Sequence 206281, A	c 792	10.6	50.5	25	6	US-10-956-160-143384	Sequence 143384, A
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721	10.6	50.5	25	6	US-10-956-157-207519	Sequence 207519, A	c 794	10.6	50.5	25	6	US-10-956-160-162800	Sequence 162800, A
722	10.6	50.5	25	6	US-10-956-157-212603	Sequence 212603, A	c 795	10.6	50.5	25	6	US-10-956-160-165571	Sequence 165571, A
723	10.6	50.5	25	6	US-10-956-157-213847	Sequence 213847, A	c 796	10.6	50.5	25	6	US-10-956-160-167851	Sequence 167851, A
724	10.6	50.5	25	6	US-10-956-157-221016	Sequence 221016, A	c 797	10.6	50.5	25	6	US-10-956-160-169577	Sequence 169577, A
725	10.6	50.5	25	6	US-10-956-157-221784	Sequence 221784, A	c 798	10.6	50.5	25	6	US-10-956-160-178558	Sequence 178558, A
726	10.6	50.5	25	6	US-10-956-157-224351	Sequence 224351, A	c 799	10.6	50.5	25	6	US-10-956-160-181550	Sequence 181550, A
727	10.6	50.5	25	6	US-10-956-157-228517	Sequence 228517, A	c 800	10.6	50.5	25	6	US-10-956-160-189909	Sequence 189909, A
728	10.6	50.5	25	6	US-10-956-157-230555	Sequence 230555, A	c 801	10.6	50.5	25	6	US-10-956-160-197024	Sequence 197024, A
729	10.6	50.5	25	6	US-10-956-157-230613	Sequence 230613, A	c 802	10.6	50.5	25	6	US-10-956-160-200814	Sequence 200814, A
730	10.6	50.5	25	6	US-10-956-157-230994	Sequence 230994, A	c 803	10.6	50.5	25	6	US-10-956-160-201129	Sequence 201129, A
731	10.6	50.5	25	6	US-10-956-157-231474	Sequence 231474, A	c 804	10.6	50.5	25	6	US-10-956-160-202738	Sequence 202738, A
732	10.6	50.5	25	6	US-10-956-157-232047	Sequence 232047, A	c 805	10.6	50.5	25	6	US-10-956-160-204212	Sequence 204212, A
733	10.6	50.5	25	6	US-10-956-157-232048	Sequence 232048, A	c 806	10.6	50.5	25	6	US-10-956-160-205453	Sequence 205453, A
734	10.6	50.5	25	6	US-10-956-157-242503	Sequence 242503, A	c 807	10.6	50.5	25	6	US-10-956-160-207465	Sequence 207465, A
735	10.6	50.5	25	6	US-10-956-157-259510	Sequence 259510, A	c 808	10.6	50.5	25	6	US-10-956-160-207466	Sequence 207466, A
736	10.6	50.5	25	6	US-10-956-157-260352	Sequence 260352, A	c 809	10.6	50.5	25	6	US-10-956-160-209044	Sequence 209044, A
737	10.6	50.5	25	6	US-10-956-157-270922	Sequence 270922, A	c 810	10.6	50.5	29	6	US-10-742-442-36	Sequence 36, Appl
738	10.6	50.5	25	6	US-10-956-157-271708	Sequence 271708, A	c 811	10.6	50.5	30	6	US-10-831-286A-11711	Sequence 11711, A
739	10.6	50.5	25	6	US-10-956-157-283828	Sequence 283828, A	c 812	10.6	50.5	30	6	US-10-831-286A-12224	Sequence 12224, A
740	10.6	50.5	25	6	US-10-956-157-284804	Sequence 284804, A	c 813	10.6	50.5	30	6	US-10-850-359-879	Sequence 879, Appl
741	10.6	50.5	25	6	US-10-956-157-284805	Sequence 284805, A	c 814	10.6	50.5	48	6	US-10-837-904-78	Sequence 78, Appl
742	10.6	50.5	25	6	US-10-956-157-289121	Sequence 289121, A	c 815	10.6	50.5	50	6	US-09-686-148B-302	Sequence 302, Appl
743	10.6	50.5	25	6	US-10-956-157-289404	Sequence 289404, A	c 816	10.4	49.5	16	8	US-60-522-459-10016	Sequence 10016, A
744	10.6	50.5	25	6	US-10-956-157-289525	Sequence 289525, A	c 817	10.4	49.5	17	6	US-10-951-303-2270	Sequence 2270, Appl
745	10.6	50.5	25	6	US-10-956-157-294658	Sequence 294658, A	c 818	10.4	49.5	17	6	US-10-951-303-2271	Sequence 2271, Appl
746	10.6	50.5	25	6	US-10-956-157-298265	Sequence 298265, A	c 819	10.4	49.5	18	6	US-10-951-303-2977	Sequence 2977, Appl
747	10.6	50.5	25	6	US-10-956-157-310007	Sequence 310007, A	c 820	10.4	49.5	20	6	US-10-873-332-50	Sequence 50, Appl
748	10.6	50.5	25	6	US-10-956-157-315166	Sequence 315166, A	c 821	10.4	49.5	20	6	US-10-831-286A-13213	Sequence 13213, A
749	10.6	50.5	25	6	US-10-956-157-318462	Sequence 318462, A	c 822	10.4	49.5	20	6	US-10-831-286A-34459	Sequence 34459, A
750	10.6	50.5	25	6	US-10-956-160-16367	Sequence 16367, A	c 823	10.4	49.5	20	6	US-10-831-286A-34517	Sequence 34517, A
751	10.6	50.5	25	6	US-10-956-160-16943	Sequence 16943, A	c 824	10.4	49.5	20	6	US-10-831-286A-46299	Sequence 46299, A
752	10.6	50.5	25	6	US-10-956-160-23698	Sequence 23698, A	c 825	10.4	49.5	20	6	US-10-513-255-6	Sequence 6, Appl
753	10.6	50.5	25	6	US-10-956-160-25667	Sequence 25667, A	c 826	10.4	49.5	22	6	US-10-490-955-30	Sequence 30, Appl
754	10.6	50.5	25	6	US-10-956-160-31540	Sequence 31540, A	c 827	10.4	49.5	22	6	US-10-490-955-93	Sequence 93, Appl
755	10.6	50.5	25	6	US-10-956-160-35819	Sequence 35819, A	c 828	10.4	49.5	22	6	US-10-490-955-130	Sequence 130, Appl

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830	10.4	49.5	22	8	US-10-522-459-1752	Sequence 1752, Ap	C 903	10.4	49.5	25	6	US-10-956-157-195121	Sequence 195121,
831	10.4	49.5	23	6	US-10-758-155-2620	Sequence 2620, Ap	C 904	10.4	49.5	25	6	US-10-956-157-195583	Sequence 195583,
832	10.4	49.5	23	6	US-10-758-155-2621	Sequence 2621, Ap	C 905	10.4	49.5	25	6	US-10-956-157-199466	Sequence 199466,
833	10.4	49.5	23	6	US-10-758-155-2623	Sequence 2623, Ap	C 906	10.4	49.5	25	6	US-10-956-157-199505	Sequence 199505,
834	10.4	49.5	23	6	US-10-844-076-2620	Sequence 2620, Ap	C 907	10.4	49.5	25	6	US-10-956-157-200337	Sequence 200337,
835	10.4	49.5	23	6	US-10-844-076-2621	Sequence 2621, Ap	C 908	10.4	49.5	25	6	US-10-956-157-200348	Sequence 200348,
836	10.4	49.5	23	6	US-10-844-076-2623	Sequence 2623, Ap	C 909	10.4	49.5	25	6	US-10-956-157-200402	Sequence 200402,
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C 838	10.4	49.5	25	6	US-10-956-157-12056	Sequence 12056, A	C 911	10.4	49.5	25	6	US-10-956-157-201006	Sequence 201006,
C 839	10.4	49.5	25	6	US-10-956-157-15301	Sequence 15301, A	C 912	10.4	49.5	25	6	US-10-956-157-201201	Sequence 201201,
840	10.4	49.5	25	6	US-10-956-157-15302	Sequence 15302, A	C 913	10.4	49.5	25	6	US-10-956-157-201202	Sequence 201202,
841	10.4	49.5	25	6	US-10-956-157-15303	Sequence 15303, A	C 914	10.4	49.5	25	6	US-10-956-157-201203	Sequence 201203,
842	10.4	49.5	25	6	US-10-956-157-15315	Sequence 15315, A	C 915	10.4	49.5	25	6	US-10-956-157-202091	Sequence 202091,
843	10.4	49.5	25	6	US-10-956-157-15316	Sequence 15316, A	C 916	10.4	49.5	25	6	US-10-956-157-202772	Sequence 202772,
844	10.4	49.5	25	6	US-10-956-157-15317	Sequence 15317, A	C 917	10.4	49.5	25	6	US-10-956-157-206696	Sequence 206696,
845	10.4	49.5	25	6	US-10-956-157-15318	Sequence 15318, A	C 918	10.4	49.5	25	6	US-10-956-157-207192	Sequence 207192,
846	10.4	49.5	25	6	US-10-956-157-15323	Sequence 15323, A	C 919	10.4	49.5	25	6	US-10-956-157-210807	Sequence 210807,
847	10.4	49.5	25	6	US-10-956-157-15333	Sequence 15333, A	C 920	10.4	49.5	25	6	US-10-956-157-210849	Sequence 210849,
848	10.4	49.5	25	6	US-10-956-157-21303	Sequence 21303, A	C 921	10.4	49.5	25	6	US-10-956-157-212029	Sequence 212029,
849	10.4	49.5	25	6	US-10-956-157-21305	Sequence 21305, A	C 922	10.4	49.5	25	6	US-10-956-157-212145	Sequence 212145,
850	10.4	49.5	25	6	US-10-956-157-21306	Sequence 21306, A	C 923	10.4	49.5	25	6	US-10-956-157-213074	Sequence 213074,
851	10.4	49.5	25	6	US-10-956-157-21307	Sequence 21307, A	C 924	10.4	49.5	25	6	US-10-956-157-223709	Sequence 223709,
852	10.4	49.5	25	6	US-10-956-157-21309	Sequence 21309, A	C 925	10.4	49.5	25	6	US-10-956-157-223716	Sequence 223716,
853	10.4	49.5	25	6	US-10-956-157-21312	Sequence 21312, A	C 926	10.4	49.5	25	6	US-10-956-157-233125	Sequence 233125,
854	10.4	49.5	25	6	US-10-956-157-21316	Sequence 21316, A	C 927	10.4	49.5	25	6	US-10-956-157-233126	Sequence 233126,
855	10.4	49.5	25	6	US-10-956-157-21317	Sequence 21317, A	C 928	10.4	49.5	25	6	US-10-956-157-233378	Sequence 233378,
856	10.4	49.5	25	6	US-10-956-157-21318	Sequence 21318, A	C 929	10.4	49.5	25	6	US-10-956-157-236128	Sequence 236128,
857	10.4	49.5	25	6	US-10-956-157-43274	Sequence 43274, A	C 930	10.4	49.5	25	6	US-10-956-157-238489	Sequence 238489,
858	10.4	49.5	25	6	US-10-956-157-89178	Sequence 89178, A	C 931	10.4	49.5	25	6	US-10-956-157-241348	Sequence 241348,
C 859	10.4	49.5	25	6	US-10-956-157-105330	Sequence 105330, A	C 932	10.4	49.5	25	6	US-10-956-157-254176	Sequence 254176,
C 860	10.4	49.5	25	6	US-10-956-157-105331	Sequence 105331, A	C 933	10.4	49.5	25	6	US-10-956-157-257636	Sequence 257636,
C 861	10.4	49.5	25	6	US-10-956-157-105334	Sequence 105334, A	C 934	10.4	49.5	25	6	US-10-956-157-258575	Sequence 258575,
C 862	10.4	49.5	25	6	US-10-956-157-105336	Sequence 105336, A	C 935	10.4	49.5	25	6	US-10-956-157-259021	Sequence 259021,
C 863	10.4	49.5	25	6	US-10-956-157-105339	Sequence 105339, A	C 936	10.4	49.5	25	6	US-10-956-157-259022	Sequence 259022,
C 864	10.4	49.5	25	6	US-10-956-157-105347	Sequence 105347, A	C 937	10.4	49.5	25	6	US-10-956-157-259614	Sequence 259614,
865	10.4	49.5	25	6	US-10-956-157-115171	Sequence 115171, A	C 938	10.4	49.5	25	6	US-10-956-157-261586	Sequence 261586,
866	10.4	49.5	25	6	US-10-956-157-115178	Sequence 115178, A	C 939	10.4	49.5	25	6	US-10-956-157-271093	Sequence 271093,
867	10.4	49.5	25	6	US-10-956-157-115181	Sequence 115181, A	C 940	10.4	49.5	25	6	US-10-956-157-272379	Sequence 272379,
868	10.4	49.5	25	6	US-10-956-157-115185	Sequence 115185, A	C 941	10.4	49.5	25	6	US-10-956-157-272404	Sequence 272404,
869	10.4	49.5	25	6	US-10-956-157-117348	Sequence 117348, A	C 942	10.4	49.5	25	6	US-10-956-157-273708	Sequence 273708,
870	10.4	49.5	25	6	US-10-956-157-125355	Sequence 125355, A	C 943	10.4	49.5	25	6	US-10-956-157-275844	Sequence 275844,
871	10.4	49.5	25	6	US-10-956-157-128655	Sequence 128655, A	C 944	10.4	49.5	25	6	US-10-956-157-278037	Sequence 278037,
872	10.4	49.5	25	6	US-10-956-157-129788	Sequence 129788, A	C 945	10.4	49.5	25	6	US-10-956-157-284179	Sequence 284179,
873	10.4	49.5	25	6	US-10-956-157-130170	Sequence 130170, A	C 946	10.4	49.5	25	6	US-10-956-157-284429	Sequence 284429,
C 874	10.4	49.5	25	6	US-10-956-157-135913	Sequence 135913, A	C 947	10.4	49.5	25	6	US-10-956-157-290768	Sequence 290768,
C 875	10.4	49.5	25	6	US-10-956-157-135914	Sequence 135914, A	C 948	10.4	49.5	25	6	US-10-956-157-298993	Sequence 298993,
C 876	10.4	49.5	25	6	US-10-956-157-135915	Sequence 135915, A	C 949	10.4	49.5	25	6	US-10-956-157-300239	Sequence 300239,
C 877	10.4	49.5	25	6	US-10-956-157-137045	Sequence 137045, A	C 950	10.4	49.5	25	6	US-10-956-157-300484	Sequence 300484,
878	10.4	49.5	25	6	US-10-956-157-138856	Sequence 138856, A	C 951	10.4	49.5	25	6	US-10-956-157-303330	Sequence 303330,
C 879	10.4	49.5	25	6	US-10-956-157-140727	Sequence 140727, A	C 952	10.4	49.5	25	6	US-10-956-157-303364	Sequence 303364,
C 880	10.4	49.5	25	6	US-10-956-157-142525	Sequence 142525, A	C 953	10.4	49.5	25	6	US-10-956-157-303799	Sequence 303799,
881	10.4	49.5	25	6	US-10-956-157-143976	Sequence 143976, A	C 954	10.4	49.5	25	6	US-10-956-157-309378	Sequence 309378,
882	10.4	49.5	25	6	US-10-956-157-144683	Sequence 144683, A	C 955	10.4	49.5	25	6	US-10-956-157-312861	Sequence 312861,
C 883	10.4	49.5	25	6	US-10-956-157-145817	Sequence 145817, A	C 956	10.4	49.5	25	6	US-10-956-157-314057	Sequence 314057,
884	10.4	49.5	25	6	US-10-956-157-148462	Sequence 148462, A	C 957	10.4	49.5	25	6	US-10-956-160-14258	Sequence 14258, A
885	10.4	49.5	25	6	US-10-956-157-151910	Sequence 151910, A	C 958	10.4	49.5	25	6	US-10-956-160-17145	Sequence 17145, A
886	10.4	49.5	25	6	US-10-956-157-153072	Sequence 153072, A	C 959	10.4	49.5	25	6	US-10-956-160-26617	Sequence 26617, A
887	10.4	49.5	25	6	US-10-956-157-172724	Sequence 172724, A	C 960	10.4	49.5	25	6	US-10-956-160-29800	Sequence 29800, A
C 888	10.4	49.5	25	6	US-10-956-157-159134	Sequence 159134, A	C 961	10.4	49.5	25	6	US-10-956-160-32617	Sequence 32617, A
C 889	10.4	49.5	25	6	US-10-956-157-162256	Sequence 162256, A	C 962	10.4	49.5	25	6	US-10-956-160-36508	Sequence 36508, A
890	10.4	49.5	25	6	US-10-956-157-169624	Sequence 169624, A	C 963	10.4	49.5	25	6	US-10-956-160-38178	Sequence 38178, A
891	10.4	49.5	25	6	US-10-956-157-174531	Sequence 174531, A	C 964	10.4	49.5	25	6	US-10-956-160-38187	Sequence 38187, A
C 892	10.4	49.5	25	6	US-10-956-157-175934	Sequence 175934, A	C 965	10.4	49.5	25	6	US-10-956-160-43842	Sequence 43842, A
C 893	10.4	49.5	25	6	US-10-956-157-182324	Sequence 182324, A	C 966	10.4	49.5	25	6	US-10-956-160-46442	Sequence 46442, A
894	10.4	49.5	25	6	US-10-956-157-184324	Sequence 184324, A	C 967	10.4	49.5	25	6	US-10-956-160-48013	Sequence 48013, A
895	10.4	49.5	25	6	US-10-956-157-187620	Sequence 187620, A	C 968	10.4	49.5	25	6	US-10-956-160-48113	Sequence 48113, A
896	10.4	49.5	25	6	US-10-956-157-187621	Sequence 187621, A	C 969	10.4	49.5	25	6	US-10-956-160-48538	Sequence 48538, A
C 897	10.4	49.5	25	6	US-10-956-157-188302	Sequence 188302, A	C 970	10.4	49.5	25	6	US-10-956-160-48680	Sequence 48680, A
C 898	10.4	49.5	25	6	US-10-956-157-191330	Sequence 191330, A	C 971	10.4	49.5	25	6	US-10-956-160-48706	Sequence 48706, A
899	10.4	49.5	25	6	US-10-956-157-192688	Sequence 192688, A	C 972	10.4	49.5	25	6	US-10-956-160-50071	Sequence 50071, A
900	10.4	49.5	25	6	US-10-956-157-192802	Sequence 192802, A	C 973	10.4	49.5	25	6	US-10-956-160-54901	Sequence 54901, A
C 901	10.4	49.5	25	6	US-10-956-157-193759	Sequence 193759, A	C 974	10.4	49.5	25	6	US-10-956-160-62160	Sequence 62160, A

975 10.4 49.5 25 6 US-10-956-160-66911 Sequence 66911, A
976 10.4 49.5 25 6 US-10-956-160-74361 Sequence 74361, A
977 10.4 49.5 25 6 US-10-956-160-76955 Sequence 76955, A
978 10.4 49.5 25 6 US-10-956-160-78917 Sequence 78917, A
979 10.4 49.5 25 6 US-10-956-160-79776 Sequence 79776, A
980 10.4 49.5 25 6 US-10-956-160-79777 Sequence 79777, A
981 10.4 49.5 25 6 US-10-956-160-86455 Sequence 86455, A
982 10.4 49.5 25 6 US-10-956-160-87553 Sequence 87553, A
983 10.4 49.5 25 6 US-10-956-160-88930 Sequence 88930, A
984 10.4 49.5 25 6 US-10-956-160-91414 Sequence 91414, A
985 10.4 49.5 25 6 US-10-956-160-92535 Sequence 92535, A
986 10.4 49.5 25 6 US-10-956-160-93789 Sequence 93789, A
987 10.4 49.5 25 6 US-10-956-160-93906 Sequence 93906, A
988 10.4 49.5 25 6 US-10-956-160-94548 Sequence 94548, A
989 10.4 49.5 25 6 US-10-956-160-95889 Sequence 95889, A
990 10.4 49.5 25 6 US-10-956-160-102309 Sequence 102309, A
991 10.4 49.5 25 6 US-10-956-160-104757 Sequence 104757, A
992 10.4 49.5 25 6 US-10-956-160-107155 Sequence 107155, A
993 10.4 49.5 25 6 US-10-956-160-107298 Sequence 107298, A
994 10.4 49.5 25 6 US-10-956-160-110571 Sequence 110571, A
995 10.4 49.5 25 6 US-10-956-160-116310 Sequence 116310, A
996 10.4 49.5 25 6 US-10-956-160-119668 Sequence 119668, A
997 10.4 49.5 25 6 US-10-956-160-120407 Sequence 120407, A
998 10.4 49.5 25 6 US-10-956-160-120757 Sequence 120757, A
999 10.4 49.5 25 6 US-10-956-160-128692 Sequence 128692, A
1000 10.4 49.5 25 6 US-10-956-160-128794 Sequence 128794, A

ALIGNMENTS

RESULT 1
US-10-956-157-281467/c
; Sequence 281467, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-281467
Query Match 71.4%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCATGCCAGATTACT 18
Db 23 GCATGCCAGATTACT 9
RESULT 2
US-10-956-160-158095
; Sequence 158095, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158095

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158095
Query Match 70.5%; Score 14.8; DB 6; Length 25;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GCGCATGCCAGATTACTG 19
Db 2 GAGCGTGCAGATTACTG 19
RESULT 3
US-10-956-160-158096
; Sequence 158096, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158096
Query Match 70.5%; Score 14.8; DB 6; Length 25;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GCGCATGCCAGATTACTG 19
Db 2 GAGCGTGCAGATTACTG 19

RESULT 4
US-10-956-157-209367/c
; Sequence 209367, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-209367
Query Match 65.7%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GCATGCCAGATTACTGG 20
Db 25 GCATGCCAGATTACTGG 9
RESULT 5
US-10-956-160-164697
; Sequence 164697, Application US/10956160

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES

; FILE REFERENCE: 031896-044000 (AM101084)

; CURRENT APPLICATION NUMBER: US/10/956,160

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 222274

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 164697

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Canis familiaris

; US-10-956-160-164697

Query Match

Best Local Similarity 65.7%; Score 13.8; DB 6; Length 25;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGGC 21

Db 9 CAAGCCAGATTGCTGGC 25

RESULT 6

US-10-956-157-288293/c

; Sequence 288293, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 288293

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

; US-10-956-157-288293

Query Match

Best Local Similarity 64.8%; Score 13.6; DB 6; Length 25;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGGC 21

Db 21 GTGCATGCCAGACAGCTGGC 2

RESULT 7

US-10-956-160-119577

; Sequence 119577, Application US/10956160

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES

; FILE REFERENCE: 031896-044000 (AM101084)

; CURRENT APPLICATION NUMBER: US/10/956,160

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 222274

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 119577

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Canis familiaris

; US-10-956-160-119577

Query Match

Best Local Similarity 64.8%; Score 13.6; DB 6; Length 25;

Best Local Similarity 80.0%; Pred. No. 3.1e+02;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGG 20

Db 2 AGCGCATGCTGGAATTTGTCG 21

RESULT 8

US-10-956-157-150549/c

; Sequence 150549, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 150549

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

; US-10-956-157-150549

Query Match

Best Local Similarity 62.9%; Score 13.2; DB 6; Length 25;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21

Db 24 GCATGCCAGACAGCTGGC 7

RESULT 9

US-10-956-160-44697/c

; Sequence 44697, Application US/10956160

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES

; FILE REFERENCE: 031896-044000 (AM101084)

; CURRENT APPLICATION NUMBER: US/10/956,160

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 222274

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 44697

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Canis familiaris

; US-10-956-160-44697

Query Match

Best Local Similarity 62.9%; Score 13.2; DB 6; Length 25;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGGC 21

Db 23 GCAGGCCAAATTAATGGC 6

RESULT 10

US-10-956-160-179056

; Sequence 179056, Application US/10956160

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES

; FILE REFERENCE: 031896-044000 (AM101084)

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; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-179056

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Query Match          62.9%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 11
US-10-956-160-109185
; Sequence 109185, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109185.
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-109185

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Query Match      61.9%; Score 13; DB 6; Length 25;
Best Local Similarity 76.2%; Pred. No. 6.3e+02;
Matches 16: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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RESULT 12
US-10-956-157-85795
; Sequence 85795, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2

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Query Match      61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 13
US-10-956-157-85796
; Sequence 85796, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85796

```

```

Query Match      61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTG 19
          | | | | | | | | | |
Db      10 GTATTCAGATTACTG 25

```

```

RESULT 14
US-10-956-157-85797
; Sequence 85797, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85797

```

```

Query Match      61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTG 19
          | | | | | | | | | |
Db      9 GTATTCAGATTACTG 24

```

```

RESULT 15
US-10-956-157-85802
; Sequence 85802, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85802
; LENGTH: 25

```

; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-85802

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 7 GTATTCAGATTACTG 22

RESULT 16

US-10-956-157-85805
; Sequence 85805, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 85805

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-85805

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 6 GTATTCAGATTACTG 21

RESULT 17

US-10-956-157-161273

; Sequence 161273, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 161273

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-161273

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
| | | | | | | | | |
Db 10 GTATTCAGATTACTG 25

RESULT 18

US-10-956-157-171287

; Sequence 171287, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 171287

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-171287

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 171287

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-171287

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGCG 21
| | | | | | | | | |
Db 4 ATGCCAGTTACTGCG 19

RESULT 19

US-10-956-157-210009/c

; Sequence 210009, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 210009

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-210009

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTGG 20
| | | | | | | | | |
Db 22 CATGCCATAATACTGG 7

RESULT 20

US-10-956-157-237787

; Sequence 237787, Application US/10956157

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956.157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 237787

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-237787

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;

```
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GCATGCCAGATTACTG 19
Db 4 GTATCCAGATTACTG 19

RESULT 21
US-10-956-160-16692
; Sequence 16692, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-16692

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACTGGC 21
Db 3 ATGACAGACTACTGGC 18

RESULT 22
US-10-956-160-77247/c
; Sequence 77247, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77247
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-77247

Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGG 20
Db 25 CATGCCACATAACTGG 10

RESULT 23
US-10-956-160-96989/c
; Sequence 96989, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
```

```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96989
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-96989
```

```
Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 CATGCCAGATTACTGG 20
Db 23 CATGCCACATAACTGG 8
```

```
RESULT 24
US-10-956-160-159211/c
; Sequence 159211, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-159211
```

```
Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 CATGCCAGATTACTGG 20
Db 19 CATGCCACATAACTGG 4
```

```
RESULT 25
US-10-956-160-180069
; Sequence 180069, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180069
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-180069
```

```
Query Match 61.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 CATGCCAGATTACTGG 20
Db 3 CTGGCAGATTACTGG 18
```

```
RESULT 26
US-10-956-157-123326
; Sequence 123326, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-123326
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGATGCCAGATTACTG 19
| | | | | | | | | | | | | | | | | | | | |
Db 6 AGTGTCTCCAGATTATTG 24
| | | | | | | | | | | | | | | | | | | | |

RESULT 27
US-10-956-157-206484
; Sequence 206484, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-206484
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCAGATGCCAGATTACTGG 20
| | | | | | | | | | | | | | | | | | | | |
Db 1 GCCTTGTCCAGATTCTCG 19
| | | | | | | | | | | | | | | | | | | | |

RESULT 28
US-10-956-157-301261/c
; Sequence 301261, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301261
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Probe Sequence
US-10-956-157-301261
Query Match 60.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | |
Db 25 CTCCTGGCGGATTACTGGC 7
| | | | | | | | | | | | | | | | | | | | |

RESULT 29
US-10-956-157-306098/c
; Sequence 306098, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 306098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-306098
Query Match 59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | |
Db 20 GCCAGATTACTGGC 7
| | | | | | | | | | | | | | | | | | | | |

RESULT 30
US-10-956-160-47893/c
; Sequence 47893, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-47893
Query Match 59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCCAGATTACTGGC 21
| | | | | | | | | | | | | | | | | | | | |
Db 22 GCCAGATTACTGGC 9
| | | | | | | | | | | | | | | | | | | | |

RESULT 31
US-10-956-160-55930
; Sequence 55930, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-55930

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 ATGCCAGATTACTG 19
DB      11 ATGCCTGATTACTG 24
          ||||| |||||
RESULT 32
US-10-956-160-76438/c
; Sequence 76438, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-76438

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      7 TGCCAGATTACTGG 20
DB      24 TGCCAGATCACTGG 11
          ||||| |||||
RESULT 33
US-10-956-160-158546
; Sequence 158546, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-158546

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GCGCATGCCAGATT 15
DB      2 GAGCATGCCAGATT 15
          ||||| |||||
RESULT 34
US-10-956-160-167178/c
; Sequence 167178, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167178
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-167178

Query Match          59.0%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 GCCAGATTACTGGC 21
DB      20 GCCAGAGTACTGGC 7
          ||||| |||||
RESULT 35
US-10-489-273-35
; Sequence 35, Application US/10489273
; GENERAL INFORMATION:
; APPLICANT: Turner, Arthur Keith
; APPLICANT: Greenwood, Judith
; APPLICANT: Stephens, Jonathan Clive
; APPLICANT: Beavis, Juliet Claire
; APPLICANT: Darsley, Michael James
; TITLE OF INVENTION: Attenuated Bacteria Useful in Vaccines
; FILE REFERENCE: 117-499 / N83542B
; CURRENT APPLICATION NUMBER: US/10/489,273
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/GB02/04164
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: GB 0121998.9
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-489-273-35

Query Match          59.0%; Score 12.4; DB 6; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCGCATGCCAGATT 15
DB      2 GCGCATGCCAGATT 15
          ||||| |||||
RESULT 36
US-10-758-155-2666
; Sequence 2666, Application US/10758155
```



```
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBHB02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
US-10-758-155-2666

Query Match      58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      5 CATGCCAGATTACTGGC 21
      ||:|||:|||:|||
Db      1 CAUGCUGAUGGUGGCG 17

RESULT 37
US-10-758-155-2667
; Sequence 2667, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBHB02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
US-10-758-155-2666

Query Match      58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      5 CATGCCAGATTACTGGC 21
      ||:|||:|||:|||
Db      1 CAUGCUGAUGGUGGCG 17

RESULT 38
US-10-758-155-2732
; Sequence 2732, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBHB02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2732
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
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; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBHB02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
US-10-758-155-2667

Query Match      58.1%; Score 12.2; DB 6; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      5 CATGCCAGATTACTGGC 21
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Db      1 CAUGCUGAUGGUGGCG 17

RESULT 38
US-10-758-155-2732
; Sequence 2732, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBHB02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
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; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2732
    Query Match      58.1%; Score 12.2; DB 6; Length 19;
    Best Local Similarity 58.8%; Pred. No. 1.6e+03;
    Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
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Db 3 CAUGCUGGAUUGCUGGC 19

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US-10-758-155-2733
; Sequence 2733, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBH02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2733
    Query Match      58.1%; Score 12.2; DB 6; Length 19;
    Best Local Similarity 58.8%; Pred. No. 1.6e+03;
    Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
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Db 3 CAUGCUGGAUUGCUGGC 19

RESULT 40
US-10-758-155-2738
; Sequence 2738, Application US/10758155
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
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; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBH02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2738
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence
; US-10-758-155-2738
    Query Match      58.1%; Score 12.2; DB 6; Length 19;
    Best Local Similarity 58.8%; Pred. No. 1.6e+03;
    Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
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Db 2 CAUGCUGGAUUGCUGGC 18

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Job time : 35.2697 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 112.708 Seconds
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978.085 Million cell updates/sec

Title: US-10-087-631B-1
Perfect score: 21
Sequence: 1 agcgcagccagattactgac 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	6	AD43736 DNA seq
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5	13.6	64.8	44	2	AAT65036 Aspergill
6	13.2	62.9	19	4	AAT65036 Aspergill
7	13.2	62.9	20	10	ADF91091 Microorga
8	13.2	62.9	21	2	AX833448 ZAM retro
9	13.2	62.9	22	6	AX833448 ZAM retro
10	13.2	62.9	32	6	ABQ87925 Enterohae
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12	13.2	62.9	32	6	ABQ87926 Enterohae
13	13	61.9	18	2	AZ41030 Cellular
14	13	61.9	18	2	AZ41030 Cellular
15	13	61.9	18	10	AAD60500 Human c-I
16	13	61.9	20	12	ADP81733 Human mel
17	13	61.9	20	12	ADP81733 Human mel
18	13	61.9	32	4	AC93092 E. coli c
19	13	61.9	32	4	AC93092 E. coli c
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	23	12.8	61.0	6	ABSS7999	Abss7999 PCR prime
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c	25	12.8	61.0	6	ABQ05495	Abq05495 Oligonucl
c	26	12.8	61.0	24	ABQ11823	Abq11823 Oligonucl
c	27	12.8	61.0	6	ABQ00780	Abq00780 Oligonucl
	28	12.8	61.0	6	ABQ05536	Abq05536 Oligonucl
	29	12.8	61.0	6	ABQ11857	Abq11857 Oligonucl
c	30	12.8	61.0	24	AAI62586	Aai62586 Human A2
c	31	12.8	61.0	25	ABQ13359	Abq13359 Oligonucl
c	32	12.8	61.0	25	ABQ13393	Abq13393 Oligonucl
c	33	12.8	61.0	28	AAQ46940	Aaq46940 Human bFG
	34	12.8	61.0	28	AAT59860	Aat59860 Sense pri
	35	12.8	61.0	33	AAH48106	Aah48106 Ribulose
	36	12.8	61.0	41	AAH48109	Aah48109 Ribulose
	37	12.8	61.0	49	AAT05760	Aat05760 Thermophi
c	38	12.6	60.0	19	AAAF82407	Aaf82407 Mealworm
c	39	12.6	60.0	20	AAAX94343	Aax94343 PCR prime
	40	12.6	60.0	21	AAZ21594	Aaz21594 PCR prime
	41	12.6	60.0	21	ABL42959	Abi42959 Human chr
	42	12.6	60.0	25	AAI61787	Aai61787 Soybean 2
c	43	12.6	60.0	34	AAA95696	Aaa95696 Bacillus
	44	12.6	60.0	38	AAQ46917	Aaq46917 PCR prime
	45	12.6	60.0	41	ABZ44895	Abz44895 Human cyt
	46	12.6	60.0	41	ABZ50445	Abz50445 Human cyt
c	47	12.6	60.0	46	ABA90115	Abi90115 Oestrogen
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	78	12.4	59.0	21	AAI67796	Aai67796 E. coli O
	79	12.4	59.0	23	ACF35777	Acf35777 Mouse MMP
c	80	12.4	59.0	25	ACI96905	Act96905 Human mic
	81	12.4	59.0	25	ACK05636	Ack05636 Human mic
	82	12.4	59.0	28	ACC79451	Acc79451 EAS1 del
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c	84	12.4	59.0	42	AAT31710	Aat31710 Respirato
c	85	12.4	59.0	42	AAZ30538	Aaz30538 RSV G pro
c	86	12.4	59.0	42	AAZ30537	Aaz30537 RSV G pro
c	87	12.4	59.0	42	AAF90137	Aaf90137 Nucleotid
c	88	12.4	59.0	42	AAF90138	Aaf90138 Nucleotid
c	89	12.4	59.0	45	AAQ44969	Aaq44969 FIV gag g
	90	12.4	59.0	48	ABZ45718	Abz45718 Human ATP
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c	94	12.2	58.1	19	AAA94562	Aaa94562 Oligonucl

c 95	12.2	58.1	20	2	AAZ02084	Aaz02084 PCR prime	c 168	11.8	56.2	20	12	ADK96648	Adk96648 Primer of
c 96	12.2	58.1	20	6	ABL44022	AbL44022 Human chr	169	11.8	56.2	21	4	AAE97043	Aaf97043 Human gen
c 97	12.2	58.1	20	10	ADH93713	Adh93713 Human gen	c 170	11.8	56.2	21	4	AAE97599	Aaf97599 Human gen
c 98	12.2	58.1	22	6	AAK99354	Aak99354 Antisense	c 171	11.8	56.2	21	12	ADN00683	Adn00683 reca PCR
c 99	12.2	58.1	22	6	AAK51433	Aak51433 Starfish	c 172	11.8	56.2	22	6	ABL44143	AbL44143 Human chr
c 100	12.2	58.1	25	3	AAAL14076	AaAl14076 Human SPR	c 173	11.8	56.2	25	9	ACK26950	Ack26950 Human mic
c 101	12.2	58.1	25	9	AAI62155	AaI62155 Soybean 3	c 174	11.8	56.2	25	9	ACK03103	Ack03103 Human mic
c 102	12.2	58.1	25	9	ACK15960	Ack15960 Human mic	c 175	11.8	56.2	25	9	ACI23522	AcI23522 Human mic
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c 105	12.2	58.1	26	10	ADR44635	Adr44635 Human ICO	c 178	11.8	56.2	30	2	AAQ25301	Aaq25301 T-cell re
c 106	12.2	58.1	27	6	AAQ25095	Aaq25095 DR-A enha	c 179	11.8	56.2	31	12	ADQ79971	Adq79971 Synthetic
c 107	12.2	58.1	27	6	ABA03313	AbA03313 Streptomy	c 180	11.8	56.2	38	12	ADM36298	Adm36298 Modified
c 108	12.2	58.1	27	6	ABA03313	AbA03313 Streptomy	c 181	11.8	56.2	39	2	AAQ75898	Aaq75898 CDR-graft
c 109	12.2	58.1	27	10	ADF44634	Adf44634 Human ICO	c 182	11.8	56.2	20	2	AAAT41033	AaA41033 Human gen
c 110	12.2	58.1	30	2	AAQ36789	Aaq36789 Mycobacte	c 183	11.6	55.2	20	2	AAQ93394	Aax93394 PCR prime
c 111	12.2	58.1	31	6	ABA03319	AbA03319 Streptomy	c 184	11.6	55.2	22	2	AAQ93394	Aax93394 PCR prime
c 112	12.2	58.1	32	6	ABQ87932	Abq87932 Enterohae	c 185	11.6	55.2	22	3	AAA95571	AaA95571 TCR Valph
c 113	12.2	58.1	32	6	ABQ87946	Abq87946 Enterohae	c 186	11.6	55.2	22	12	ADK67740	Adk67740 Murine fa
c 114	12.2	58.1	34	6	ABK87179	Abk87179 A. pernix	c 187	11.6	55.2	23	6	ABA04844	AbA04844 Human PCR
c 115	12.2	58.1	34	6	ABS52447	Abs52447 Thermophi	c 188	11.6	55.2	23	8	ACC71766	Acc71766 PCR prime
c 116	12.2	58.1	42	2	AAT90107	Aat90107 Ha-ras fr	c 189	11.6	55.2	24	2	AAK86555	Aax86555 Primer re
c 117	12.2	58.1	44	2	AAE65037	Aae65037 Aspergill	c 190	11.6	55.2	25	6	AAU50060	AaU50060 Murine al
c 118	12.2	58.1	44	2	AAQ02757	Aaq02757 Oligonucl	c 191	11.6	55.2	25	6	ABV81964	Abv81964 Human HTP
c 119	12.2	58.1	44	10	ABZ57904	Abz57904 RNA secon	c 192	11.6	55.2	25	9	ACI93929	AcI93929 Human HTP
c 120	12.2	58.1	50	4	AAI77361	AaI77361 Human sil	c 193	11.6	55.2	25	9	ACI93929	AcI93929 Human mic
c 121	12.2	58.1	20	5	AAO9105	Aao9105 Human MEK	c 194	11.6	55.2	30	2	AAQ84732	Aaq84732 Primer to
c 122	12.2	58.1	20	6	ABL45362	AbL45362 Human chr	c 195	11.6	55.2	30	2	AAQ84732	Aaq84732 Primer to
c 123	12.2	58.1	20	6	ABY93220	AbY93220 Capture o	c 196	11.6	55.2	30	2	AAZ07618	Aaz07618 HCV NS1/5
c 124	12.2	58.1	20	12	ADU25471	AdJ25471 Human end	c 197	11.6	55.2	30	2	AAZ00428	Aaz00428 Hepatitis
c 125	12.2	58.1	23	8	AAQ49636	Aaq49636 Human KPO	c 198	11.6	55.2	30	2	AAZ26763	Aaz26763 PCR prime
c 126	12.2	58.1	24	6	ACC57383	Acc57383 Human BPA	c 199	11.6	55.2	30	2	ADF66097	Adf66097 Hepatitis
c 127	12.2	58.1	24	6	ABI83010	Abi83010 Capture o	c 200	11.6	55.2	30	2	ADP66102	Adp66102 Hepatitis
c 128	12.2	58.1	24	6	ABI83011	Abi83011 Capture o	c 201	11.6	55.2	30	3	AAZ55031	Aaz55031 Neisseria
c 129	12.2	58.1	24	6	ABY92277	AbY92277 Capture o	c 202	11.6	55.2	31	2	AAAT66766	Aat66766 Human DF3
c 130	12.2	58.1	24	6	ABY92276	AbY92276 Capture o	c 203	11.6	55.2	31	3	AAZ35908	Aaz35908 Human gen
c 131	12.2	58.1	25	6	ABV81962	Abv81962 Human HTP	c 204	11.6	55.2	31	6	AAAL37984	AaL37984 Human imm
c 132	12.2	58.1	25	6	ABV81962	Abv81962 Human HTP	c 205	11.6	55.2	31	10	ADF69474	Adf69474 Tapesia y
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c 134	12.2	58.1	25	6	ABV81961	Abv81961 Human HTP	c 207	11.6	55.2	33	6	ABZ22187	Abz22187 Human glu
c 135	12.2	58.1	25	6	ABV81961	Abv81961 Human HTP	c 208	11.6	55.2	35	9	ACC84746	Acc84746 E. coli p
c 136	12.2	58.1	25	6	ABV81958	Abv81958 Human HTP	c 209	11.6	55.2	36	2	AAQ99619	Aaq99619 Human Ah
c 137	12.2	58.1	25	9	ACD26693	AcI26693 Human mic	c 210	11.6	55.2	37	2	AAV16041	Aav16041 PCR prime
c 138	12.2	58.1	25	12	ADG76734	Adg76734 Human olf	c 211	11.6	55.2	37	3	AAZ43300	Aaz43300 Murine ty
c 139	12.2	58.1	27	10	ABZ84571	Abz84571 Toxicolog	c 212	11.6	55.2	37	3	AAA05285	AaA05285 PCR prime
c 140	12.2	58.1	28	4	AAE75355	Aae75355 Pestiviru	c 213	11.6	55.2	37	8	ACD53443	AcD53443 HBV G-cle
c 141	12.2	58.1	29	3	AAQ04125	AaA04125 Polymorph	c 214	11.6	55.2	37	12	ADM61953	Adm61953 Hepatitis
c 142	12.2	58.1	29	3	AAZ54569	Aaz54569 Neisseria	c 215	11.6	55.2	45	6	ABK86059	Abk86059 Protein C
c 143	12.2	58.1	29	3	AAZ54761	Aaz54761 Neisseria	c 216	11.6	55.2	46	4	AAH93855	Aah93855 Human pro
c 144	12.2	58.1	29	3	AAZ54803	Aaz54803 Neisseria	c 217	11.6	55.2	46	4	AAH93859	Aah93859 Human pro
c 145	12.2	58.1	29	3	AAAL1314	AaAL1314 N. mening	c 218	11.6	55.2	46	4	AAAG63948	AaG63948 Human pro
c 146	12.2	58.1	29	3	AAZ21599	Aaz21599 Neisseria	c 219	11.6	55.2	46	4	AAAG63952	AaG63952 Human pro
c 147	12.2	58.1	30	2	AAZ99188	Aaz99188 N. mening	c 220	11.6	55.2	46	5	ACA59760	AcA59760 Prostate
c 148	12.2	58.1	30	5	AAAB89117	AaAB89117 Neisseria	c 221	11.6	55.2	46	5	ACA59756	AcA59756 Prostate
c 149	12.2	58.1	33	4	AAH48797	Aah48797 Erythropro	c 222	11.6	55.2	46	6	ABL95319	AbL95319 Human cod
c 150	12.2	58.1	34	4	AAH91676	Aah91676 Human inf	c 223	11.6	55.2	46	6	ABL95323	AbL95323 Human cod
c 151	12.2	58.1	37	6	AAH96699	Aah96699 Human Chk	c 224	11.6	55.2	46	6	ABA90113	AbA90113 Oestrogen
c 152	12.2	58.1	37	6	ABK59224	Abk59224 Human CUC	c 225	11.6	55.2	46	6	ABA90102	AbA90102 Oestrogen
c 153	12.2	58.1	37	6	ABK59203	Abk59203 Human CUC	c 226	11.6	55.2	46	6	ABA90125	AbA90125 Oestrogen
c 154	12.2	58.1	37	8	ACD53542	AcD53542 HBV G-cle	c 227	11.6	55.2	46	6	ABA90174	AbA90174 Oestrogen
c 155	12.2	58.1	37	8	ACD53452	AcD53452 HBV G-cle	c 228	11.6	55.2	46	6	ABA90133	AbA90133 Oestrogen
c 156	12.2	58.1	37	12	ADM62001	Adm62001 Hepatitis	c 229	11.6	55.2	46	6	ABA90099	AbA90099 Oestrogen
c 157	12.2	58.1	37	12	ADM61962	Adm61962 Hepatitis	c 230	11.6	55.2	46	6	ABA90104	AbA90104 Oestrogen
c 158	12.2	58.1	38	2	AAAT48796	AaA48796 Erythropro	c 231	11.6	55.2	46	6	ABQ87822	AbQ87822 Human ESR
c 159	12.2	58.1	40	2	AAO88558	Aao88558 Oligonucl	c 232	11.6	55.2	46	6	ABQ87808	AbQ87808 Human ESR
c 160	12.2	58.1	40	2	AAO88557	Aao88557 Oligonucl	c 233	11.6	55.2	46	6	ABQ87811	AbQ87811 Human ESR
c 161	12.2	58.1	41	6	ABZ47661	Abz47661 Human ATP	c 234	11.6	55.2	46	6	ABQ87842	AbQ87842 Human ESR
c 162	12.2	58.1	41	6	ABZ45066	Abz45066 Human ATP	c 235	11.6	55.2	46	6	ABQ87883	AbQ87883 Human ESR
c 163	12.2	58.1	43	2	AAV19848	AaV19848 Primer fo	c 236	11.6	55.2	46	6	ABQ87834	AbQ87834 Human ESR
c 164	12.2	58.1	44	10	ADD25977	AdD25977 Human ery	c 237	11.6	55.2	46	6	ABQ87813	AbQ87813 Human ESR
c 165	12.2	58.1	44	10	ADD25979	AdD25979 Human ery	c 238	11.6	55.2	46	8	ACC95483	Acc95483 Prostate
c 166	11.8	56.2	18	2	AAO95883	Aao95883 Human bia	c 239	11.6	55.2	46	8	ACC95487	Acc95487 Prostate
c 167	11.8	56.2	20	4	AAF83480	Aaf83480 Human ADA	c 240	11.6	55.2	46	8	ABX33844	Abx33844 Human ESR

C 241	11.6	55.2	46	8	ABX33870	Human ESR	Abx33870 Human ESR	C 314	11.4	54.3	37	12	ADM61959	Hepatitis
C 242	11.6	55.2	46	8	ABX33878	Human ESR	Abx33878 Human ESR	C 315	11.4	54.3	37	12	ADM61992	Hepatitis
C 243	11.6	55.2	46	8	ABX33847	Human ESR	Abx33847 Human ESR	C 316	11.4	54.3	37	12	ADM61994	Hepatitis
C 244	11.6	55.2	46	8	ABX33849	Human ESR	Abx33849 Human ESR	C 317	11.4	54.3	38	10	ADG79103	Schizophr
C 245	11.6	55.2	46	8	ABX33858	Human ESR	Abx33858 Human ESR	C 318	11.4	54.3	39	6	ABS61225	Human pol
C 246	11.6	55.2	46	10	ADB14061	Human pro	Adb14061 Human pro	C 319	11.4	54.3	39	12	ADL65077	Human sin
C 247	11.6	55.2	46	10	ADB14065	Human mat	Adb14065 Human mat	C 320	11.4	54.3	39	12	ADL65224	Human sin
C 248	11.6	55.2	46	10	ADG26481	Human pro	Adg26481 Human pro	C 321	11.4	54.3	40	2	AAV85690	LRPS exon
C 249	11.6	55.2	46	10	ADG26477	Human pro	Adg26477 Human pro	C 322	11.4	54.3	40	6	ABN88696	E2F aptam
C 250	11.6	55.2	47	2	AAQ25091	DR-A enha	Aaq25091 DR-A enha	C 323	11.4	54.3	40	6	ABT11996	E coli ex
C 251	11.6	55.2	50	6	ABK86058	Protein C	Abk86058 Protein C	C 324	11.4	54.3	40	12	ADG25842	Human OAT
C 252	11.6	55.2	50	6	ABZ06497	Human leu	Abz06497 Human leu	C 325	11.4	54.3	41	9	ACC42022	Human SCN
C 253	11.6	55.2	50	6	ABZ06887	Human leu	Abz06887 Human leu	C 326	11.4	54.3	43	10	ADE15723	E. coli t
C 254	11.4	54.3	17	2	AAQ07263	S-region	Aaq07263 S-region	C 327	11.4	54.3	44	4	AAAL28558	Human SNP
C 255	11.4	54.3	20	2	AAAT1880	TCL-1 gen	Aat1880 TCL-1 gen	C 328	11.4	54.3	45	2	AAV01772	C. tracho
C 256	11.4	54.3	20	4	AAH45015	PCR prime	Aah45015 PCR prime	C 329	11.4	54.3	45	6	ABZ22133	Thioredox
C 257	11.4	54.3	20	6	ABK99735	Human RAI	Abk99735 Human RAI	C 330	11.4	54.3	45	6	ABZ22133	Thioredox
C 258	11.4	54.3	20	6	ABQ62344	Human syn	Abq62344 Human syn	C 331	11.4	54.3	46	2	AAAT15858	Thioredox
C 259	11.4	54.3	20	12	ADOS1318	Human UBE	Ados1318 Human UBE	C 332	11.4	54.3	47	3	AAZ67307	Human map
C 260	11.4	54.3	20	12	ADP81720	Human MAG	Adp81720 Human MAG	C 333	11.4	54.3	47	12	ADO18168	Primer of
C 261	11.4	54.3	20	12	ADP81750	Human mel	Adp81750 Human mel	C 334	11.4	54.3	48	6	ABN85198	Mutagenic
C 262	11.4	54.3	21	9	ADA113899	Short int	Ada113899 Short int	C 335	11.4	54.3	50	2	AAAX86588	PCR prime
C 263	11.4	54.3	22	5	ASL11698	Human odo	Asl11698 Human odo	C 336	11.2	53.3	50	3	AAZ61244	Primer Ac
C 264	11.4	54.3	22	6	ABK95513	Novel G-p	Abk95513 Novel G-p	C 337	11.2	53.3	50	3	AAZ61244	Primer Ac
C 265	11.4	54.3	22	6	ABK95513	Novel G-p	Abk95513 Novel G-p	C 338	11.2	53.3	50	3	AAZ61244	Primer Ac
C 266	11.4	54.3	22	11	ADL98011	Human olf	Adl98011 Human olf	C 339	11.2	53.3	50	3	AAZ61244	Primer Ac
C 267	11.4	54.3	22	12	ADH42719	Novel hum	Adh42719 Novel hum	C 340	11.2	53.3	19	3	AAAX86588	PCR prime
C 268	11.4	54.3	22	12	ADQ07020	Novel siR	Adq07020 Novel siR	C 341	11.2	53.3	19	3	AAAX86588	PCR prime
C 269	11.4	54.3	23	4	AAH23021	VEGPR-2 g	Aah23021 VEGPR-2 g	C 342	11.2	53.3	19	6	ABN91922	Vascular
C 270	11.4	54.3	23	10	ABX90512	Human VEG	Abx90512 Human VEG	C 343	11.2	53.3	19	6	ABN91922	Vascular
C 271	11.4	54.3	24	2	AAAT59862	Sense pri	Aat59862 Sense pri	C 344	11.2	53.3	20	4	AAAD02844	A. thalia
C 272	11.4	54.3	24	6	ABQ06153	Oligonuc1	Abq06153 Oligonuc1	C 345	11.2	53.3	20	6	AAAD1799	Human RBC
C 273	11.4	54.3	24	6	ABQ06111	Oligonuc1	Abq06111 Oligonuc1	C 346	11.2	53.3	20	6	ABN95151	Capture o
C 274	11.4	54.3	24	6	ABQ06194	Oligonuc1	Abq06194 Oligonuc1	C 347	11.2	53.3	20	12	ADJ56706	Rat hypot
C 275	11.4	54.3	24	6	ABN91269	Capture o	Abn91269 Capture o	C 348	11.2	53.3	20	12	ADJ56706	Rat hypot
C 276	11.4	54.3	24	6	ABN91268	Capture o	Abn91268 Capture o	C 349	11.2	53.3	20	12	ADJ56706	Rat hypot
C 277	11.4	54.3	25	2	AAAT61970	Primer co	Aat61970 Primer co	C 350	11.2	53.3	21	4	AAAF97527	Human Not
C 278	11.4	54.3	25	9	ACI19934	Human mic	Act19934 Human mic	C 351	11.2	53.3	21	4	AAAF97527	Human Not
C 279	11.4	54.3	25	9	ACI19934	Human mic	Act19934 Human mic	C 352	11.2	53.3	21	4	AAAF97527	Human Not
C 280	11.4	54.3	25	10	ADE34184	Plastid t	Ade34184 Plastid t	C 353	11.2	53.3	21	10	ADH72752	PCR prime
C 281	11.4	54.3	26	2	AAQ89943	Listeria	Aaq89943 Listeria	C 354	11.2	53.3	21	10	ADH72752	PCR prime
C 282	11.4	54.3	27	2	AAQ47090	Lymphotox	Aaq47090 Lymphotox	C 355	11.2	53.3	21	12	ADK96397	Primer of
C 283	11.4	54.3	27	2	AAAT73380	Primer ol	Aat73380 Primer ol	C 356	11.2	53.3	21	12	ADK96397	Primer of
C 284	11.4	54.3	27	2	AAV21946	Nuclease	Aav21946 Nuclease	C 357	11.2	53.3	21	12	ADK96397	Primer of
C 285	11.4	54.3	27	12	ADM98067	Mouse try	Adm98067 Mouse try	C 358	11.2	53.3	21	12	ADK96397	Primer of
C 286	11.4	54.3	27	12	ADM96248	Mouse try	Adm96248 Mouse try	C 359	11.2	53.3	22	12	ADK94910	Primer of
C 287	11.4	54.3	28	2	AAZ76390	Human tum	Aaz76390 Human tum	C 360	11.2	53.3	22	12	ADK94910	Primer of
C 288	11.4	54.3	28	2	AAAX5439	Human ade	Aax5439 Human ade	C 361	11.2	53.3	23	2	AAAT89558	Bloom's s
C 289	11.4	54.3	28	2	AAV55606	Primer fo	Aav55606 Primer fo	C 362	11.2	53.3	23	10	ADD89840	Human CAM
C 290	11.4	54.3	28	3	AAAX33983	Low adeno	Aax33983 Low adeno	C 363	11.2	53.3	23	10	ADD89840	Human CAM
C 291	11.4	54.3	28	3	AAAF20105	Human tum	Aaf20105 Human tum	C 364	11.2	53.3	24	6	ABQ04658	Human inf
C 292	11.4	54.3	28	4	AAAC62135	PCR prime	Aac62135 PCR prime	C 365	11.2	53.3	24	6	ABQ00342	Oligonuc1
C 293	11.4	54.3	28	10	ABZ95799	Human tum	Abz95799 Human tum	C 366	11.2	53.3	24	6	ABQ07006	Oligonuc1
C 294	11.4	54.3	28	11	ABD19539	Human tum	Abd19539 Human tum	C 367	11.2	53.3	24	6	ABQ10986	Oligonuc1
C 295	11.4	54.3	29	2	AAZ20234	Brassica	Aaz20234 Brassica	C 368	11.2	53.3	24	6	ABQ01521	Oligonuc1
C 296	11.4	54.3	29	2	AAZ20241	Mustard r	Aaz20241 Mustard r	C 369	11.2	53.3	24	6	ABQ01521	Oligonuc1
C 297	11.4	54.3	29	9	ADA27217	PCR prime	Ada27217 PCR prime	C 370	11.2	53.3	24	6	ABQ04699	Oligonuc1
C 298	11.4	54.3	30	2	AAQ45374	Primer to	Aaq45374 Primer to	C 371	11.2	53.3	24	6	ABQ06965	Oligonuc1
C 299	11.4	54.3	32	3	AAZ880592	P73-2-4 p	Aaz880592 P73-2-4 p	C 372	11.2	53.3	24	6	ABQ06965	Oligonuc1
C 300	11.4	54.3	33	3	AAZ880592	Human TRF	Aaz880592 Human TRF	C 373	11.2	53.3	24	6	ABQ06965	Oligonuc1
C 301	11.4	54.3	33	3	AAAC60124	Oligomer	Aac60124 Oligomer	C 374	11.2	53.3	24	10	ACC57628	Mouse MAP
C 302	11.4	54.3	33	3	AAAC60125	Oligomer	Aac60125 Oligomer	C 375	11.2	53.3	25	6	AAV15566	Sequence
C 303	11.4	54.3	33	3	AAAO7456	PCR prime	Aaa07456 PCR prime	C 376	11.2	53.3	25	6	ABQ12522	Oligonuc1
C 304	11.4	54.3	33	3	AAZ48628	Light cha	Aaz48628 Light cha	C 377	11.2	53.3	25	6	ABQ12522	Oligonuc1
C 305	11.4	54.3	33	3	AAAL12363	Feline hu	Aal12363 Feline hu	C 378	11.2	53.3	25	6	ABQ12563	Oligonuc1
C 306	11.4	54.3	33	5	AAAC83238	Anti-EGFR	Aac83238 Anti-EGFR	C 379	11.2	53.3	25	9	ACI43718	Human mic
C 307	11.4	54.3	33	6	ABK11443	Mouse DNA	Abk11443 Mouse DNA	C 380	11.2	53.3	25	9	ACI43718	Human mic
C 308	11.4	54.3	34	2	AAAT15853	Thermosta	Aat15853 Thermosta	C 381	11.2	53.3	25	9	ACK22648	Human mic
C 309	11.4	54.3	35	10	ADE50872	Human TRP	Ade50872 Human TRP	C 382	11.2	53.3	25	9	ACI05942	Human mic
C 310	11.4	54.3	35	12	ADL65324	Lactobaci	Adl65324 Lactobaci	C 383	11.2	53.3	25	9	ACI05942	Human mic
C 311	11.4	54.3	37	8	ACD53535	HBV G-cle	Acd53535 HBV G-cle	C 384	11.2	53.3	25	9	ACK22649	Human mic
C 312	11.4	54.3	37	8	ACD53533	HBV G-cle	Acd53533 HBV G-cle	C 385	11.2	53.3	25	9	ACK22649	Human mic
C 313	11.4	54.3	37	8	ACD53449	HBV G-cle	Acd53449 HBV G-cle	C 386	11.2	53.3	25	10	ABQ84410	DPPI0 PCR

387	11.2	53.3	26	2	AA0707447	Aax07447 Rhodother	C 460	11	52.4	21	9	ADAI13906	Adai13906 Short int
388	11.2	53.3	26	6	ABT04218	Abt04218 Human G-p	C 461	11	52.4	21	9	ADAI13902	Adai13902 Short int
389	11.2	53.3	26	8	ABZ69360	Abz69360 Bacteriop	C 462	11	52.4	21	9	ADAI13905	Adai13905 Short int
390	11.2	53.3	26	8	ABZ69364	Abz69364 Bacteriop	C 463	11	52.4	21	9	ADAI13900	Adai13900 Short int
391	11.2	53.3	26	12	ADH30968	Adh30968 Human G-p	C 464	11	52.4	21	9	ADAI13903	Adai13903 Short int
392	11.2	53.3	29	3	AAZ88270	Aaz88270 Sec B nuc	C 465	11	52.4	21	9	ADAI13898	Adai13898 Short int
393	11.2	53.3	29	3	AAQ49367	Aaq49367 PCR prime	C 466	11	52.4	21	9	ADAI13907	Adai13907 Short int
394	11.2	53.3	30	6	ABX67560	Abx67560 Novel Hel	C 467	11	52.4	21	9	ADAI13904	Adai13904 Short int
395	11.2	53.3	30	10	ADE15918	Ade15918 Non-antib	C 468	11	52.4	21	10	ADB88626	Adb88626 Frizzled-
396	11.2	53.3	31	8	AA053243	Aa053243 PCR prime	C 469	11	52.4	21	12	ADK97255	Adk97255 Primer of
397	11.2	53.3	31	10	AA053243	Aa053243 PCR prime	C 470	11	52.4	22	2	AAQ05279	Aaq05279 Sequence
398	11.2	53.3	31	12	AA053243	Aa053243 PCR prime	C 471	11	52.4	22	2	AAQ05279	Aaq05279 Sequence
399	11.2	53.3	31	12	ADL08094	Adl08094 Human SNP	C 472	11	52.4	22	3	AA05326	Aa05326 Hepatitis
400	11.2	53.3	32	9	ACF57397	Acf57397 Pichia pa	C 473	11	52.4	22	6	ABQ94026	Abq94026 NOV13 for
401	11.2	53.3	33	6	AAK99233	Aak99233 Corynebac	C 474	11	52.4	22	6	ABQ94026	Abq94026 NOV13 for
402	11.2	53.3	33	6	ABX2145	Abx2145 Corynebac	C 475	11	52.4	22	6	AD117602	Adi117602 Forward P
403	11.2	53.3	34	2	AA059674	Aa059674 Mutagenic	C 476	11	52.4	22	12	ADN42690	Adn42690 Human NOV
404	11.2	53.3	34	2	AA059674	Aa059674 Mutagenic	C 477	11	52.4	22	12	ADN42690	Adn42690 Human NOV
405	11.2	53.3	34	2	AA059674	Aa059674 Mutagenic	C 478	11	52.4	22	12	ADN42690	Adn42690 Human NOV
406	11.2	53.3	34	3	AAA14935	Aa14935 PCR prime	C 479	11	52.4	22	4	AAF28015	Aaf28015 Human TR1
407	11.2	53.3	36	6	AA046831	Aa046831 Sheep alp	C 480	11	52.4	24	4	AAF28015	Aaf28015 Human TR1
408	11.2	53.3	36	6	AA026509	Aa026509 199001 PC	C 481	11	52.4	24	6	ABA05138	Ab05138 Human cla
409	11.2	53.3	36	6	AA046797	Aa046797 199001 pr	C 482	11	52.4	24	6	ABA05138	Ab05138 Human cla
410	11.2	53.3	36	10	ADE15912	Ade15912 Non-antib	C 483	11	52.4	24	6	ABA05138	Ab05138 Human cla
411	11.2	53.3	36	12	ADM93359	Adm93359 Chimeric	C 484	11	52.4	24	8	ABV77201	Abv77201 PCR prime
412	11.2	53.3	38	10	ADG78987	Adg78987 Schizophr	C 485	11	52.4	24	9	ACH66209	Ach66209 Human tum
413	11.2	53.3	40	2	AA0796608	Aa0796608 Cycloitol-	C 486	11	52.4	24	9	ACH66209	Ach66209 Human tum
414	11.2	53.3	41	3	AA053863	Aa053863 Primer GD	C 487	11	52.4	25	2	AA053863	Aa053863 Primer GD
415	11.2	53.3	41	4	AA048110	Aa048110 Ribulose	C 488	11	52.4	25	2	AA053863	Aa053863 Primer GD
416	11.2	53.3	41	6	AB0860083	Ab0860083 Human DNA	C 489	11	52.4	25	2	AA053863	Aa053863 Primer GD
417	11.2	53.3	41	6	AB0860083	Ab0860083 Human DNA	C 490	11	52.4	25	2	AA053863	Aa053863 Primer GD
418	11.2	53.3	41	6	AB0860083	Ab0860083 Human DNA	C 491	11	52.4	25	2	AA053863	Aa053863 Primer GD
419	11.2	53.3	41	6	AB0860083	Ab0860083 Human DNA	C 492	11	52.4	25	2	AA053863	Aa053863 Primer GD
420	11.2	53.3	41	12	ADM95046	Adm95046 Nitrosomo	C 493	11	52.4	25	5	AA053863	Aa053863 Primer GD
421	11.2	53.3	44	10	ACC79660	Acc79660 Camel ant	C 494	11	52.4	25	8	ABV81957	Abv81957 Human HTP
422	11.2	53.3	45	12	ADH27909	Adh27909 Human chr	C 495	11	52.4	25	8	ABV81957	Abv81957 Human HTP
423	11.2	53.3	46	6	ABA90154	Ab090154 Oestrogen	C 496	11	52.4	25	8	ABV81957	Abv81957 Human HTP
424	11.2	53.3	46	6	AB087833	Ab087833 Human ESR	C 497	11	52.4	25	8	ABV81957	Abv81957 Human HTP
425	11.2	53.3	46	6	AB087863	Ab087863 Human ESR	C 498	11	52.4	25	8	ABV81957	Abv81957 Human HTP
426	11.2	53.3	46	8	ABX33859	Abx33859 Human ESR	C 499	11	52.4	25	9	ACK19865	Ack19865 Human mic
427	11.2	53.3	46	8	ABX33869	Abx33869 Human ESR	C 500	11	52.4	25	9	ACK19865	Ack19865 Human mic
428	11.2	53.3	47	3	AA0268191	Aa0268191 Human map	C 501	11	52.4	25	9	ACK19865	Ack19865 Human mic
429	11.2	53.3	47	8	AB0225341	Ab0225341 PCR prime	C 502	11	52.4	25	9	ACK19865	Ack19865 Human mic
430	11.2	53.3	47	8	AB0225341	Ab0225341 PCR prime	C 503	11	52.4	25	9	ACK19865	Ack19865 Human mic
431	11.2	53.3	49	3	AA099358	Aa099358 Human ser	C 504	11	52.4	25	9	ACK19865	Ack19865 Human mic
432	11.2	53.3	49	3	AA099358	Aa099358 Human ser	C 505	11	52.4	25	9	ACK19865	Ack19865 Human mic
433	11.2	53.3	50	4	AA028113	Aa028113 Human SNP	C 506	11	52.4	25	9	ACK19865	Ack19865 Human mic
434	11.2	53.3	50	4	AA028113	Aa028113 Human SNP	C 507	11	52.4	25	9	ACK19865	Ack19865 Human mic
435	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 508	11	52.4	25	10	ADB73746	Adb73746 Human PRO
436	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 509	11	52.4	25	10	ADB73746	Adb73746 Human PRO
437	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 510	11	52.4	25	10	ADB73746	Adb73746 Human PRO
438	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 511	11	52.4	25	10	ADB73746	Adb73746 Human PRO
439	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 512	11	52.4	25	10	ADB73746	Adb73746 Human PRO
440	11.2	53.3	50	6	AB0207111	Ab0207111 Human leu	C 513	11	52.4	25	10	ADB73746	Adb73746 Human PRO
441	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 514	11	52.4	25	10	ADB73746	Adb73746 Human PRO
442	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 515	11	52.4	25	10	ADB73746	Adb73746 Human PRO
443	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 516	11	52.4	25	10	ADB73746	Adb73746 Human PRO
444	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 517	11	52.4	25	10	ADB73746	Adb73746 Human PRO
445	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 518	11	52.4	25	10	ADB73746	Adb73746 Human PRO
446	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 519	11	52.4	25	10	ADB73746	Adb73746 Human PRO
447	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 520	11	52.4	25	10	ADB73746	Adb73746 Human PRO
448	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 521	11	52.4	25	10	ADB73746	Adb73746 Human PRO
449	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 522	11	52.4	25	10	ADB73746	Adb73746 Human PRO
450	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 523	11	52.4	25	10	ADB73746	Adb73746 Human PRO
451	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 524	11	52.4	25	10	ADB73746	Adb73746 Human PRO
452	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 525	11	52.4	25	10	ADB73746	Adb73746 Human PRO
453	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 526	11	52.4	25	10	ADB73746	Adb73746 Human PRO
454	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 527	11	52.4	25	10	ADB73746	Adb73746 Human PRO
455	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 528	11	52.4	25	10	ADB73746	Adb73746 Human PRO
456	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 529	11	52.4	25	10	ADB73746	Adb73746 Human PRO
457	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 530	11	52.4	25	10	ADB73746	Adb73746 Human PRO
458	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 531	11	52.4	25	10	ADB73746	Adb73746 Human PRO
459	11.2	53.3	50	12	ADP12693	Adp12693 50-mer ol	C 532	11	52.4	25	12	ADB48574	Adb48574 Human PRO

C 533	11	52.4	25	12	AD89675	Human PRO	Ad89675	Human PRO	11	52.4	36	8	ACD56094	Ad56094	HBV enzym
C 534	11	52.4	25	12	AD61315	Human PRO	Ad61315	Human PRO	11	52.4	36	10	AD606506	Ad606506	Vector pg
C 535	11	52.4	25	12	AD640007	Human PRO	Ad640007	Human PRO	11	52.4	36	10	AD606505	Ad606505	Vector pg
C 536	11	52.4	25	12	AD645803	Human PRO	Ad645803	Human PRO	11	52.4	36	12	AD63897	Ad63897	Plant lip
C 537	11	52.4	25	12	AD624199	Human PRO	Ad624199	Human PRO	11	52.4	36	12	AD63897	Ad63897	Plant lip
C 538	11	52.4	25	12	AD640631	Human PRO	Ad640631	Human PRO	11	52.4	36	12	AD649147	Ad649147	PDGF rece
C 539	11	52.4	25	12	AD633575	Human PRO	Ad633575	Human PRO	11	52.4	37	3	AC68506	Ac68506	Periplaki
C 540	11	52.4	25	12	AD633558	Human PRO	Ad633558	Human PRO	11	52.4	37	4	AAH96740	Aah96740	Human Chk
C 541	11	52.4	25	12	AD627025	Human PRO	Ad627025	Human PRO	11	52.4	37	4	AAH96771	Aah96771	Human Chk
C 542	11	52.4	25	12	AD627661	Human PRO	Ad627661	Human PRO	11	52.4	37	4	ABK05536	Abk05536	Human NOG
C 543	11	52.4	25	12	AD641255	Human PRO	Ad641255	Human PRO	11	52.4	37	4	ABK05562	Abk05562	Human NOG
C 544	11	52.4	25	12	AD632934	Human PRO	Ad632934	Human PRO	11	52.4	37	4	ABL47776	Ab147776	Human GRI
C 545	11	52.4	25	12	AD625300	Human PRO	Ad625300	Human PRO	11	52.4	37	6	ABK20763	Abk20763	Human ERG
C 546	11	52.4	25	12	AD626401	Human PRO	Ad626401	Human PRO	11	52.4	37	6	ABK20828	Abk20828	Human ERG
C 547	11	52.4	25	12	AD634190	Human PRO	Ad634190	Human PRO	11	52.4	37	6	ABK59194	Abk59194	Human CLC
C 548	11	52.4	25	12	AD646427	Human PRO	Ad646427	Human PRO	11	52.4	37	6	ABK59214	Abk59214	Human CLC
C 549	11	52.4	25	12	AD650413	Human PRO	Ad650413	Human PRO	11	52.4	37	6	ABK59220	Abk59220	Human CLC
C 548	11	52.4	25	12	AD650413	Human PRO	Ad650413	Human PRO	11	52.4	37	8	ACD53445	AcD53445	HBV G-cle
C 550	11	52.4	25	12	AD649789	Human PRO	Ad649789	Human PRO	11	52.4	37	8	ACC70729	Acc70729	Yeast PCR
C 551	11	52.4	25	12	AD651661	Human PRO	Ad651661	Human PRO	11	52.4	37	11	ADM55096	Adm55096	G-cleaver
C 552	11	52.4	25	12	AD649165	Human PRO	Ad649165	Human PRO	11	52.4	37	12	ADM64057	Adm64057	Hepatitis
C 553	11	52.4	25	12	AD648541	Human PRO	Ad648541	Human PRO	11	52.4	37	12	ADM61955	Adm61955	Hepatitis
C 554	11	52.4	25	12	AD651037	Human PRO	Ad651037	Human PRO	11	52.4	38	2	AAT66699	Aat66699	Primer cy
C 555	11	52.4	25	12	AD658981	Human PRO	Ad658981	Human PRO	11	52.4	38	2	AX01663	Ax01663	E. coli a
C 556	11	52.4	25	12	AD682437	Human PRO	Ad682437	Human PRO	11	52.4	38	4	AAF89669	Aaf89669	Probe use
C 557	11	52.4	25	12	ADH25462	Human neu	Adh25462	Human neu	11	52.4	39	4	ABS611354	Abs611354	Human bra
C 558	11	52.4	25	12	ADL07073	Human PRO	Adl07073	Human PRO	11	52.4	40	2	AAV36565	Aav36565	Self-clea
C 559	11	52.4	25	12	ADL07073	Human PRO	Adl07073	Human PRO	11	52.4	40	6	ABQ74999	Abq74999	T7 1.2 ge
C 560	11	52.4	25	12	AD049125	Human ade	Ado49125	Human ade	11	52.4	41	4	AAF24108	Aaf24108	Corynebac
C 561	11	52.4	25	12	ADP16496	Renal cel	Adp16496	Renal cel	11	52.4	41	6	AA242897	Aa1242897	Human syn
C 562	11	52.4	26	3	AA55838	Histone d	Aa55838	Histone d	11	52.4	41	6	ABZ43794	Abz43794	Human ary
C 563	11	52.4	26	3	AA55838	Human his	Aa55838	Human his	11	52.4	41	6	ABZ45033	Abz45033	Human ald
C 564	11	52.4	26	3	AAH43120	Antisense	Aah43120	Antisense	11	52.4	41	6	ABZ49136	Abz49136	Human ald
C 565	11	52.4	26	4	AAH43120	Antisense	Aah43120	Antisense	11	52.4	41	6	ABZ50831	Abz50831	Human ary
C 566	11	52.4	26	4	AAH43120	Antisense	Aah43120	Antisense	11	52.4	41	10	ACC42768	Acc42768	Histone H
C 567	11	52.4	26	4	AAH43120	Antisense	Aah43120	Antisense	11	52.4	41	10	ACC42768	Acc42768	Histone H
C 568	11	52.4	26	4	AAH43120	Antisense	Aah43120	Antisense	11	52.4	41	10	ACC42768	Acc42768	Histone H
C 569	11	52.4	26	10	ADC51190	Human cel	Adc51190	Human cel	11	52.4	42	6	ABQ74985	Abq74985	Bacteriop
C 570	11	52.4	27	2	AAQ34832	PCR prime	Aaq34832	PCR prime	11	52.4	42	3	AAZ96525	Aaz96525	T cell an
C 571	11	52.4	27	2	AAQ34832	PCR prime	Aaq34832	PCR prime	11	52.4	42	12	ADG27621	Adg27621	Nucleic a
C 572	11	52.4	27	6	ABK15325	PCR prime	Abk15325	PCR prime	11	52.4	46	3	AAZ96525	Aaz96525	T cell an
C 573	11	52.4	27	12	ADN06126	Cricetulu	Adn06126	Cricetulu	11	52.4	46	5	AAZ44096	Aaz44096	Neisseria
C 574	11	52.4	28	2	AA51027	5' primer	Aat51027	5' primer	11	52.4	46	5	AAZ44096	Aaz44096	Neisseria
C 575	11	52.4	28	2	AA51028	5' primer	Aat51028	5' primer	11	52.4	46	6	ABA90117	AbA90117	Oestrogen
C 576	11	52.4	28	2	AAV10595	Primer us	Aav10595	Primer us	11	52.4	46	6	ABA90149	AbA90149	Oestrogen
C 577	11	52.4	28	3	AAAL5116	PCR prime	AaA51116	PCR prime	11	52.4	46	6	ABA90168	AbA90168	Oestrogen
C 578	11	52.4	28	4	AAAD03560	Oligonucl	Aad03560	Oligonucl	11	52.4	46	6	ABA90110	AbA90110	Oestrogen
C 579	11	52.4	28	4	AAAF82467	Phagemid	Aaf82467	Phagemid	11	52.4	46	6	ABA90118	AbA90118	Oestrogen
C 580	11	52.4	28	6	AAAF82467	Phagemid	Aaf82467	Phagemid	11	52.4	46	6	ABA90127	AbA90127	Oestrogen
C 581	11	52.4	28	10	ACF03379	Mycoplasma	Acf03379	Mycoplasma	11	52.4	46	6	ABA90129	AbA90129	Oestrogen
C 582	11	52.4	28	12	ADJ76691	OAS2 reve	Adj76691	OAS2 reve	11	52.4	46	6	ABA90131	AbA90131	Oestrogen
C 583	11	52.4	29	2	AAV09775	Human mar	Aav09775	Human mar	11	52.4	46	6	ABA90103	AbA90103	Oestrogen
C 584	11	52.4	29	2	AAV09775	Human mar	Aav09775	Human mar	11	52.4	46	6	ABA90119	AbA90119	Oestrogen
C 585	11	52.4	29	3	AAV09775	Human mar	Aav09775	Human mar	11	52.4	46	6	ABA90136	AbA90136	Oestrogen
C 586	11	52.4	30	2	AAQ28031	Primer T4	Aaq28031	Primer T4	11	52.4	46	6	ABA90167	AbA90167	Oestrogen
C 587	11	52.4	30	6	ABK89309	N-acetyl g	Abk89309	N-acetyl g	11	52.4	46	6	ABQ87827	Abq87827	Human ESR
C 588	11	52.4	30	6	ABK89309	N-acetyl g	Abk89309	N-acetyl g	11	52.4	46	6	ABQ87819	Abq87819	Human ESR
C 589	11	52.4	30	8	ABT16385	Gene ther	Abt16385	Gene ther	11	52.4	46	6	ABQ87836	Abq87836	Human ESR
C 590	11	52.4	30	10	AD606104	BMMI DNA	Ad606104	BMMI DNA	11	52.4	46	6	ABQ87858	Abq87858	Human ESR
C 591	11	52.4	30	12	AD022111	Taqman pr	Ado22111	Taqman pr	11	52.4	46	6	ABQ87828	Abq87828	Human ESR
C 592	11	52.4	31	3	AA788676	Human gen	Aa788676	Human gen	11	52.4	46	6	ABQ87877	Abq87877	Human ESR
C 593	11	52.4	32	3	AAZ55176	Neisseria	Aaz55176	Neisseria	11	52.4	46	6	ABQ87826	Abq87826	Human ESR
C 594	11	52.4	33	6	AAZ42895	Human syn	Aal42895	Human syn	11	52.4	46	6	ABQ87876	Abq87876	Human ESR
C 595	11	52.4	33	10	ACC42766	Histone H	Acc42766	Histone H	11	52.4	46	6	ABQ87812	Abq87812	Human ESR
C 596	11	52.4	34	6	ABA99727	Bovine BG	AbA99727	Bovine BG	11	52.4	46	6	ABQ87838	Abq87838	Human ESR
C 597	11	52.4	34	6	ABK85579	Newcastle	Abk85579	Newcastle	11	52.4	46	6	ABQ87840	Abq87840	Human ESR
C 598	11	52.4	34	6	ABK85580	Newcastle	Abk85580	Newcastle	11	52.4	46	6	ABQ87845	Abq87845	Human ESR
C 599	11	52.4	35	2	AAV07321	Nucleotid	Aav07321	Nucleotid	11	52.4	46	8	ABX33855	Abx33855	Human ESR
C 600	11	52.4	35	4	AAAF62583	Oligonucl	Aaf62583	Oligonucl	11	52.4	46	8	ABX33876	Abx33876	Human ESR
C 601	11	52.4	35	6	AB567610	PCR prime	Ab567610	PCR prime	11	52.4	46	8	ABX33864	Abx33864	Human ESR
C 602	11	52.4	35	11	ADM79773	Group B S	Adm79773	Group B S	11	52.4	46	8	ABX33894	Abx33894	Human ESR
C 603	11	52.4	35	11	ADM79667	Group B S	Adm79667	Group B S	11	52.4	46	8	ABX33872	Abx33872	Human ESR
C 604	11	52.4	35	12	ADF91754	Human cat	Adf91754	Human cat	11	52.4	46	8	ABX33881	Abx33881	Human ESR
C 605	11	52.4	35	12	ADO18989	Sequence	Ado18989	Sequence	11	52.4	46	8	ABX33863	Abx33863	Human ESR

c 679	11	52.4	46	8	ABX333862	Abx33862 Human ESR	752	11	52.4	50	12	ADG51765	Adg51765 Human PRO
c 680	11	52.4	46	8	ABX33912	Abx33912 Human ESR	753	11	52.4	50	12	ADG49269	Adg49269 Human PRO
c 681	11	52.4	46	8	ABX33913	Abx33913 Human ESR	754	11	52.4	50	12	ADG48645	Adg48645 Human PRO
c 682	11	52.4	46	8	ABX33848	Abx33848 Human ESR	755	11	52.4	50	12	ADG51141	Adg51141 Human PRO
c 683	11	52.4	46	8	ABX33874	Abx33874 Human ESR	756	11	52.4	50	12	ADG59085	Adg59085 Human PRO
c 684	11	52.4	48	3	AAA30308	Aaa30308 M. tuberc	757	11	52.4	50	12	ADG62541	Adg62541 Human PRO
c 685	11	52.4	48	6	ABQ94452	Abq94452 Tumour su	758	11	52.4	50	12	ADH25566	Adh25566 Human neu
c 686	11	52.4	49	6	ABQ75061	Abq75061 Vector co	759	11	52.4	50	12	ADM17343	Adm17343 Human PRO
c 687	11	52.4	50	2	AAT02969	Aat02969 Interleuk	760	11	52.4	50	12	ADL07177	Adl07177 Human PRO
c 688	11	52.4	50	2	AA234184	Aa234184 Human PRO	761	10.8	51.4	16	2	AAT43395	Aat43395 Octopine
c 689	11	52.4	50	3	AAC58480	Aac58480 Human PRO	c 762	10.8	51.4	16	2	AAV64339	Aav64339 A. tumefa
c 690	11	52.4	50	3	AAAC78806	Aaa78806 Human PRO	c 763	10.8	51.4	17	8	ABT38386	Abt38386 Tumour su
c 691	11	52.4	50	3	AAA77646	Aaa77646 Human PRO	764	10.8	51.4	17	10	ADI50569	Adi50569 Human tum
c 692	11	52.4	50	4	AAL32133	Aal32133 Human SNP	c 765	10.8	51.4	17	10	ADI48125	Adi48125 Human tum
c 693	11	52.4	50	4	AAL32134	Aal32134 Human SNP	c 766	10.8	51.4	17	11	ADM43630	Adm43630 Signature
c 694	11	52.4	50	4	AAL32098	Aal32098 Human SNP	767	10.8	51.4	18	8	ABX79721	Abx79721 EST poly
c 695	11	52.4	50	4	AAH90486	Aah90486 Human cto	c 768	10.8	51.4	18	10	ADF48806	Adf48806 Vibrio pa
c 696	11	52.4	50	6	AB202787	Ab202787 Human leu	769	10.8	51.4	19	10	ADC84328	Adc84328 Human pap
c 697	11	52.4	50	6	AB204399	Ab204399 Human leu	770	10.8	51.4	19	10	ADF44230	Adf44230 HPV CP806
c 698	11	52.4	50	6	AB201657	Ab201657 Human leu	c 771	10.8	51.4	19	12	ADQ60771	Adq60771 Anti-AKT3
c 699	11	52.4	50	8	AB204224	Ab204224 Human leu	772	10.8	51.4	20	2	ABX79128	Abx79128 Primer At
c 700	11	52.4	50	8	ACA63752	Aca63752 Novel hum	773	10.8	51.4	20	6	ABQ92652	Abq92652 Human leu
c 701	11	52.4	50	8	ACA71916	Aca71916 Human PRO	774	10.8	51.4	20	6	ABZ30709	Abz30709 Candida a
c 702	11	52.4	50	8	ABX92556	Abx92556 Human PRO	775	10.8	51.4	20	6	ABN89725	Abn89725 Human ABC
c 703	11	52.4	50	8	ACA66297	Aca66297 Human sec	c 776	10.8	51.4	20	6	ABN89725	Abn89725 Human ABC
c 704	11	52.4	50	9	ADA24883	Ada24883 Secreted	c 777	10.8	51.4	20	12	ADH10876	Adh10876 Human cat
c 705	11	52.4	50	9	ACD29898	Acd29898 Novel hum	778	10.8	51.4	20	12	ADH10803	Adh10803 Human cat
c 706	11	52.4	50	9	ADA12544	Ada12544 Human sec	c 779	10.8	51.4	20	12	ADI1686	Adi1686 Human pro
c 707	11	52.4	50	9	ACD29313	Acd29313 Novel hum	c 780	10.8	51.4	20	12	ADI181745	Adi181745 Human pro
c 708	11	52.4	50	10	ADB73850	Adb73850 Human PRO	781	10.8	51.4	20	12	ADJ86940	Adj86940 Nucleic a
c 709	11	52.4	50	10	ADB76566	Adb76566 Human PRO	c 782	10.8	51.4	20	12	ADK95978	Adk95978 Primer of
c 710	11	52.4	50	10	ADC43992	Adc43992 Human PRO	c 783	10.8	51.4	20	12	ADK94362	Adk94362 Forward p
c 711	11	52.4	50	10	ADC61752	Adc61752 Human PRO	c 784	10.8	51.4	20	12	ADM11814	Adm11814 Endotheli
c 712	11	52.4	50	10	ADC63716	Adc63716 Human PRO	785	10.8	51.4	20	12	ADN01352	Adn01352 Endotheli
c 713	11	52.4	50	10	ADC66816	Adc66816 Human PRO	c 786	10.8	51.4	20	12	ADN01281	Adn01281 Endotheli
c 714	11	52.4	50	10	ADC68940	Adc68940 Human PRO	c 787	10.8	51.4	20	12	ADP68662	Adp68662 Human PPA
c 715	11	52.4	50	10	ADC63000	Adc63000 Human PRO	c 788	10.8	51.4	21	2	AAH83448	Aah83448 ZAM retro
c 716	11	52.4	50	10	ADC68065	Adc68065 Human PRO	c 789	10.8	51.4	21	4	AAFA96690	Aafa96690 Human gen
c 717	11	52.4	50	10	ADC41385	Adc41385 Human PRO	c 790	10.8	51.4	21	6	ABA04885	Ab04885 TT virus
c 718	11	52.4	50	10	ADC67440	Adc67440 Human PRO	c 791	10.8	51.4	21	10	ABV75972	Abv75972 Mouse GLU
c 719	11	52.4	50	10	ADC62376	Adc62376 Human PRO	792	10.8	51.4	21	10	ADL07578	Adl07578 R. picket
c 720	11	52.4	50	10	ADC42009	Adc42009 Human PRO	c 793	10.8	51.4	21	11	ADJ12916	Adj12916 Human DNA
c 721	11	52.4	50	10	ADE49378	Ad49378 Human PRO	c 794	10.8	51.4	21	11	ADJ13508	Adj13508 Human DNA
c 722	11	52.4	50	10	ADE35432	Ad35432 Human PRO	c 795	10.8	51.4	21	11	ADM65359	Adm65359 NRY polym
c 723	11	52.4	50	10	ADE16546	Ad16546 Human PRO	c 796	10.8	51.4	22	2	AAQ92322	Aaq92322 Mango thi
c 724	11	52.4	50	10	ADB73161	Adb73161 Human PRO	797	10.8	51.4	22	2	AAQ09940	Aaq09940 Human bta
c 725	11	52.4	50	10	ADD72519	Ad72519 Human PRO	c 798	10.8	51.4	22	2	AAV15247	Aav15247 Thioester
c 726	11	52.4	50	10	ABE11710	Ab11710 Human PRO	c 799	10.8	51.4	22	3	AAAG6728	Aag6728 Dog genom
c 727	11	52.4	50	10	ADF47184	Adf47184 Human PRO	800	10.8	51.4	22	8	ABZ76438	Abz76438 IBV S-1 g
c 728	11	52.4	50	10	ADG33407	Adg33407 Human DNA	c 801	10.8	51.4	23	8	AAZ55207	Aaz55207 HIV-1 tar
c 729	11	52.4	50	10	ADG52941	Adg52941 Human PRO	c 802	10.8	51.4	24	2	AAT43545	Aat43545 Primer 72
c 730	11	52.4	50	10	ADG60261	Adg60261 Human PRO	803	10.8	51.4	24	2	AAV81937	Aav81937 Caenorhab
c 731	11	52.4	50	10	ADL61021	Adl61021 Human PRO	804	10.8	51.4	24	3	AAA12813	Aaa12813 PCR prime
c 732	11	52.4	50	10	ACD42717	Acd42717 Secreted	805	10.8	51.4	24	6	ADJ2635	Adj2635 acea18b
c 733	11	52.4	50	12	ADE48678	Ad48678 Human PRO	806	10.8	51.4	24	11	ADL95470	Adl95470 Angiotens
c 734	11	52.4	50	12	ADE89779	Ad89779 Human PRO	807	10.8	51.4	24	12	ADQ90193	Adq90193 Chlamydia
c 735	11	52.4	50	12	ADP61419	Adp61419 Human PRO	808	10.8	51.4	25	2	AZF221338	Aaz21338 Shigella
c 736	11	52.4	50	12	ADP40111	Adp40111 Human PRO	809	10.8	51.4	25	4	AAAF79599	Aaf79599 Human Akt
c 737	11	52.4	50	12	ADP45907	Adp45907 Human PRO	c 810	10.8	51.4	25	4	AAH40525	Aah40525 SNP speci
c 738	11	52.4	50	12	ADP24303	Adp24303 Human PRO	c 811	10.8	51.4	25	5	AAI62117	Aai62117 Soybean 3
c 739	11	52.4	50	12	ADP40735	Adp40735 Human PRO	812	10.8	51.4	25	9	ACI85321	Act85321 Human mic
c 740	11	52.4	50	12	ADP23679	Adp23679 Human PRO	813	10.8	51.4	25	9	ACI85320	Act85320 Human mic
c 741	11	52.4	50	12	ADP33662	Adp33662 Human PRO	814	10.8	51.4	25	9	ACK05637	Ack05637 Human mic
c 742	11	52.4	50	12	ADP27129	Adp27129 Human PRO	c 815	10.8	51.4	25	9	ACI65687	Act65687 Human mic
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c 746	11	52.4	50	12	ADP25404	Adp25404 Human PRO	c 819	10.8	51.4	25	9	ACK181476	Act181476 Human mic
c 747	11	52.4	50	12	ADP26505	Adp26505 Human PRO	c 820	10.8	51.4	25	9	ACH52970	Ach52970 DNA targe
c 748	11	52.4	50	12	ADP34294	Adp34294 Human PRO	c 821	10.8	51.4	25	10	ADC26465	Adc26465 NOV prote
c 749	11	52.4	50	12	ADP46531	Adp46531 Human PRO	822	10.8	51.4	26	2	AAQ63946	Aaq63946 Probe for
c 750	11	52.4	50	12	ADG50517	Adg50517 Human PRO	c 823	10.8	51.4	26	3	AAZ91983	Aaz91983 Mahogany
c 751	11	52.4	50	12	ADG49893	Adg49893 Human PRO	c 824	10.8	51.4	26	6	ABL49982	Ab149982 Rice OSSA

C 825	10.8	51.4	27	4	AH21598	Human hyp	Aah21598	Human hyp	C 898	10.8	51.4	50	4	AA28112	Human SNP
C 826	10.8	51.4	27	8	ABZ68363	Primer Te	Abz68363	Primer Te	C 899	10.8	51.4	50	4	AAI78425	Human sil
C 827	10.8	51.4	27	8	ABT16214	NOVX rela	Abt16214	NOVX rela	C 900	10.8	51.4	50	6	ABZ01191	Human leu
C 828	10.8	51.4	27	10	ADC26483	NOV prote	Adc26483	NOV prote	C 901	10.8	51.4	50	6	ABZ03490	Human leu
C 829	10.8	51.4	27	10	ADC51654	5' PCR pr	Adc51654	5' PCR pr	C 902	10.8	51.4	50	10	ADG33470	Human DNA
C 830	10.8	51.4	27	12	ADO14905	Novel hum	Ado14905	Novel hum	C 903	10.6	50.5	17	2	AAT53604	Rat ICAM
C 831	10.8	51.4	27	12	ADP69073	Novel hum	Adp69073	Novel hum	C 904	10.6	50.5	17	6	ABV79960	Human HTP
C 832	10.8	51.4	28	2	AX15329	Oligonuc	Ax15329	Oligonuc	C 905	10.6	50.5	17	6	ABV79961	Human HTP
C 833	10.8	51.4	28	3	AZ237290	PCR prime	Aaz37290	PCR prime	C 906	10.6	50.5	17	10	ADF62571	Human PCC
C 834	10.8	51.4	28	3	AA10286	Lambda ph	Aaa10286	Lambda ph	C 907	10.6	50.5	18	3	AAA66931	Dog genom
C 835	10.8	51.4	28	4	AZ26450	HIV-1 pol	Aaf26450	HIV-1 pol	C 908	10.6	50.5	18	4	AAH74505	PCR prime
C 836	10.8	51.4	28	6	ABL60690	S. enteri	Abi60690	S. enteri	C 909	10.6	50.5	18	4	AAH74505	PCR prime
C 837	10.8	51.4	28	6	ABK96401	PCR prime	Abk96401	PCR prime	C 910	10.6	50.5	19	12	ADP71078	Mutant hu
C 838	10.8	51.4	29	3	AA16765	Human sec	Aax16765	Human sec	C 911	10.6	50.5	19	3	AAZ37296	PCR prime
C 839	10.8	51.4	29	10	ADC22115	Group II	Aac22115	Group II	C 912	10.6	50.5	19	6	AAZ37296	PCR prime
C 840	10.8	51.4	30	2	AAV4583	Primer 40	Aav44583	Primer 40	C 913	10.6	50.5	19	12	ADM16144	Murine SA
C 841	10.8	51.4	30	6	ABX68919	Novel Hel	Abx68919	Novel Hel	C 914	10.6	50.5	20	2	AAQ93439	Equine cl
C 842	10.8	51.4	30	12	ADM11826	Composite	Adm11826	Composite	C 915	10.6	50.5	20	2	AAQ93440	Equine cl
C 843	10.8	51.4	30	12	ADP08008	Human RAD	Adp08008	Human RAD	C 916	10.6	50.5	20	2	AAQ93440	Equine cl
C 844	10.8	51.4	31	2	AAV67583	Nucleotid	Aav67583	Nucleotid	C 917	10.6	50.5	20	2	AAQ93440	Equine cl
C 845	10.8	51.4	31	2	AAZ06354	Human bia	Aax06354	Human bia	C 918	10.6	50.5	20	2	AAQ93440	Equine cl
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C 847	10.8	51.4	31	3	AZ45640	PCR prime	Aaz45640	PCR prime	C 920	10.6	50.5	20	2	AAQ93440	Equine cl
C 848	10.8	51.4	31	3	AAZ79211	Human gen	Aaz79211	Human gen	C 921	10.6	50.5	20	2	AAQ93440	Equine cl
C 849	10.8	51.4	31	3	AAZ79211	Human gen	Aaz79211	Human gen	C 922	10.6	50.5	20	2	AAQ93440	Equine cl
C 850	10.8	51.4	31	12	ADO79546	KIAA0783	Ado79546	KIAA0783	C 923	10.6	50.5	20	2	AAQ93440	Equine cl
C 851	10.8	51.4	31	12	ADO79546	KIAA0783	Ado79546	KIAA0783	C 924	10.6	50.5	20	2	AAQ93440	Equine cl
C 852	10.8	51.4	32	2	AAZ87128	platelet	Aax87128	platelet	C 925	10.6	50.5	20	3	AAQ93440	Equine cl
C 853	10.8	51.4	32	6	ABK53072	Tobacco s	Abk53072	Tobacco s	C 926	10.6	50.5	20	3	AAQ93440	Equine cl
C 854	10.8	51.4	33	2	AAQ46735	HIV ampli	Aaq46735	HIV ampli	C 927	10.6	50.5	20	3	AAQ93440	Equine cl
C 855	10.8	51.4	33	2	AAQ44311	HIV-1 am	Aaq44311	HIV-1 am	C 928	10.6	50.5	20	4	AAH24675	Nucleotid
C 856	10.8	51.4	33	2	AAQ49511	Human imm	Aaq49511	Human imm	C 929	10.6	50.5	20	4	AAH24675	Nucleotid
C 857	10.8	51.4	33	5	AB197660	Endogenou	Abi97660	Endogenou	C 930	10.6	50.5	20	4	AAH24675	Nucleotid
C 858	10.8	51.4	33	6	ABQ76004	Human ger	Abq76004	Human ger	C 931	10.6	50.5	20	5	AAQ93440	Equine cl
C 859	10.8	51.4	34	12	ADJ93351	Bpntase 3	Adj93351	Bpntase 3	C 932	10.6	50.5	20	5	AAQ93440	Equine cl
C 860	10.8	51.4	35	10	ADF50493	Mutagenic	Adf50493	Mutagenic	C 933	10.6	50.5	20	5	AAQ93440	Equine cl
C 861	10.8	51.4	35	10	ADF50494	Mutagenic	Adf50494	Mutagenic	C 934	10.6	50.5	20	6	ABN86460	E. coli h
C 862	10.8	51.4	35	10	ADF76038	RNA PCR p	Adf76038	RNA PCR p	C 935	10.6	50.5	20	6	ABN86460	E. coli h
C 863	10.8	51.4	35	10	ADF75958	DNA PCR p	Adf75958	DNA PCR p	C 936	10.6	50.5	20	8	ACC49979	SYNTHETIC
C 864	10.8	51.4	36	2	AAQ74610	Primer fo	Aaq74610	Primer fo	C 937	10.6	50.5	20	8	ACC49979	SYNTHETIC
C 865	10.8	51.4	36	6	ABL49295	Human lun	Abi49295	Human lun	C 938	10.6	50.5	20	8	ACC49979	SYNTHETIC
C 866	10.8	51.4	36	6	ABQ92481	Human lun	Abq92481	Human lun	C 939	10.6	50.5	20	9	ACC49979	SYNTHETIC
C 867	10.8	51.4	36	9	ADA28534	Lung tumo	Ada28534	Lung tumo	C 940	10.6	50.5	20	10	ADB99384	Human PCR
C 868	10.8	51.4	36	10	ADH37098	Lung can	Adh37098	Lung can	C 941	10.6	50.5	20	10	ADB99384	Human PCR
C 869	10.8	51.4	36	12	ADM56901	Human lun	Adm56901	Human lun	C 942	10.6	50.5	20	10	ADB99384	Human PCR
C 870	10.8	51.4	37	2	AAV74519	Primer fo	Aav74519	Primer fo	C 943	10.6	50.5	20	12	ACA88968	Selection
C 871	10.8	51.4	37	2	AAV72392	A. nidula	Aav72392	A. nidula	C 944	10.6	50.5	20	12	ACA88968	Selection
C 872	10.8	51.4	38	2	AAZ86025	PCR prime	Aaz86025	PCR prime	C 945	10.6	50.5	20	12	ADH63406	Human glu
C 873	10.8	51.4	38	3	AAI12834	Bacterial	Aai12834	Bacterial	C 946	10.6	50.5	20	12	ADH63406	Human glu
C 874	10.8	51.4	38	6	ABL39950	HIV type	Abi39950	HIV type	C 947	10.6	50.5	20	12	ADH63406	Human glu
C 875	10.8	51.4	38	9	ACD28028	Human pol	Acd28028	Human pol	C 948	10.6	50.5	20	12	ADJ25370	Primer of
C 876	10.8	51.4	38	12	ADG79067	Schizophr	Adg79067	Schizophr	C 949	10.6	50.5	20	12	ADJ25370	Primer of
C 877	10.8	51.4	38	12	ADM73776	HIV-1 typ	Adm73776	HIV-1 typ	C 950	10.6	50.5	20	12	ADJ25370	Primer of
C 878	10.8	51.4	40	2	AAZ76461	Human BRC	Aaz76461	Human BRC	C 951	10.6	50.5	20	12	ADK80244	Chimeric
C 879	10.8	51.4	40	10	ADH11095	E.coli AT	Adh11095	E.coli AT	C 952	10.6	50.5	20	12	ADK80244	Chimeric
C 880	10.8	51.4	41	2	AAV81512	Oligonuc	Aav81512	Oligonuc	C 953	10.6	50.5	20	12	ADK80244	Chimeric
C 881	10.8	51.4	41	3	AAZ73029	Transglut	Aaz73029	Transglut	C 954	10.6	50.5	20	12	ADK80244	Chimeric
C 882	10.8	51.4	41	6	ABQ76007	Human ger	Abq76007	Human ger	C 955	10.6	50.5	20	12	ADK80244	Chimeric
C 883	10.8	51.4	41	6	ABQ76006	Human ger	Abq76006	Human ger	C 956	10.6	50.5	20	12	ADK80244	Chimeric
C 884	10.8	51.4	41	8	ABT14775	Human Bcl	Abt14775	Human Bcl	C 957	10.6	50.5	20	12	ADK80244	Chimeric
C 885	10.8	51.4	43	9	ABK16527	Hamster D	Abk16527	Hamster D	C 958	10.6	50.5	20	12	ADK80244	Chimeric
C 886	10.8	51.4	45	2	AAV68583	Nucleotid	Aav68583	Nucleotid	C 959	10.6	50.5	20	12	ADK80244	Chimeric
C 887	10.8	51.4	45	2	AAV01771	C. tracho	Aav01771	C. tracho	C 960	10.6	50.5	20	12	ADK80244	Chimeric
C 888	10.8	51.4	45	2	AAZ78454	Primer 1	Aaz78454	Primer 1	C 961	10.6	50.5	20	12	ADK80244	Chimeric
C 889	10.8	51.4	45	2	AAZ30006	Amplifica	Aaz30006	Amplifica	C 962	10.6	50.5	20	12	ADK80244	Chimeric
C 890	10.8	51.4	45	2	AAZ82661	Amplifica	Aaz82661	Amplifica	C 963	10.6	50.5	20	12	ADK80244	Chimeric
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C 892	10.8	51.4	45	3	AAZ296678	T cell an	Aaz296678	T cell an	C 965	10.6	50.5	20	12	ADK80244	Chimeric
C 893	10.8	51.4	45	4	AAZ82169	Human ret	Aaz82169	Human ret	C 966	10.6	50.5	20	12	ADK80244	Chimeric
C 894	10.8	51.4	45	5	AAZ30829	Group II	Aaz30829	Group II	C 967	10.6	50.5	20	12	ADK80244	Chimeric
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C 896	10.8	51.4	50	2	AAQ25602	NANBH det	Aaq25602	NANBH det	C 969	10.6	50.5	20	12	ADK80244	Chimeric
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c	971	10.6	50.5	21	12	AD159763	Ad159763 Antisense
	972	10.6	50.5	21	12	ADK71066	AdK71066 HIV gp41
	973	10.6	50.5	21	12	ADP83662	ADP83662 Poly-DNP-
c	974	10.6	50.5	21	12	ADQ26803	ADQ26803 Beta-cate
	975	10.6	50.5	22	4	AAC84332	AAC84332 C. soroki
c	976	10.6	50.5	22	8	ADA06060	ADA06060 Human NOV
c	977	10.6	50.5	22	8	ABX72432	ABX72432 Human NOV
c	978	10.6	50.5	22	10	ADJ95231	ADJ95231 Novel NOV
c	979	10.6	50.5	22	12	ADN63211	ADN63211 Human NOV
c	980	10.6	50.5	22	12	ADP11050	ADP11050 Set 1 rig
	981	10.6	50.5	23	10	ADF31891	ADF31891 Human IGF
	982	10.6	50.5	23	12	ADI30523	ADI30523 Murine an
c	983	10.6	50.5	23	12	ADI59981	ADI59981 SiRNA -ve
c	984	10.6	50.5	23	12	ADI59869	ADI59869 SiRNA +ve
c	985	10.6	50.5	23	12	ADI59872	ADI59872 SiRNA +ve
c	986	10.6	50.5	23	12	ADI59978	ADI59978 SiRNA -ve
c	987	10.6	50.5	24	6	AQ13972	AQ13972 PE-Glu247
c	988	10.6	50.5	24	6	ABQ11011	ABQ11011 Oligonuc1
c	989	10.6	50.5	24	6	ABQ04724	ABQ04724 Oligonuc1
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	993	10.6	50.5	24	6	AB185441	AB185441 Capture o
c	994	10.6	50.5	24	6	AB184436	AB184436 Capture o
c	995	10.6	50.5	24	6	AB185440	AB185440 Capture o
	996	10.6	50.5	24	6	AB184437	AB184437 Capture o
c	997	10.6	50.5	24	10	ADE85981	ADE85981 Human t1s
c	998	10.6	50.5	25	2	AAT04462	AAT04462 M. tuberc
c	999	10.6	50.5	25	3	AAZ91935	AAZ91935 Mahogany
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ALIGNMENTS

RESULT 1	
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ID	AAD43284 standard; DNA; 21 BP.
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AC	AAD43284;
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DT	14-NOV-2002 (first entry)
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KW	Amplification; target nucleic acid; ds.
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OS	Unidentified.
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EP	EP1236805-A1.
PN	
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PD	04-SEP-2002.
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PF	27-FEB-2002; 2002EP-00004483.
XX	
PR	02-MAR-2001; 2001EP-00105172.
XX	
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.
XX	(HOFF) HOFFMANN LA ROCHE & CO AG F.
PI	Jaeger S;
XX	
DR	WPI; 2002-610695/66.
XX	
PT	Amplification of a target nucleic acid region using

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PT sequence.
XX
XX Disclosure; Page 16; 28pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region in a sample using a specific control sequence. The invention
XX is also directed to a method of determination of a target nucleic acid
XX using a special control nucleic acid. Nucleic acids of the invention are
XX used as a control in a reaction for amplifying target nucleic acids and
XX as a control in a hybridisation reaction for determination of target
XX nucleic acids. The present sequence is a DNA used to illustrate the
XX methods of the invention
XX
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XX
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XX Query Match 100.0%; Score 21; DB 6; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 0.85;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 AGCGCATGCCAGATTACTGGC 21
XX | | | | | | | | | | | | | | | | | | | |
XX Db 1 AGCGCATGCCAGATTACTGGC 21
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XX RESULT 2
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XX ID AAD43736 standard; DNA; 21 BP.
XX AC AAD43736;
XX
XX 14-NOV-2002 (first entry)
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XX DNA sequence to illustrate the method of the invention.
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XX Amplification; target nucleic acid; control nucleic acid; ds.
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XX 04-SEP-2002.
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XX 02-MAR-2001; 2001EP-00105172.
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XX 02-MAR-2001; 2001EP-00105172.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
XX
XX WPI; 2002-610694/66.
XX
XX Amplification of a target nucleic acid region using control sequences.
XX
XX Disclosure; Page 15; 29pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region. The method is useful for amplification of a nucleic acid
XX molecule using control nucleic acid sequences. The control nucleic acid
XX sequences are at least in part parallel-complementary to the sequence of
XX the target nucleic acid. The present sequence is a DNA used to illustrate
XX the method of the invention
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
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Query Match      100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCGCATGCCAGATTACTGGC 21
    |||||
Db 1 AGCGCATGCCAGATTACTGGC 21

RESULT 3
ADE29100/c
ID ADE29100 standard; RNA; 21 BP.
XX
AC ADE29100;
XX
DT 29-JAN-2004 (first entry)
XX
DE SNUOPTIN antisense silencing RNA - SEQ ID 86.
XX
KW anti-HIV; SID; selected interacting domain; HIV; gene therapy; siRNA;
KW silencing RNA; HIV-1 integrase; LEDGF; MCM7; HBO1; Snurportin; VP1;
KW Transportin-SR; EIF3S3; ss; SNUOPTIN.
XX
OS Unidentified.
XX
PN WO2003046176-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-EP013868.
XX
PR 26-NOV-2001; 2001US-0333346P.
XX
PR 31-MAY-2002; 2002US-0385132P.
XX
PA (HYBR-) HYBRIGENICS.
XX
PI Legrain P, Rain J, Benarous R, Emiliani S, Berlioz-Torrent C;
PI Blot G;
XX
DR WPI; 2003-505199/47.
XX
PT New complex between two interacting proteins, useful for screening a
PT molecules that inhibit human immunodeficiency virus or for preparing a
PT medicament for treating HIV-1.
XX
PS Example 8; SEQ ID NO 86; 102pp; English.
XX
CC The invention relates to a novel complex between two interacting proteins
CC listed within the specification. The complex of the invention
CC demonstrates anti-HIV activity whilst the SID (selected interacting
CC domains) and polypeptides may be useful for screening molecules that
CC inhibit human immunodeficiency virus (HIV), as well as during gene
CC therapy procedures. The siRNAs (silencing RNAs) targeted against cellular
CC proteins interacting with HIV-1 integrase, LEDGF, MCM7, HBO1, Snurportin,
CC VP1, Transportin-SR and EIF3S3, are useful in preparing a medicament for
CC treating HIV-1. The current sequence is that of the siRNA of the
CC invention.
XX
SQ Sequence 21 BP; 3 A; 5 C; 6 G; 2 T; 5 U; 0 Other;

Query Match      65.7%; Score 13.8; DB 10; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 CATGCCAGATTACTGGC 21
    |||||
Db 18 CATGCCAGAGACTGGC 2

RESULT 4
ADE29099
ID ADE29099 standard; RNA; 21 BP.
```

```
XX ADE29099;
XX 29-JAN-2004 (first entry)
XX SNUOPTIN sense silencing RNA - SEQ ID 85.
XX anti-HIV; SID; selected interacting domain; HIV; gene therapy; siRNA;
XX silencing RNA; HIV-1 integrase; LEDGF; MCM7; HBO1; Snurportin; VP1;
XX Transportin-SR; EIF3S3; ss; SNUOPTIN.
XX Unidentified.
XX WO2003046176-A2.
XX 05-JUN-2003.
XX 26-NOV-2002; 2002WO-EP013868.
XX 26-NOV-2001; 2001US-0333346P.
XX 31-MAY-2002; 2002US-0385132P.
XX (HYBR-) HYBRIGENICS.
XX Legrain P, Rain J, Benarous R, Emiliani S, Berlioz-Torrent C;
XX Blot G;
XX WPI; 2003-505199/47.
XX New complex between two interacting proteins, useful for screening a
XX molecules that inhibit human immunodeficiency virus or for preparing a
XX medicament for treating HIV-1.
XX Example 8; SEQ ID NO 85; 102pp; English.
XX The invention relates to a novel complex between two interacting proteins
XX listed within the specification. The complex of the invention
XX demonstrates anti-HIV activity whilst the SID (selected interacting
XX domains) and polypeptides may be useful for screening molecules that
XX inhibit human immunodeficiency virus (HIV), as well as during gene
XX therapy procedures. The siRNAs (silencing RNAs) targeted against cellular
XX proteins interacting with HIV-1 integrase, LEDGF, MCM7, HBO1, Snurportin,
XX VP1, Transportin-SR and EIF3S3, are useful in preparing a medicament for
XX treating HIV-1. The current sequence is that of the siRNA of the
XX invention.
XX SQ Sequence 21 BP; 5 A; 6 C; 5 G; 2 T; 3 U; 0 Other;

Query Match      65.7%; Score 13.8; DB 10; Length 21;
Best Local Similarity 76.5%; Pred. No. 3.8e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 5 CATGCCAGATTACTGGC 21
    |||||
Db 2 CAUGCCAGAGACUGGC 18

RESULT 5
AAT65036
ID AAT65036 standard; DNA; 44 BP.
XX
AC AAT65036;
XX
DT 19-JUN-1997 (first entry)
XX
DE Aspergillus oryzae alpha-glucosidase gene PCR sense primer.
XX Fungus; fungal; enhancer element; terminator; recombinant protein;
XX polymerase chain reaction; amplification primer; ss.
XX Synthetic.
XX JP09009968-A.
```

XX 14-JAN-1997.
PD
XX
XX 29-JUN-1995; 95JP-00163579.
XX
XX 29-JUN-1995; 95JP-00163579.
XX
XX (OZEK-) OZEKI KK.
PA (KOKU-) KOKUZEI CHO CHORHAN.
XX
XX WPI; 1997-126425/12.
XX
XX Fungal DNA enhancer element - used to transform other host fungus e.g
PT Aspergillus oryzae, to produce large quantities of a gene product.
XX
XX Example 11; Page 12; 25pp; Japanese.
XX
XX The promoter region of the alpha-glucosidase (agda) gene of Aspergillus
CC oryzae contains two novel enhancer elements: one (designated "enhancer-
CC B") corresponds to the consensus sequence CGGNATTGA and the other
CC (designated "enhancer-C") is of sequence CCAATCAGCGT. By inserting at
CC least one of the enhancer elements into a promoter region which is
CC functional in fungi, the activity of the promoter is enhanced. Using such
CC improved promoters, a gene of interest can be expressed efficiently in
CC transformed fungi. An oligonucleotide primer of the present sequence was
CC used in the construction of a high expression plasmid which contained an
CC enhanced promoter
XX
XX Sequence 44 BP; 10 A; 12 C; 13 G; 9 T; 0 U; 0 Other;
SQ Query Match 64.8%; Score 13.6; DB 2; Length 44;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGCGATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 3 AGAGCATGCCATATGACTAG 22

RESULT 6
AAF58409
ID AAF58409 standard; DNA; 19 BP.
XX
XX AAF58409;
AC
XX 25-APR-2001 (first entry)
DT
XX Murine mOCILrP1 clone PCR primer OCILm47.
DE
XX Osteopathic; mononuclear osteoclast precursor formation inhibition;
KW calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;
KW osteoclast differentiation; bone resorption; primary hyperparathyroidism;
KW Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;
KW humoral hypercalcaemia; cancer; PCR primer; ss.
XX
XX Mus musculus.
OS
XX WO200105964-A1.
PN
XX 25-JAN-2001.
PD
XX 19-JUL-2000; 2000WO-AU000864.
PF
XX 19-JUL-1999; 99AU-00001675.
XX
XX (SVIN-) ST VINCENTS INST MEDICAL RES.
PA
XX Zhou H, Kartsogiannis V, Hu Y, Gillespie MT, Ng KW;
PI WPI; 2001-103148/11.
XX
XX Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
PT on an osteoblast cell surface and used for treating excessive bone

PT resorption in conditions such as osteoporosis and Paget's disease.
XX Claim 35; Page 17; 131pp; English.
XX
XX The present invention relates to osteoclast inhibitory lectin coding
CC sequences and proteins (OCIL; see AAF58407). OCIL is a type II membrane
CC protein which is expressed on osteoblast cell surfaces. OCIL inhibits
CC osteoclast differentiation from haematopoietic cell precursors. OCIL is
CC useful for treating a condition with excessive bone resorption, including
CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
XX conditions where cancer has metastasised to the bone
XX Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
SQ Query Match 62.9%; Score 13.2; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CGCATGCCAGATTACTGG 20
||| ||||| ||||| |||||
Db 2 CCCATGCCAGATTGCTTG 19

RESULT 7
ADF91091/c
ID ADF91091 standard; DNA; 20 BP.
XX
XX ADF91091;
AC
XX 26-FEB-2004 (first entry)
DT
XX Microorganism detection PCR primer, SEQ ID 174.
DE
XX Detection; microorganism; PCR; primer; bacterium; fungus; protozoan;
KW virus; diarrhoea; food poisoning; ss.
XX
XX Escherichia coli.
OS
XX JP2003164282-A.
PN
XX 10-JUN-2003.
PD
XX 29-NOV-2001; 2001JP-00365153.
PF
XX 29-NOV-2001; 2001JP-00365153.
XX
XX (RAKA-) RAKAN KK.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
XX WPI; 2003-793230/75.
DR
XX Rapid, sensitive detection of specific or unspecified microbes causing
PT diarrhea and food poisoning, using primers which target universal and
PT specific genes, and amplifying by PCR under heat cycle conditions
PT suitable for many detections.
XX
XX Claim 1; SEQ ID NO 174; 69pp; Japanese.
PS
XX The present invention relates to a method for detecting microorganisms
CC using primers (ADF90918-ADF91145). The method is used for detecting
CC microorganisms (bacteria, fungi, protozoa, viruses) which cause diarrhoea
CC symptoms, and pathogenic microbes of food poisoning. The method can be
CC used to detect unspecified microbes, or specific pathogens, or for the
CC simultaneous detection of many kinds of microorganism.
XX
XX Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
SQ Query Match 62.9%; Score 13.2; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 GCATGCCAGATTACTGGC 21

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Db      | ||| ||||| |||||
        18 GAATGTCAGATACTGGC 1

RESULT 8
AAx83448/c
ID  AAx83448 standard; DNA; 21 BP.
XX  AC
XX  AC
XX  27-AUG-2003 (revised)
XX  DT 14-SEP-1999 (first entry)
XX  XX
DE  ZAM retroelement genome PCR primer o2.
XX  XX
XX  Genome; retroelement; retrovirus; ZAM; gag; pol; env; LTR; vector;
XX  KW long terminal repeat; gene therapy; primer; PCR; amplification; ss.
XX  XX
XX  Synthetic.
XX  OS Drosophila melanogaster.
XX  XX
XX  FR2772045-A1.
XX  PN
XX  11-JUN-1999.
XX  PD
XX  10-DEC-1997; 97FR-00015655.
XX  PF
XX  10-DEC-1997; 97FR-00015655.
XX  PR
XX  (UYAU-) UNIV AUVERGNE.
XX  PA
XX  Leblanc P, Vaury C;
XX  PI
XX  WPI; 1999-359998/31.
XX  DR
XX  New Drosophila ZAM retroelement nucleic acid - useful in gene transfer or
XX  PT gene therapy.
XX  FT
XX  PS
XX  Example 1; Page 11; 55pp; French.
XX  XX
XX  Primers AAX83446-X83447 were used to PCR amplify the complete genomic DNA
XX  CC sequence of a novel retroelement ZAM (AAX83445) found in Drosophila
XX  CC melanogaster. Similarly to other retroelements and retroviruses, ZAM
XX  CC contains 3 genes (gag, pol and env) and long terminal repeats (LTR's) at
XX  CC either end of the genome. Vectors containing the sequence can be used for
XX  CC gene transfer or gene therapy. (Updated on 27-AUG-2003 to correct OS
XX  CC field.)
XX  CC
XX  SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGGC 21
        ||||| |||||
Db      20 GAATGCCAGTTAACTGGC 3

RESULT 9
ABN83493/c
ID  ABN83493 standard; DNA; 22 BP.
XX  XX
XX  AC
XX  ABN83493;
XX  XX
XX  30-AUG-2002 (first entry)
XX  DT
XX  DE Escherichia coli O157:H7 PCR primer stx2R.
XX  XX
XX  KW PCR; primer; bacterium strain typing; enterohaemorrhagic; ss.
XX  XX
XX  OS Escherichia coli O157:H7.
XX  PT

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PN      WO200236827-A1.
XX      10-MAY-2002.
XX      01-NOV-2001; 2001WO-US044963.
XX      01-NOV-2000; 2000US-0244973P.
XX      (GEHO) GEN HOSPITAL CORP.
XX      Kudva I, Calderwood SB, Ausubel FW;
XX      WPI; 2002-519260/55.
XX      Typing the strain of bacterial isolate, by providing genomic DNA from the
XX      isolate, performing polymerization on DNA using primers comprising
XX      restriction nuclease site, thus producing amplicon having restriction
XX      site.
XX      Example 2; Page 43; 87pp; English.
XX      The present invention relates to a method for typing the strain of a
XX      bacterial isolate (I). The method involves providing genomic DNA (GDNA)
XX      from (I), performing PCR on GDNA using a first and second primer to
XX      amplify GDNA comprising a restriction nuclease restriction site, thus
XX      producing an amplicon having the restriction site, and characterising the
XX      amplicon and thus typing the strain of (I). To illustrate the method a
XX      genomic sequence, comprising O-islands, from enterohaemorrhagic
XX      Escherichia coli O157:H7 was used. The present sequence is a PCR primer
XX      used to amplify a virulence gene from E. coli O157:H7
XX      SQ Sequence 22 BP; 4 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 6; Length 22;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGGC 21
        ||||| |||||
Db      20 GAATGTCAGATACTGGC 3

RESULT 10
ABQ87925/c
ID  ABQ87925 standard; DNA; 32 BP.
XX  AC
XX  ABQ87925;
XX  XX
XX  10-SEP-2002 (first entry).
XX  DT
XX  DE Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 24.
XX  XX
XX  KW Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
XX  KW hlyA; detection; food; PCR; primer; ss.
XX  XX
XX  OS Escherichia coli.
XX  XX
XX  WO200253771-A2.
XX  PN
XX  11-JUL-2002.
XX  PD
XX  15-OCT-2001; 2001WO-EP011901.
XX  PF
XX  08-JAN-2001; 2001DE-01000493.
XX  PR
XX  (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX  FA
XX  Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
XX  PI
XX  WPI; 2002-528864/56.
XX  DR
XX  Detecting enterohaemorrhagic Escherichia coli, from the presence of
XX  PT sequences from the Shigella-like toxin locus and at least one of eae and

```

PT hlyA loci.
 XX Claim 3; Page 18; 86pp; German.
 PS
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 4 A; 8 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 26 GAATGTCAGATAACTGGC 9
 RESULT 11
 ABQ87940
 ID ABQ87940 standard; DNA; 32 BP.
 XX AC
 XX ABQ87940;
 XX
 DT 10-SEP-2002 (first entry)
 DE Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 39.
 XX
 XX Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
 KW hlyA; detection; food; PCR; primer; ss.
 XX Escherichia coli.
 OS
 XX WO200253771-A2.
 FN
 PD 11-JUL-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011901.
 XX
 PR 08-JAN-2001; 2001DE-01000493.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 XX
 PI Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
 XX WPI; 2002-528864/56.
 DR
 XX
 XX 11-JUL-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011901.
 XX
 PR 08-JAN-2001; 2001DE-01000493.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 XX
 PI Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
 XX WPI; 2002-528864/56.
 DR
 XX
 XX Detecting enterohaemorrhagic Escherichia coli, from the presence of
 PT sequences from the Shigella-like toxin locus and at least one of eae and
 PT hlyA loci.
 PS Claim 3; Page 19; 86pp; German.
 XX
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 11 A; 9 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 7 GAATGTCAGATAACTGGC 24
 RESULT 12
 ABQ87926/c
 ID ABQ87926 standard; DNA; 32 BP.
 XX AC
 XX ABQ87926;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Enterohaemorrhagic Escherichia coli detection PCR primer SEQ ID NO 25.
 XX
 XX Enterohaemorrhagic Escherichia coli; EHEC; slt; Shigella-like toxin; eae;
 KW hlyA; detection; food; PCR; primer; ss.
 XX Escherichia coli.
 OS
 XX WO200253771-A2.
 FN
 PD 11-JUL-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011901.
 XX
 PR 08-JAN-2001; 2001DE-01000493.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 XX
 PI Grabowski R, Groenewald C, Schneider A, Pardigol A, Berghof K;
 XX WPI; 2002-528864/56.
 DR
 XX
 XX Detecting enterohaemorrhagic Escherichia coli, from the presence of
 PT sequences from the Shigella-like toxin locus and at least one of eae and
 PT hlyA loci.
 PS Claim 3; Page 18; 86pp; German.
 XX
 CC The invention relates to detection (M1) of enterohaemorrhagic Escherichia
 CC coli (EHEC) in a sample from the presence of nucleic acid sequences from
 CC the slt (Shigella-like toxin) locus and the eae and/or hlyA loci. (M1) is
 CC useful for detecting of EHEC e.g. in foods. The method provides secure
 CC detection of EHEC (including differentiation from other types of E.
 CC coli), with minimal interference from other sample components such as
 CC inhibitors of the polymerase chain reaction, DNA of non-pathogenic
 CC bacteria or the quenching phenomenon. The present sequence is that of one
 CC of the PCR primers of the invention (ABQ87902-ABQ87999)
 XX
 SQ Sequence 32 BP; 4 A; 8 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 32;
 Best Local Similarity 83.3%; Pred. No. 8e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GCATGCCAGATTACTGGC 21
 DB 26 GAATGTCAGATAACTGGC 9
 RESULT 13
 AA241030/c
 ID AA241030 standard; DNA; 18 BP.
 XX AC
 XX AA241030;
 XX
 DT 26-JAN-2000 (first entry)
 DE Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #22.

XX Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9953101-A1.

XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US008268.

XX 13-APR-1998; 98US-0081483P.

XX 28-APR-1998; 98US-00067638.

XX (ISIS-) ISIS PHARM INC.

XX Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;

XX WPI; 1999-620446/53.

XX Identifying compounds which modulate expression of nucleic acids, used to
 PT provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity.

XX Example 21; Page 100; 264pp; English.

XX A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (TNA) sequence via binding of the
 CC compounds with the TNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the TNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a TNA sequence via binding of the ONs with the TNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the TNA according to defined criteria; and (2) a method of defining a set
 CC of compounds that modulate the expression of a TNA sequence via binding
 CC of the compounds with the TNA. The methods can be used for the generation
 CC and identification of synthetic compounds having defined physical,
 CC chemical or bioactive properties. Information gathered from assays of
 CC such compounds is used to identify nucleic acid sequences that are
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of
 CC the present invention

XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 61.9%; Score 13; DB 2; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 9.6e+03;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 6 ATGCCAGATTACT 18

XX DB 16 ATGCCAGATTACT 4

XX RESULT 14

XX AAZ22124/c

XX ID AAZ22124 standard; DNA; 18 BP.

XX AC AAZ22124;

XX DT 26-NOV-1999 (first entry)

XX DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23433.

XX

KW Cellular Inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
 KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.

XX Synthetic.

OS Homo sapiens.

XX US5958771-A.

XX 28-SEP-1999.

XX 03-DEC-1998; 98US-00205144.

XX 03-DEC-1998; 98US-00205144.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsert LM, Ackermann EJ;

XX WPI; 1999-561046/47.

XX Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
 PT useful for e.g. diagnostics, therapeutics, and as research reagents.

XX Example 15; Col 39; 33pp; English.

XX The invention provides antisense compounds of 8-30 nucleotides that
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-
 CC 2). The antisense compounds may be used for diagnostics, therapeutics
 CC (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent
 CC or delay infection, inflammation, or tumor formation), as research
 CC reagents (e.g. to distinguish between members of a biological pathway)
 CC and in kits. Sequences AAZ22103-142 represent phosphorothioate
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of
 CC apoptosis-2

XX Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 61.9%; Score 13; DB 2; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 9.6e+03;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 6 ATGCCAGATTACT 18

XX DB 16 ATGCCAGATTACT 4

XX RESULT 15

XX AAD60500/c

XX ID AAD60500 standard; DNA; 18 BP.

XX AC AAD60500;

XX 18-DEC-2003 (first entry)

XX Human c-IAP-2 antisense oligonucleotide #ISIS #23473.

XX Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;
 KW hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;
 KW API-1; hIAP-1; MHC; gene therapy; phosphorothioate; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..18

XX /tag= a

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"

XX modified_base 1..4

XX /tag= b

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX

PF 10-DEC-2002; 2002US-00317278.
XX
PR 10-DEC-2002; 2002US-00317278.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Dobie KW;
XX WPI; 2004-440382/41.
DR
XX
XX
PT New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding melanoma antigen E-D1 (MAGE-D1), useful for treating diseases
PT associated with MAGE-D1, e.g. hyperproliferative disorders.
XX
PS Example 15; SEQ ID NO 17; 36pp; English.
XX
CC The invention relates to compounds, compositions and methods for
CC modulating the expression of melanoma antigen E-D1 (MAGE-D1). MAGE-D1 is
CC also called as melanoma antigen, family D, 1, neurotrophin receptor-
CC interacting MAGE homologue (NRAGE) and Dlxin-1. The composition comprise
CC antisense oligonucleotides targeted to MAGE-D1. The compound, composition
CC and methods are useful for treating a disease or condition associated
CC with MAGE-D1, such as a hyperproliferative disorder. They are also useful
CC in research and diagnostics for modulating the expression of MAGE-D1. The
CC present sequence is an antisense oligonucleotide targeted to human MAGE-
CC D1 DNA. This sequence is used to illustrate the method of the invention.
XX
SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGCCAGATTACTG 19
Db 8 TGCCAGATTACTG 20

RESULT 18
AAC93092
ID AAC93092 standard; DNA; 32 BP.
XX
AC AAC93092;
XX
DT 28-MAR-2001 (first entry)
XX
DE E. coli cerulenin mutagenic primer I197A Antisense.
XX
KW Beta-ketoacyl ACP synthase; KAS; cell fatty acid composition;
KW oilseed crop; cancer; immunosuppressant; anti-parasitic agent;
KW antibiotic; PCR primer; ss.
XX
OS Escherichia coli.
XX
FN WO200075343-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US016151.
XX
PR 09-JUN-1999; 99US-0138308P.
XX
PA (CALJ) CALGENE LLC.
XX
PI Dehesh K, Val D;
XX
DR WPI; 2001-061730/07.
XX
PT Engineering beta-ketoacyl-ACP synthase useful for altering the fatty acid
PT composition of a host cell, comprises modifying the sequence encoding KAS
PT and expressing the modified sequence in the host cell.
XX
PS Example 2; Page 22; 145pp; English.

XX The present invention provides a method for obtaining an altered beta-
CC ketoacyl ACP synthase (KAS) protein. These engineered proteins have
CC altered substrate specificity and are produced by modifying the coding
CC sequence and then expressing it in a host cell. The proteins are useful
CC in the altering of the fatty acid composition of a plant, particularly in
CC the modification of oilseed crops, and in the identification of molecules
CC for use in cancer therapy, as immunosuppressants, anti-parasitic agents
CC and antibiotics
XX
SQ Sequence 32 BP; 5 A; 14 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 4; Length 32;
Best Local Similarity 76.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGGC 21
Db 6 AACGCCGCCGGAGTACTGGC 26

RESULT 19
AAC93091/C
ID AAC93091 standard; DNA; 32 BP.
XX
AC AAC93091;
XX
DT 28-MAR-2001 (first entry)
XX
DE E. coli cerulenin mutagenic primer I197A Sense.
XX
KW Beta-ketoacyl ACP synthase; KAS; cell fatty acid composition;
KW oilseed crop; cancer; immunosuppressant; anti-parasitic agent;
KW antibiotic; PCR primer; ss.
XX
OS Escherichia coli.
XX
FN WO200075343-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US016151.
XX
PR 09-JUN-1999; 99US-0138308P.
XX
PA (CALJ) CALGENE LLC.
XX
PI Dehesh K, Val D;
XX
DR WPI; 2001-061730/07.
XX
PT Engineering beta-ketoacyl-ACP synthase useful for altering the fatty acid
PT composition of a host cell, comprises modifying the sequence encoding KAS
PT and expressing the modified sequence in the host cell.
XX
PS Example 2; Page 22; 145pp; English.
XX
CC The present invention provides a method for obtaining an altered beta-
CC ketoacyl ACP synthase (KAS) protein. These engineered proteins have
CC altered substrate specificity and are produced by modifying the coding
CC sequence and then expressing it in a host cell. The proteins are useful
CC in the altering of the fatty acid composition of a plant, particularly in
CC the modification of oilseed crops, and in the identification of molecules
CC for use in cancer therapy, as immunosuppressants, anti-parasitic agents
CC and antibiotics
XX
SQ Sequence 32 BP; 6 A; 7 C; 14 G; 5 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 4; Length 32;
Best Local Similarity 76.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGGC 21

Db 27 AACGCCCGCGGAGTACTGGC 7
||||| ||| ||| ||| ||| |||

RESULT 20
ADI80472
ID ADI80472 standard; DNA; 32 BP.
XX AC ADI80472;
XX DT 22-APR-2004 (first entry)
XX DE E. coli KAS II PCR site-directed mutagenesis I197A antisense primer.
XX KW beta-ketoacyl-ACP synthase; KAS; enzyme; acyl-ACP substrate;
XX KW altered substrate specificity; PCR; site-directed mutagenesis; primer;
XX SS.
XX OS Escherichia coli.
XX OS Synthetic.
XX PN WO2004007744-A2.
XX PD 22-JAN-2004.
XX PF 31-JUL-2000; 2000WO-US022359.
XX PR 31-JUL-2000; 2000WO-US022359.
XX PA (CALJ) CALGENE LLC.
XX PI Kaytayoon D, Val D;
XX DR WPI; 2004-122971/12.
XX PT Obtaining engineered approximately-beta-ketoacyl-ACP synthase (KAS), useful
PT for preparing constructs to direct expression in a host cell comprising
PT modifying a gene sequence encoding a first KAS protein to produce a
PT modified KAS gene sequence.
XX PS Example 2; SEQ ID NO 16; 40pp; English.

The present invention describes a method for obtaining an engineered beta
-ketoacyl-ACP synthase (KAS) having an altered substrate specificity with
respect to the acyl-ACP substrates utilised by the KAS. Also described:
(1) an amino acid sequence encoding a KAS protein, where the sequence has
at least one substitution, insertion or deletion of at least one amino
acid residue selected from residue 105-120, 130-140, 190-205 and 340-400
and the protein has an altered substrate specificity; (2) a nucleic acid
construct comprising an operably linked components in the 5' to 3',
direction of transcription: (a) a transcriptional initiation region; and
(b) a polynucleotide sequence encoding a KAS having an altered substrate
specificity; and (3) a method for altering the fatty acid composition of
a host cell. The method is useful for obtaining an engineered KAS having
an altered substrate specificity with respect to the acyl-ACP substrates
utilised by the KAS. The engineered nucleic acid sequences are useful in
the preparation of constructs to direct expression in a host cell. It can
also be used in the preparation of plant expression constructs to alter
the fatty acid composition of a plant cell. The DNA constructs can be
used for transcription or translation and translation (expression) of
an engineered KAS protein having altered substrate specificity with
respect to the native KAS protein. The present sequence represents a PCR
site-directed mutagenesis primer for E. coli KAS II, which is used in an
example from the present invention.

Sequence 32 BP; 5 A; 14 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 32;
Best Local Similarity 76.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
||||| ||| ||| ||| ||| |||

Db 6 AACGCCCGCGGAGTACTGGC 26

RESULT 21
ADI80471/c
ID ADI80471 standard; DNA; 32 BP.
XX AC ADI80471;
XX DT 22-APR-2004 (first entry)
XX DE E. coli KAS II PCR site-directed mutagenesis I197A sense primer.
XX KW beta-ketoacyl-ACP synthase; KAS; enzyme; acyl-ACP substrate;
XX KW altered substrate specificity; PCR; site-directed mutagenesis; primer;
XX SS.
XX OS Escherichia coli.
XX OS Synthetic.
XX PN WO2004007744-A2.
XX PD 22-JAN-2004.
XX PF 31-JUL-2000; 2000WO-US022359.
XX PR 31-JUL-2000; 2000WO-US022359.
XX PA (CALJ) CALGENE LLC.
XX PI Kaytayoon D, Val D;
XX DR WPI; 2004-122971/12.
XX PT Obtaining engineered approximately-beta-ketoacyl-ACP synthase (KAS), useful
PT for preparing constructs to direct expression in a host cell comprising
PT modifying a gene sequence encoding a first KAS protein to produce a
PT modified KAS gene sequence.
XX PS Example 2; SEQ ID NO 15; 40pp; English.

The present invention describes a method for obtaining an engineered beta
-ketoacyl-ACP synthase (KAS) having an altered substrate specificity with
respect to the acyl-ACP substrates utilised by the KAS. Also described:
(1) an amino acid sequence encoding a KAS protein, where the sequence has
at least one substitution, insertion or deletion of at least one amino
acid residue selected from residue 105-120, 130-140, 190-205 and 340-400
and the protein has an altered substrate specificity; (2) a nucleic acid
construct comprising an operably linked components in the 5' to 3',
direction of transcription: (a) a transcriptional initiation region; and
(b) a polynucleotide sequence encoding a KAS having an altered substrate
specificity; and (3) a method for altering the fatty acid composition of
a host cell. The method is useful for obtaining an engineered KAS having
an altered substrate specificity with respect to the acyl-ACP substrates
utilised by the KAS. The engineered nucleic acid sequences are useful in
the preparation of constructs to direct expression in a host cell. It can
also be used in the preparation of plant expression constructs to alter
the fatty acid composition of a plant cell. The DNA constructs can be
used for transcription or translation and translation (expression) of
an engineered KAS protein having altered substrate specificity with
respect to the native KAS protein. The present sequence represents a PCR
site-directed mutagenesis primer for E. coli KAS II, which is used in an
example from the present invention.

Sequence 32 BP; 6 A; 7 C; 14 G; 5 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 12; Length 32;
Best Local Similarity 76.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
||||| ||| ||| ||| ||| |||
Db 27 AACGCCCGCGGAGTACTGGC 7

```

RESULT 22
AAH62283/c
ID   AAH62283 standard; DNA; 21 BP.
XX
AC   AAH62283;
XX
DT   09-SEP-2004 (revised)
DT   12-SEP-2001 (first entry)
XX
DE   NRIP1 polymorphism containing DNA fragment #184.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key Location/Qualifiers
FT   variation      11
FT                       /*tag= a
FT                       /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 200WO-USO31639.
XX
PR   24-NOV-1999; 99US-O167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M, Ireland JS, Lander ES;
PT   WFI; 2001-367705/38.
DR
XX
PT   New nucleic acid segments of the human genome, particularly from genes including polymorphic sites,for phenotype correlation, forensics,paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 44; 80pp; English.
CC
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences'. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture CC of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis
CC
CC   Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ   Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match          61.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred.No.1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY    4 GCATGCCAGATTACTG 19
     |||||
DB    21 GCATGCCAGATCCCTG 6


RESULT 23
ABS57999
ID   ABS57999 standard; DNA; 23 BP.
```



```
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 CGCATGCCAGATTACT 18
Db 20 CGCATGCCAAATTCCT 5
RESULT 27
ABQ00780/c
ID ABQ00780 standard; DNA; 24 BP.
AC ABQ00780;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 771.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
XX
PT 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 62; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 CGCATGCCAGATTACT 18
Db 20 CGCATGCCAAATTCCT 5
RESULT 27
ABQ00780/c
ID ABQ00780 standard; DNA; 24 BP.
AC ABQ00780;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 771.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
XX
PT 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 62; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 CGCATGCCAGATTACT 18
Db 20 CGCATGCCAAATTCCT 5
```

```
Db 20 CGCATGCCAAATTCCT 5
RESULT 28
ABQ05536
ID ABQ05536 standard; DNA; 24 BP.
XX
AC ABQ05536;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 5527.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
XX
PT 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 157; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 11 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 CGCATGCCAGATTACT 18
Db 5 CGCATGCCAAATTCCT 20
RESULT 29
ABQ11857
ID ABQ11857 standard; DNA; 24 BP.
XX
AC ABQ11857;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11848.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
```


CC comprises detecting the presence of the modified target nucleic acid

XX Sequence 25 BP; 5 A; 3 C; 11 G; 6 T; 0 U; 0 Other;

SQ

Query Match 61.0%; Score 12.8; DB 6; Length 25;

Best Local Similarity 87.5%; Pred. No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 CGCATGCCAGATTACT 18
|||||

Db 21 CGCATGCCAAATTCCT 6

RESULT 32

ABQ13393

ID ABQ13393 standard; DNA; 25 BP.

XX

AC ABQ13393;

XX

DT 11-JUN-2002 (first entry)

XX

DE Oligonucleotide adapter/capture probe 13384.

XX

KW Oligonucleotide array; adapter sequence; probe; ss.

XX

OS Synthetic.

XX

PN WO200216649-A2.

XX

PD 28-FEB-2002.

XX

PF 27-AUG-2001; 2001WO-US026519.

XX

PR 25-AUG-2000; 2000US-0227948P.

XX

PR 29-AUG-2000; 2000US-0228854P.

XX

XX (ILLU-) ILLUMINA INC.

FA

PI Gunderson K;

XX

DR WPI; 2002-292068/33.

XX

XX

PT Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.

PT

XX

PS Claim 1; Page 254; 261pp; English.

XX

CC The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

XX

SQ Sequence 25 BP; 5 A; 11 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 6; Length 25;

Best Local Similarity 87.5%; Pred. No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 CGCATGCCAGATTACT 18
|||||

Db 6 CGCATGCCAAATTCCT 21

RESULT 33

AAQ46940/c

ID AAQ46940 standard; DNA; 28 BP.

XX

AC AAQ46940;

XX

DT 07-FEB-1994 (first entry)

XX

DE Human bFGF primer 4.

XX

KW Human; fibronectin; FN; fibroblast cell growth factor; FGF; amplify; fusion; cell adhesion; cell growth; anti-aging; cosmetics; primer; wound healing; surgery; polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN JP05178897-A.

XX

PD 20-JUL-1993.

XX

PF 05-MAR-1992; 92JP-00083220.

XX

PR 14-OCT-1991; 91JP-00291959.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1993-261656/33.

XX

PT Synthetic functional polypeptide to promote wound healing, etc. - contg. cell adhesion polypeptide from fibronectin and fibroblast growth factor polypeptide, opt. linked by spacer.

PT

XX

PS Example 1; Page 11; 13pp; Japanese.

XX

CC The sequences given in AAQ46937-42 are primers which were used in the amplification of the DNA encoding the human fibronectin (FN) and fibroblast cell growth factor (FGF) fragments which were used in the production of the fusion polypeptides of the invention. These polypeptides were able to stimulate cell adhesion and cell growth, and may be used for anti-aging cosmetics and in wound healing after surgery

CC

XX

SQ Sequence 28 BP; 9 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 28;

Best Local Similarity 87.5%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 ATGCCAGATTACTGGC 21
|||||

Db 27 ATGGAAGATTACTGGC 12

RESULT 34

AAAT59860

ID AAAT59860 standard; DNA; 28 BP.

XX

AC AAAT59860;

XX

DT 09-DEC-1997 (first entry)

XX

DE Sense primer #1 for phosphate translocator protein fragment.

XX

KW Phosphate translocator protein; inner envelope membrane; plastid; pea; chloroplast; photosynthate; chimeric gene; promoter; transporter protein; permeability barrier; plant; translocator protein; membrane permeability; metabolism; starch production; plant growth; primer; PCR; amplify; polymerase chain reaction; ss.

XX

OS Synthetic.

XX

PN WO9708329-A1.

XX

PD 06-MAR-1997.

XX

PF 28-AUG-1996; 96WO-GB002129.

XX

Query Match 61.0%; Score 12.8; DB 4; Length 41;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGG 20
 |||||
 Db 8 CATGCCAGAGACTGG 23

RESULT 37
 AAT05760
 ID AAT05760 standard; DNA; 49 BP.
 XX AC AAT05760;
 XX DT 10-JUN-1996 (first entry)
 XX DE Thermophilic strand displacement amplification template oligo primer.
 XX KW Primer; template oligonucleotide; recognition; cleavage; site;
 XX KW restriction endonuclease; strand displacement assay; thermostable;
 XX KW strand displacement amplification reaction; diagnosis; HincII;
 XX KW genetic diseases; gene isolation; forensic medicine; ss.
 XX OS Synthetic.
 XX PN AU9514776-A.
 XX PD 26-OCT-1995.
 XX PF 13-MAR-1995; 95AU-00014776.
 XX PR 18-APR-1994; 94US-00229279.
 XX PA (BECT) BECTON DICKINSON CO.
 XX PI Fraiser MS, Spargo CA, Walker GT, Van Cleve M, Wright DU;
 XX WPI; 1995-383306/50.
 XX DR Amplifying target nucleic acid by strand displacement amplification -
 XX PT using thermophilic DNA polymerase and thermophilic restriction
 XX PT endonuclease.
 XX PS Example 5; Page 35; 47pp; English.
 XX CC The primer AAT05760 was used to prime the template oligonucleotide
 CC AAT05761, which contains a recognition/cleavage site for the restriction
 CC endonuclease HincII. The template was used in an thermophilic strand
 CC displacement amplification, to compare conventional and the claimed
 CC thermophilic strand displacement amplification reaction of the invention,
 CC which is useful in the diagnosis of genetic diseases, isolation of genes
 CC and forensic medicine
 XX SQ Sequence 49 BP; 12 A; 8 C; 16 G; 13 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 49;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGG 20
 |||||
 Db 22 CATGCCCGTACTGG 37

RESULT 38
 AAF82407
 ID AAF82407 standard; DNA; 19 BP.
 XX AC AAF82407;
 XX DT 26-JUN-2001 (first entry)

XX DE Mealworm encapsulation protein DNA primer #12.
 XX KW Mealworm; encapsulation; immunostimulant; primer; ss.
 XX OS Tenebrio molitor.
 XX PN JP2001037488-A.
 XX PD 13-FEB-2001.
 XX PF 29-NOV-1999; 99JP-00338594.
 XX PR 07-JUL-1999; 99KR-00027933.
 XX PR 26-JUL-1999; 99KR-00031172.
 XX PA (SAMY-) SAMYANG GENEX CORP.
 XX DR WPI; 2001-285602/30.
 XX PT Novel protein involved in encapsulation, used as an immunological
 XX PT activity enhancer.
 XX PS Example 4; Page 6; 23pp; Japanese.
 XX CC The present primer is provided in a specification relating a mealworm
 CC protein that participates in encapsulation, which is a cellular defensive
 CC reaction. The invention provides an encapsulation polypeptide comprising
 CC residues 1-754 or 18-754 of a 754 amino acid sequence, or 1-579 or 16-579
 CC of a 579 amino acid sequence, both fully defined in the specification, or
 CC a mutant having a replacement, deletion or insertion of an amino acid in
 CC at least one residue of the sequence. The protein can be used as an
 CC immunological activity enhancer
 XX SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 4; Length 19;
 Best Local Similarity 78.9%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCCCATGCCAGATTACTG 19
 |||||
 Db 1 AGCTCCAGCCAGATTCTCTG 19

RESULT 39
 AAX94343/C
 ID AAX94343 standard; DNA; 20 BP.
 XX AC AAX94343;
 XX DT 13-SEP-1999 (first entry)
 XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 XX KW neutralising epitope; PCR primer; ss.
 XX OS Synthetic.
 XX OS Chlamydia pneumoniae.
 XX PN WO9927105-A2.
 XX PD 03-JUN-1999.
 XX PF 20-NOV-1998; 98WO-IB001890.
 XX PR 21-NOV-1997; 97FR-00014673.
 XX PR 04-NOV-1998; 98US-0107078P.
 XX PA (GEST) GENSET.

PI Griffais R;
 XX WPI; 1999-357842/30.
 XX Genome sequence of Chlamydia pneumoniae.
 XX Page 1662; Disclosure; 1912pp; English.
 PS AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-AAY35875) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
 SQ Query Match 60.0%; Score 12.6; DB 2; Length 20;
 Best Local Similarity 78.9%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AGCGCATGCCAGATTACTG 19
 DB 20 AACGCTGCCAATTACAG 2

RESULT 40
 AAZ21594
 ID AAZ21594 standard; DNA; 21 BP.
 XX AAZ21594;
 XX 02-DEC-1999 (first entry)
 XX PCR primer INSPr for amplifying HIV integrase cDNA.
 DE PCR primer; HIV; integrase; IN; inhibitor; DNA insertion; treatment;
 KW viral replication; reverse transcriptase; protease inhibitor;
 KW combination therapy; resistant strain; ss.
 XX Synthetic.
 OS Human immunodeficiency virus.
 XX WO9948371-A1.
 PN 30-SEP-1999.
 XX 26-MAR-1999; 99WO-US006700.
 XX 27-MAR-1998; 98US-0079764P.
 PR 17-JUL-1998; 98US-0093208P.
 XX (REGC) UNIV CALIFORNIA.
 PA Robinson WE, King PJ, Reinecke MG;
 PI WPI; 1999-571930/48.
 XX bis-(3,4-Dihydroxycinnamoyl)tartaric acid analogues for treatment of HIV
 XX infections.
 PT Disclosure; Page 35; 68pp; English.
 PS PCR primers AAZ21589-Z21594 are used to amplify the HIV integrase cDNA.
 CC This primer corresponds to nucleotides 4016-4036 of the integrase
 CC sequence. The HIV integrase (IN) cDNA was used in the generation of an L-
 CC chioric acid resistant strain of HIV. The invention relates to new
 CC compounds that are IN inhibitors. The inhibitors are novel compounds that

CC potentially and selectively inhibit HIV integrase. The inhibitors are
 CC structural analogues of bis-(3,4-Dihydroxycinnamoyl) tartaric acid.
 CC Integrase has the minimal activities needed for integration. In vitro the
 CC enzyme processes the HIV DNA for insertion in to the host cell's nucleus.
 CC IN also cleaves double stranded DNA and facilitates the insertion of the
 CC HIV DNA in to the cleavage site. IN also covalently links the HIV DNA to
 CC the cleaved ends of the host DNA. The new compounds block the actions of
 CC IN, and therefore block viral replication. The compounds are synergistic
 CC with reverse transcriptase and protease inhibitors, acting at a different
 CC part of the HIV replication cycle. The new inhibitors are used,
 CC preferably in combination therapy with reverse transcriptase inhibitors
 CC and protease inhibitors in the treatment of HIV
 XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 SQ Query Match 60.0%; Score 12.6; DB 2; Length 21;
 Best Local Similarity 78.9%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AGCGCATGCCAGATTACTG 19
 DB 3 AGGGAATGCCAAATTCCTG 21

Search completed: November 23, 2004, 17:27:12
 Job time : 145.708 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21
Sequence: 1 agcgatgccagattactggc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.2	62.9	40	6	5521093-6
C 2	13	61.9	18	2	US-09-205-144-29
C 3	13	61.9	32	4	US-09-591-279A-15
C 4	13	61.9	32	4	US-09-591-279A-16
C 5	12.8	61.0	24	4	US-09-780-752-20
C 6	12.8	61.0	28	1	US-07-959-369-19
C 7	12.8	61.0	28	3	US-09-023-341-5
C 8	12.8	61.0	49	1	US-08-223-279-17
C 9	12.8	61.0	49	1	US-08-701-269-17
C 10	12.6	60.0	20	4	US-09-198-452A-3669
C 11	12.6	60.0	36	4	US-09-371-772B-12766
C 12	12.4	59.0	21	3	US-09-179-221D-7
C 13	12.4	59.0	42	3	US-08-721-979A-71
C 14	12.4	59.0	42	3	US-08-721-979A-72
C 15	12.4	59.0	42	3	US-08-836-501-71
C 16	12.4	59.0	42	3	US-08-836-501-72
C 17	12.4	59.0	42	4	US-09-654-289-71
C 18	12.4	59.0	42	4	US-09-654-289-72
C 19	12.4	59.0	42	4	US-09-582-876-71
C 20	12.4	59.0	42	4	US-09-582-876-72
C 21	12.4	59.0	42	4	US-09-626-830-71
C 22	12.4	59.0	42	4	US-09-626-830-72
C 23	12.4	59.0	42	4	US-10-091-257-71
C 24	12.4	59.0	42	4	US-10-091-257-72
C 25	12.4	59.0	45	5	PCT-US93-09070-5
C 26	12.2	58.1	19	1	US-08-328-710A-15
C 27	12.2	58.1	19	3	US-08-968-046-15

30	1	US-07-915-922-9	Sequence 9, Appli
44	4	US-09-464-122A-13	Sequence 13, Appli
47	4	US-09-641-638-1195	Sequence 1195, Ap
47	4	US-10-170-097-1195	Sequence 1195, Ap
20	3	US-09-488-744A-71	Sequence 71, Appli
29	4	US-09-304-232-325	Sequence 325, App
29	4	US-09-302-626B-132	Sequence 132, App
33	3	US-08-776-511-7	Sequence 7, Appli
33	3	US-08-776-511-6	Sequence 6, Appli
38	3	US-09-485-737B-29	Sequence 29, Appli
40	3	US-09-485-737B-30	Sequence 30, Appli
20	3	US-09-527-154-13	Sequence 13, Appli
39	2	US-08-553-501A-38	Sequence 38, Appli
39	3	US-09-205-231-38	Sequence 38, Appli
47	4	US-09-422-978-275	Sequence 275, App
20	4	US-09-198-452A-2720	Sequence 2720, Ap
30	1	US-07-862-495-4	Sequence 4, Appli
31	2	US-08-948-132-2	Sequence 2, Appli
33	2	US-08-577-492-17	Sequence 17, Appli
33	3	US-09-079-630-17	Sequence 17, Appli
36	1	US-08-045-806-21	Sequence 21, Appli
36	1	US-08-366-051B-21	Sequence 21, Appli
36	4	US-09-371-772B-12981	Sequence 12981, A
36	4	US-09-479-005A-593	Sequence 593, App
36	4	US-09-479-005A-849	Sequence 849, App
36	4	US-09-479-005A-1002	Sequence 1002, Ap
37	2	US-08-857-946-41	Sequence 41, Appli
37	3	US-08-970-740-41	Sequence 41, Appli
46	4	US-09-636-215-611	Sequence 611, App
46	4	US-09-636-215-615	Sequence 615, App
46	4	US-09-685-166A-611	Sequence 611, App
46	4	US-09-685-166A-615	Sequence 615, App
46	4	US-09-679-426-611	Sequence 611, App
46	4	US-09-679-426-615	Sequence 615, App
47	4	US-09-641-638-962	Sequence 962, App
47	4	US-10-170-097-962	Sequence 962, App
17	4	US-09-462-951B-11	Sequence 11, Appli
20	2	US-08-330-272-6	Sequence 6, Appli
20	3	US-09-407-818-15	Sequence 15, Appli
20	4	US-09-668-313A-100	Sequence 100, App
20	4	US-09-705-267A-88	Sequence 88, Appli
20	5	PCT-US95-13663-6	Sequence 6, Appli
21	4	US-09-657-472-1808	Sequence 1808, Ap
21	4	US-09-657-472-2364	Sequence 2364, Ap
22	3	US-09-029-341-7	Sequence 7, Appli
28	2	US-08-305-764C-51	Sequence 51, Appli
28	3	US-09-233-506-5	Sequence 5, Appli
33	3	US-08-300-928C-52	Sequence 52, Appli
33	3	US-08-430-944D-52	Sequence 52, Appli
33	3	US-08-430-014-52	Sequence 52, Appli
33	3	US-08-431-184-52	Sequence 52, Appli
34	2	US-08-840-236-9	Sequence 9, Appli
34	2	US-08-505-448A-9	Sequence 9, Appli
40	4	US-09-060-299-185	Sequence 185, App
40	4	US-09-402-923A-185	Sequence 185, App
45	1	US-08-661-507-2	Sequence 2, Appli
46	2	US-08-840-236-14	Sequence 14, Appli
46	2	US-08-505-448A-14	Sequence 14, Appli
47	4	US-09-671-317-661	Sequence 661, App
50	3	US-09-012-097A-50	Sequence 50, Appli
50	4	US-09-481-620A-68	Sequence 68, Appli
50	4	US-09-781-804-49	Sequence 49, Appli
50	4	US-09-060-299-383	Sequence 383, App
19	4	US-09-402-923A-383	Sequence 383, App
19	4	US-09-696-791-271	Sequence 271, App
20	3	US-09-798-096-69	Sequence 69, Appli
23	1	US-08-559-303B-48	Sequence 48, Appli
23	3	US-09-175-828-48	Sequence 48, Appli
26	3	US-09-129-075-5	Sequence 5, Appli
26	3	US-07-850-770-23	Sequence 23, Appli
26	4	US-09-544-123-5	Sequence 5, Appli
26	5	PCT-US93-01598-23	Sequence 23, Appli
30	1	US-08-313-168-4	Sequence 4, Appli

101	11.2	53.3	34	3	US-09-183-412-49	Sequence 49, Appl	174	10.8	51.4	24	3	US-09-085-476-18	Sequence 18, Appl
c 102	11.2	53.3	34	4	US-09-086-118-19	Sequence 19, Appl	175	10.8	51.4	25	2	US-08-738-922-3	Sequence 3, Appl
103	11.2	53.3	34	4	US-09-769-864-49	Sequence 49, Appl	176	10.8	51.4	25	3	US-09-474-922A-7	Sequence 7, Appl
104	11.2	53.3	36	4	US-09-371-772B-12844	Sequence 12844, A	177	10.8	51.4	26	1	US-08-148-910-4	Sequence 4, Appl
105	11.2	53.3	36	4	US-09-479-005A-674	Sequence 674, App	178	10.8	51.4	26	1	US-08-448-937A-4	Sequence 4, Appl
106	11.2	53.3	37	4	US-09-479-005A-1102	Sequence 1102, Ap	c 179	10.8	51.4	26	3	US-09-245-041-74	Sequence 74, Appl
107	11.2	53.3	41	4	US-09-479-123-15	Sequence 15, Appl	c 180	10.8	51.4	26	4	US-09-358-055B-75	Sequence 75, Appl
108	11.2	53.3	41	4	US-09-484-997-15	Sequence 15, Appl	c 181	10.8	51.4	26	4	US-09-893-238-74	Sequence 74, Appl
109	11.2	53.3	41	4	US-09-481-355-15	Sequence 15, Appl	c 182	10.8	51.4	26	4	US-09-446-504-90	Sequence 90, Appl
110	11.2	53.3	41	4	US-09-481-282-15	Sequence 15, Appl	c 183	10.8	51.4	28	3	US-09-712-266-90	Sequence 90, Appl
111	11.2	53.3	41	4	US-09-455-659A-15	Sequence 15, Appl	c 184	10.8	51.4	28	4	US-09-786-684-9	Sequence 9, Appl
112	11.2	53.3	41	4	US-09-484-996-15	Sequence 15, Appl	c 185	10.8	51.4	28	4	US-09-786-684-9	Sequence 9, Appl
113	11.2	53.3	41	4	US-09-479-123-15	Sequence 15, Appl	186	10.8	51.4	32	3	US-08-991-743C-129	Sequence 129, App
114	11.2	53.3	41	4	US-09-484-317A-15	Sequence 15, Appl	187	10.8	51.4	32	4	US-09-851-486-129	Sequence 129, App
115	11.2	53.3	41	4	US-08-435-350-52	Sequence 52, Appl	188	10.8	51.4	33	3	US-08-437-569-16	Sequence 16, Appl
116	11.2	52.4	14	1	US-09-474-432B-419	Sequence 419, App	189	10.8	51.4	33	3	US-08-169-715-37	Sequence 37, Appl
117	11.2	52.4	17	4	US-09-474-432B-420	Sequence 420, App	190	10.8	51.4	35	1	US-08-479-852-38	Sequence 38, Appl
118	11.2	52.4	17	4	US-09-476-387-418	Sequence 418, App	191	10.8	51.4	35	1	US-08-479-852-38	Sequence 38, Appl
119	11.2	52.4	17	4	US-09-476-387-419	Sequence 419, App	192	10.8	51.4	35	2	US-08-462-646-38	Sequence 38, Appl
120	11.2	52.4	18	4	US-10-066-130-14	Sequence 14, Appl	193	10.8	51.4	35	2	US-08-462-646-38	Sequence 38, Appl
121	11.2	52.4	20	3	US-09-488-744A-70	Sequence 70, Appl	194	10.8	51.4	35	3	US-09-013-406-38	Sequence 38, Appl
122	11.2	52.4	22	4	US-08-469-260A-114	Sequence 114, App	195	10.8	51.4	35	3	US-09-013-406-38	Sequence 38, Appl
123	11.2	52.4	22	4	US-08-488-446-114	Sequence 114, App	196	10.8	51.4	35	4	US-09-766-095-38	Sequence 38, Appl
124	11.2	52.4	22	4	US-08-467-344A-114	Sequence 114, App	197	10.8	51.4	35	4	US-09-766-095-38	Sequence 38, Appl
125	11.2	52.4	22	4	US-08-424-550B-114	Sequence 114, App	198	10.8	51.4	36	4	US-09-479-005A-778	Sequence 778, App
126	11.2	52.4	23	4	US-09-181-585-6	Sequence 6, Appl	199	10.8	51.4	37	4	US-09-196-270-21	Sequence 21, Appl
127	11.2	52.4	24	3	US-09-139-617-16	Sequence 16, Appl	c 200	10.8	51.4	37	4	US-09-823-823-62	Sequence 62, Appl
128	11.2	52.4	24	4	US-09-561-741A-16	Sequence 16, Appl	201	10.8	51.4	38	4	US-09-823-823-62	Sequence 62, Appl
129	11.2	52.4	24	4	US-09-558-795-16	Sequence 16, Appl	202	10.8	51.4	39	2	US-08-467-963C-37	Sequence 37, Appl
130	11.2	52.4	25	4	US-09-402-631A-48	Sequence 48, Appl	203	10.8	51.4	39	2	US-08-838-189D-37	Sequence 37, Appl
131	11.2	52.4	27	1	US-07-796-106-10	Sequence 10, Appl	204	10.8	51.4	39	3	US-08-852-344D-37	Sequence 37, Appl
c 132	11.2	52.4	27	3	US-08-584-040-430	Sequence 430, App	205	10.8	51.4	40	3	US-08-344-639E-37	Sequence 37, Appl
133	11.2	52.4	28	4	US-09-067-453-3	Sequence 3, Appl	206	10.8	51.4	40	3	US-08-975-703-22	Sequence 22, Appl
134	11.2	52.4	28	4	US-09-067-453-4	Sequence 4, Appl	c 207	10.8	51.4	41	3	US-09-515-884-22	Sequence 22, Appl
c 135	11.2	52.4	29	2	US-08-794-793-3	Sequence 3, Appl	c 208	10.8	51.4	41	3	US-09-109-063-7	Sequence 7, Appl
c 136	11.2	52.4	29	3	US-09-249-200-3	Sequence 3, Appl	c 209	10.8	51.4	41	4	US-09-448-310-7	Sequence 7, Appl
c 137	11.2	52.4	29	4	US-09-304-232-784	Sequence 784, App	c 210	10.8	51.4	42	2	US-08-418-848A-61	Sequence 61, Appl
c 138	11.2	52.4	30	1	US-08-104-072B-20	Sequence 20, Appl	211	10.8	51.4	43	4	US-09-553-867A-39	Sequence 39, Appl
c 139	11.2	52.4	35	3	US-08-959-212-11	Sequence 11, Appl	212	10.8	51.4	45	1	US-08-661-507-1	Sequence 1, Appl
c 140	11.2	52.4	36	4	US-09-371-772B-12728	Sequence 12728, A	213	10.8	51.4	45	2	US-08-855-085-2	Sequence 2, Appl
c 141	11.2	52.4	36	4	US-09-371-772B-12746	Sequence 12746, A	214	10.8	51.4	45	2	US-09-186-030-2	Sequence 2, Appl
c 142	11.2	52.4	36	4	US-09-371-772B-12813	Sequence 12813, A	215	10.8	51.4	45	2	US-08-865-675-2	Sequence 2, Appl
c 143	11.2	52.4	36	4	US-09-371-772B-13005	Sequence 13005, A	216	10.8	51.4	45	2	US-08-933-749-3	Sequence 3, Appl
c 144	11.2	52.4	36	4	US-09-371-772B-13027	Sequence 13027, A	217	10.8	51.4	45	2	US-09-237-510-2	Sequence 2, Appl
c 145	11.2	52.4	36	4	US-09-371-772B-13150	Sequence 13150, A	218	10.8	51.4	45	3	US-09-120-916-2	Sequence 2, Appl
c 146	11.2	52.4	36	4	US-09-371-772B-14097	Sequence 14097, A	219	10.8	51.4	45	3	US-08-964-020-6	Sequence 6, Appl
c 147	11.2	52.4	36	4	US-09-479-005A-683	Sequence 683, App	220	10.8	51.4	45	3	US-09-235-583-3	Sequence 3, Appl
c 148	11.2	52.4	36	4	US-09-479-005A-920	Sequence 920, App	c 221	10.8	51.4	45	3	US-09-599-164-3	Sequence 3, Appl
c 149	11.2	52.4	36	4	US-09-479-005A-993	Sequence 993, App	c 222	10.8	51.4	47	4	US-09-422-978-323	Sequence 323, App
c 150	11.2	52.4	36	4	US-09-479-005A-1001	Sequence 1001, Ap	c 223	10.8	51.4	47	4	US-09-422-978-323	Sequence 323, App
c 151	11.2	52.4	36	4	US-09-479-005A-1003	Sequence 1003, Ap	224	10.8	51.4	50	4	US-09-270-767-25514	Sequence 25514, A
c 152	11.2	52.4	36	4	US-09-479-005A-1012	Sequence 1012, Ap	c 225	10.6	50.5	17	2	US-08-292-620A-1811	Sequence 1811, Ap
c 153	11.2	52.4	37	4	US-09-552-322-20	Sequence 20, Appl	c 226	10.6	50.5	17	3	US-09-071-845-1811	Sequence 1811, Ap
c 154	11.2	52.4	37	4	US-09-479-005A-1104	Sequence 1104, Ap	c 227	10.6	50.5	20	2	US-08-633-575B-3	Sequence 3, Appl
c 155	11.2	52.4	38	2	US-09-479-005A-1166	Sequence 1166, Ap	c 228	10.6	50.5	20	2	US-08-433-819-11	Sequence 11, Appl
c 156	11.2	52.4	38	2	US-09-097-759-5	Sequence 5, Appl	229	10.6	50.5	20	3	US-09-488-744A-69	Sequence 69, Appl
c 157	11.2	52.4	38	3	US-09-065-104-9	Sequence 9, Appl	c 230	10.6	50.5	20	4	US-09-199-542B-3	Sequence 3, Appl
c 158	11.2	52.4	38	4	US-09-371-772B-7548	Sequence 7548, Ap	c 231	10.6	50.5	20	4	US-09-526-193A-116	Sequence 116, App
c 159	11.2	52.4	38	4	US-09-371-772B-11378	Sequence 11378, A	c 232	10.6	50.5	21	2	US-09-574-779B-154	Sequence 154, App
c 160	11.2	52.4	40	4	US-09-849-069-44	Sequence 44, Appl	c 233	10.6	50.5	21	2	US-08-357-642A-11	Sequence 11, Appl
c 161	11.2	52.4	40	4	US-10-001-052-36	Sequence 36, Appl	c 234	10.6	50.5	21	2	US-08-460-626-23	Sequence 23, Appl
c 162	11.2	52.4	42	3	US-08-952-973-19	Sequence 19, Appl	c 235	10.6	50.5	21	2	US-08-460-626-23	Sequence 23, Appl
c 163	11.2	52.4	42	4	US-10-001-052-13	Sequence 13, Appl	c 236	10.6	50.5	24	1	US-08-467-284-12	Sequence 12, Appl
c 164	11.2	52.4	47	4	US-09-422-978-1086	Sequence 1086, Ap	c 237	10.6	50.5	24	1	US-08-467-284-12	Sequence 12, Appl
c 165	11.2	52.4	47	4	US-09-422-978-1654	Sequence 1654, Ap	c 238	10.6	50.5	25	3	US-08-737-607-36	Sequence 36, Appl
c 166	11.2	52.4	48	4	US-08-439-813-7	Sequence 7, Appl	c 239	10.6	50.5	25	3	US-09-245-041-26	Sequence 26, Appl
c 167	11.2	52.4	49	4	US-10-001-052-123	Sequence 123, App	c 240	10.6	50.5	25	4	US-09-358-055B-27	Sequence 27, Appl
c 168	10.8	51.4	18	4	US-09-475-947A-46	Sequence 46, Appl	c 241	10.6	50.5	25	4	US-09-893-238-25	Sequence 26, Appl
c 169	10.8	51.4	20	4	US-09-529-239D-65	Sequence 65, Appl	c 242	10.6	50.5	26	1	US-08-411-795B-57	Sequence 57, Appl
c 170	10.8	51.4	21	4	US-09-657-472-1455	Sequence 1455, Ap	c 243	10.6	50.5	26	1	US-08-469-319A-57	Sequence 57, Appl
c 171	10.8	51.4	21	4	US-09-657-472-2292	Sequence 2292, Ap	c 244	10.6	50.5	26	4	US-08-764-114-57	Sequence 57, Appl
c 172	10.8	51.4	22	1	US-08-464-523B-21	Sequence 21, Appl	c 245	10.6	50.5	26	4	US-08-469-419-57	Sequence 57, Appl
c 173	10.8	51.4	24	2	US-08-448-267A-7	Sequence 7, Appl	c 246	10.6	50.5	26	4	US-09-199-542B-82	Sequence 82, Appl

c 247	10.6	50.5	27	1	US-08-242-402-3	Sequence 3, Appli	c 320	10.6	50.5	47	4	US-09-422-978-3505	Sequence 3505, Ap
c 248	10.6	50.5	27	1	US-08-270-180-4	Sequence 4, Appli	c 321	10.6	50.5	48	1	US-08-137-117D-81	Sequence 81, Appl
c 249	10.6	50.5	27	1	US-08-682-423-4	Sequence 4, Appli	c 322	10.6	50.5	48	1	US-08-436-717-81	Sequence 81, Appl
c 250	10.6	50.5	27	3	US-09-246-277A-8	Sequence 8, Appli	c 323	10.4	49.5	17	3	US-08-584-040-5368	Sequence 5368, Ap
c 251	10.6	50.5	27	5	PCT-US95-05141-4	Sequence 4, Appli	c 324	10.4	49.5	17	3	US-08-584-040-5369	Sequence 5369, Ap
c 252	10.6	50.5	28	1	US-08-455-633A-24	Sequence 24, Appl	c 325	10.4	49.5	17	4	US-09-371-772B-2270	Sequence 2270, Ap
c 253	10.6	50.5	28	2	US-08-456-460C-24	Sequence 24, Appl	c 326	10.4	49.5	17	4	US-09-371-772B-2271	Sequence 2271, Ap
c 254	10.6	50.5	28	3	US-08-812-121-6	Sequence 6, Appli	c 327	10.4	49.5	18	3	US-08-584-040-6215	Sequence 6215, Ap
c 255	10.6	50.5	28	3	US-08-928-805-3	Sequence 6, Appli	c 328	10.4	49.5	18	4	US-09-157-864-14	Sequence 14, Appl
c 256	10.6	50.5	28	3	US-09-403-672-6	Sequence 6, Appli	c 329	10.4	49.5	18	4	US-09-371-772B-2977	Sequence 2977, Ap
c 257	10.6	50.5	28	5	PCT-US94-05354-24	Sequence 24, Appl	c 330	10.4	49.5	19	1	US-08-221-579A-47	Sequence 47, Appl
c 258	10.6	50.5	29	1	US-08-032-846-25	Sequence 25, Appl	c 331	10.4	49.5	19	1	US-08-753-147-6	Sequence 6, Appli
c 259	10.6	50.5	29	1	US-08-993-228-29	Sequence 29, Appl	c 332	10.4	49.5	19	1	US-08-512-681-11	Sequence 11, Appl
c 260	10.6	50.5	29	3	US-09-029-341-11	Sequence 11, Appl	c 333	10.4	49.5	19	2	US-08-704-701-47	Sequence 47, Appl
c 261	10.6	50.5	29	3	US-08-474-636-25	Sequence 25, Appl	c 334	10.4	49.5	19	2	US-08-979-385B-51	Sequence 51, Appl
c 262	10.6	50.5	30	4	US-09-522-955A-17	Sequence 17, Appl	c 335	10.4	49.5	19	3	US-09-321-461-47	Sequence 47, Appl
c 263	10.6	50.5	32	3	US-09-252-292-10	Sequence 10, Appl	c 336	10.4	49.5	19	3	US-08-357-398A-39	Sequence 39, Appl
c 264	10.6	50.5	33	4	US-09-531-056A-11	Sequence 11, Appl	c 337	10.4	49.5	19	4	US-09-422-978-9097	Sequence 9097, Ap
c 265	10.6	50.5	35	4	US-09-823-823-38	Sequence 38, Appl	c 338	10.4	49.5	19	5	PCT-US95-16206A-39	Sequence 39, Appl
c 266	10.6	50.5	35	4	US-09-736-116-65	Sequence 65, Appl	c 339	10.4	49.5	20	3	US-08-928-881-4	Sequence 4, Appli
c 267	10.6	50.5	35	4	US-09-736-116-94	Sequence 94, Appl	c 340	10.4	49.5	20	3	US-09-167-375-15	Sequence 15, Appl
c 268	10.6	50.5	36	4	US-09-371-772B-12743	Sequence 12743, A	c 341	10.4	49.5	20	3	US-09-467-642-46	Sequence 46, Appl
c 269	10.6	50.5	36	4	US-09-371-772B-12940	Sequence 12940, A	c 342	10.4	49.5	20	3	US-09-543-921-4	Sequence 4, Appli
c 270	10.6	50.5	36	4	US-09-371-772B-13109	Sequence 13109, A	c 343	10.4	49.5	20	4	US-09-517-467B-223	Sequence 223, App
c 271	10.6	50.5	36	4	US-09-479-005A-571	Sequence 571, App	c 344	10.4	49.5	20	4	US-09-266-014-9	Sequence 9, Appli
c 272	10.6	50.5	36	4	US-09-479-005A-595	Sequence 595, App	c 345	10.4	49.5	20	4	US-09-659-845A-171	Sequence 171, App
c 273	10.6	50.5	36	4	US-09-479-005A-688	Sequence 688, App	c 346	10.4	49.5	20	4	US-09-422-978-11045	Sequence 11045, A
c 274	10.6	50.5	36	4	US-09-479-005A-838	Sequence 838, App	c 347	10.4	49.5	20	4	US-09-491-759-4	Sequence 4, Appli
c 275	10.6	50.5	36	4	US-09-479-005A-903	Sequence 903, App	c 348	10.4	49.5	20	4	US-09-526-193A-147	Sequence 147, App
c 276	10.6	50.5	36	4	US-09-479-005A-975	Sequence 975, App	c 349	10.4	49.5	21	3	US-09-336-447A-66	Sequence 66, Appl
c 277	10.6	50.5	36	4	US-09-004-068-7	Sequence 7, Appli	c 350	10.4	49.5	21	3	US-09-710-200-3	Sequence 3, Appli
c 278	10.6	50.5	37	1	US-08-477-877B-27	Sequence 27, Appl	c 351	10.4	49.5	21	4	US-09-975-408-3	Sequence 3, Appli
c 279	10.6	50.5	37	2	US-08-477-881A-27	Sequence 27, Appl	c 352	10.4	49.5	21	4	US-09-422-978-1826	Sequence 1826, A
c 280	10.6	50.5	37	2	US-08-477-989B-27	Sequence 27, Appl	c 353	10.4	49.5	21	4	US-09-657-472-1826	Sequence 66, Appl
c 281	10.6	50.5	37	4	US-09-662-386-17	Sequence 17, Appl	c 354	10.4	49.5	21	4	US-09-952-267B-66	Sequence 66, Appl
c 282	10.6	50.5	37	4	US-09-479-005A-1078	Sequence 1078, Ap	c 355	10.4	49.5	23	1	US-08-242-035A-9	Sequence 9, Appl
c 283	10.6	50.5	38	4	US-10-112-802-68	Sequence 68, Appl	c 356	10.4	49.5	23	1	US-09-018-584A-47	Sequence 47, Appl
c 284	10.6	50.5	38	4	US-10-112-802-69	Sequence 69, Appl	c 357	10.4	49.5	23	3	US-09-784-423-47	Sequence 47, Appl
c 285	10.6	50.5	39	2	US-08-714-070A-21	Sequence 21, Appl	c 358	10.4	49.5	24	1	US-08-508-778A-13	Sequence 13, Appl
c 286	10.6	50.5	40	4	US-09-496-346-10	Sequence 10, Appl	c 359	10.4	49.5	24	2	US-08-202-044-14	Sequence 14, Appl
c 287	10.6	50.5	41	2	US-08-985-337A-4	Sequence 4, Appli	c 360	10.4	49.5	24	3	US-08-751-344B-14	Sequence 14, Appl
c 288	10.6	50.5	41	2	US-08-985-144A-4	Sequence 4, Appli	c 361	10.4	49.5	24	3	US-08-818-082-6	Sequence 6, Appli
c 289	10.6	50.5	41	2	US-08-985-320A-4	Sequence 4, Appli	c 362	10.4	49.5	24	4	US-09-815-585-21	Sequence 21, Appl
c 290	10.6	50.5	41	3	US-08-984-732A-4	Sequence 4, Appli	c 363	10.4	49.5	24	4	US-09-692-056-6	Sequence 6, Appli
c 291	10.6	50.5	41	3	US-09-195-578-16	Sequence 16, Appl	c 364	10.4	49.5	25	1	US-07-989-160-10	Sequence 10, Appl
c 292	10.6	50.5	41	3	US-09-170-951-16	Sequence 16, Appl	c 365	10.4	49.5	25	3	US-08-891-789B-18	Sequence 18, Appl
c 293	10.6	50.5	41	3	US-09-164-482-16	Sequence 16, Appl	c 366	10.4	49.5	25	3	US-08-849-602C-6	Sequence 6, Appli
c 294	10.6	50.5	41	3	US-09-332-769-11	Sequence 11, Appl	c 367	10.4	49.5	25	3	US-09-149-322-41	Sequence 41, Appl
c 295	10.6	50.5	41	3	US-09-456-153-11	Sequence 11, Appl	c 368	10.4	49.5	25	5	PCT-US92-08090-10	Sequence 10, Appl
c 296	10.6	50.5	41	3	US-09-167-180-16	Sequence 16, Appl	c 369	10.4	49.5	26	1	US-08-044-621D-15	Sequence 15, Appl
c 297	10.6	50.5	41	3	US-09-455-627-11	Sequence 11, Appl	c 370	10.4	49.5	26	3	US-09-534-407-28	Sequence 28, Appl
c 298	10.6	50.5	41	3	US-09-426-533-11	Sequence 11, Appl	c 371	10.4	49.5	26	4	US-09-007-288E-2	Sequence 2, Appli
c 299	10.6	50.5	41	3	US-09-609-205-12	Sequence 12, Appl	c 372	10.4	49.5	26	4	US-09-007-288E-137	Sequence 137, App
c 300	10.6	50.5	41	3	US-09-516-945-11	Sequence 11, Appl	c 373	10.4	49.5	26	4	US-09-999-201B-28	Sequence 28, Appl
c 301	10.6	50.5	41	3	US-09-757-218-12	Sequence 12, Appl	c 374	10.4	49.5	26	4	US-10-281-673A-28	Sequence 28, Appl
c 302	10.6	50.5	41	3	US-09-516-757-11	Sequence 11, Appl	c 375	10.4	49.5	27	4	US-09-630-250B-2	Sequence 2, Appli
c 303	10.6	50.5	41	3	US-09-516-750-11	Sequence 11, Appl	c 376	10.4	49.5	28	1	US-08-446-729-11	Sequence 11, Appl
c 304	10.6	50.5	41	3	US-09-342-577-12	Sequence 12, Appl	c 377	10.4	49.5	28	4	US-09-157-864-12	Sequence 12, Appl
c 305	10.6	50.5	41	3	US-09-516-756-11	Sequence 11, Appl	c 378	10.4	49.5	29	1	US-08-306-871-23	Sequence 23, Appl
c 306	10.6	50.5	41	3	US-09-828-061A-12	Sequence 12, Appl	c 379	10.4	49.5	29	1	US-08-569-959-23	Sequence 23, Appl
c 307	10.6	50.5	41	3	US-09-463-917-11	Sequence 11, Appl	c 380	10.4	49.5	29	2	US-08-930-605-5	Sequence 5, Appli
c 308	10.6	50.5	41	4	US-09-347-673-12	Sequence 12, Appl	c 381	10.4	49.5	30	1	US-08-373-124A-25	Sequence 25, Appl
c 309	10.6	50.5	41	4	US-09-757-213-12	Sequence 12, Appl	c 382	10.4	49.5	30	1	US-08-667-079B-8	Sequence 8, Appli
c 310	10.6	50.5	41	4	US-09-656-653-11	Sequence 11, Appl	c 383	10.4	49.5	30	1	US-08-435-628-25	Sequence 25, Appl
c 311	10.6	50.5	41	4	US-09-757-231-12	Sequence 12, Appl	c 384	10.4	49.5	30	2	US-08-678-039A-20	Sequence 20, Appl
c 312	10.6	50.5	41	4	US-09-828-259A-12	Sequence 12, Appl	c 385	10.4	49.5	30	3	US-08-643-704A-27	Sequence 27, Appl
c 313	10.6	50.5	41	4	US-09-719-878-12	Sequence 12, Appl	c 386	10.4	49.5	30	4	US-09-052-919-30	Sequence 30, Appl
c 314	10.6	50.5	41	4	US-09-757-217A-12	Sequence 12, Appl	c 387	10.4	49.5	30	4	US-09-953-052-30	Sequence 30, Appl
c 315	10.6	50.5	41	4	US-09-828-325A-12	Sequence 12, Appl	c 388	10.4	49.5	31	2	US-08-859-998-463	Sequence 463, App
c 316	10.6	50.5	41	4	US-09-756-248-11	Sequence 11, Appl	c 389	10.4	49.5	31	3	US-08-836-329-14	Sequence 14, Appl
c 317	10.6	50.5	44	1	US-08-340-011-20	Sequence 20, Appl	c 390	10.4	49.5	31	3	US-08-925-928-463	Sequence 463, App
c 318	10.6	50.5	44	3	US-08-901-710-20	Sequence 20, Appl	c 391	10.4	49.5	31	4	US-09-225-201B-463	Sequence 463, App
c 319	10.6	50.5	46	3	US-09-065-104-14	Sequence 14, Appl	c 392	10.4	49.5	32	1	US-08-765-081-8	Sequence 8, Appli

c 393	10.4	49.5	32	3	US-09-098-082-8	Sequence 8, Appl1	466	10.2	48.6	20	3	US-08-037-230D-27	Sequence 27, Appl
c 394	10.4	49.5	32	5	PCT-US95-06994-10	Sequence 10, Appl	467	10.2	48.6	20	3	US-08-443-580F-11	Sequence 11, Appl
c 395	10.4	49.5	34	4	US-09-978-758-14	Sequence 14, Appl	c 468	10.2	48.6	20	4	US-09-387-341-12	Sequence 12, Appl
c 396	10.4	49.5	34	4	US-10-001-052-50	Sequence 50, Appl	469	10.2	48.6	20	4	US-08-571-263-11	Sequence 11, Appl
c 397	10.4	49.5	35	2	US-08-632-470-20	Sequence 20, Appl	470	10.2	48.6	20	4	US-09-583-850-27	Sequence 27, Appl
c 398	10.4	49.5	36	1	US-08-338-992B-23	Sequence 23, Appl	c 471	10.2	48.6	20	4	US-08-754-477A-65	Sequence 65, Appl
c 399	10.4	49.5	36	3	US-09-010-733-23	Sequence 23, Appl	472	10.2	48.6	20	4	US-09-579-197-27	Sequence 27, Appl
c 400	10.4	49.5	36	4	US-09-477-135A-164	Sequence 164, Appl	473	10.2	48.6	20	4	US-09-404-026-27	Sequence 27, Appl
c 401	10.4	49.5	38	4	US-09-662-386-13	Sequence 13, Appl	c 474	10.2	48.6	20	4	US-09-068-506-57	Sequence 57, Appl
c 402	10.4	49.5	39	3	US-09-000-092-22	Sequence 22, Appl	475	10.2	48.6	20	4	US-09-249-247-211	Sequence 211, Appl
c 403	10.4	49.5	39	4	US-09-227-595-16	Sequence 16, Appl	c 476	10.2	48.6	20	4	US-09-758-881-44	Sequence 44, Appl
c 404	10.4	49.5	39	4	US-09-227-595-17	Sequence 17, Appl	c 477	10.2	48.6	20	4	US-09-899-440-11	Sequence 11, Appl
c 405	10.4	49.5	39	4	US-08-595-590B-16	Sequence 16, Appl	478	10.2	48.6	21	1	US-08-753-147-60	Sequence 60, Appl
c 406	10.4	49.5	39	4	US-08-595-590B-17	Sequence 17, Appl	479	10.2	48.6	21	3	US-08-954-536-7	Sequence 7, Appl
c 407	10.4	49.5	40	4	US-09-849-069-44	Sequence 44, Appl	480	10.2	48.6	21	3	US-09-418-641-5	Sequence 5, Appl
c 408	10.4	49.5	42	1	US-08-044-621D-5	Sequence 5, Appl	481	10.2	48.6	21	3	US-08-612-973-1	Sequence 1, Appl
c 409	10.4	49.5	45	1	US-08-171-389-62	Sequence 62, Appl	482	10.2	48.6	21	3	US-08-927-597-1	Sequence 1, Appl
c 410	10.4	49.5	45	1	US-08-123-936-62	Sequence 62, Appl	483	10.2	48.6	21	3	US-09-249-697A-17	Sequence 17, Appl
c 411	10.4	49.5	45	2	US-08-475-228A-62	Sequence 62, Appl	484	10.2	48.6	21	3	US-09-363-316B-17	Sequence 17, Appl
c 412	10.4	49.5	45	3	US-08-482-080A-62	Sequence 62, Appl	485	10.2	48.6	21	4	US-09-422-978-5867	Sequence 5867, Ap
c 413	10.4	49.5	45	3	US-09-354-947-62	Sequence 62, Appl	c 486	10.2	48.6	22	3	US-09-230-704-12	Sequence 12, Appl
c 414	10.4	49.5	45	4	US-09-981-953A-14	Sequence 14, Appl	c 487	10.2	48.6	22	3	US-08-192-946-15	Sequence 15, Appl
c 415	10.4	49.5	45	5	PCT-US93-12388-62	Sequence 62, Appl	c 488	10.2	48.6	22	3	US-09-609-162-12	Sequence 12, Appl
c 416	10.4	49.5	46	2	US-08-404-531B-48	Sequence 48, Appl	c 489	10.2	48.6	22	4	US-09-612-204B-30	Sequence 30, Appl
c 417	10.4	49.5	46	3	US-08-476-900A-48	Sequence 48, Appl	c 490	10.2	48.6	22	4	US-09-634-732-12	Sequence 12, Appl
c 418	10.4	49.5	46	3	US-08-488-546A-48	Sequence 48, Appl	c 491	10.2	48.6	23	3	US-09-338-907-172	Sequence 172, Appl
c 419	10.4	49.5	47	1	US-08-723-896-20	Sequence 20, Appl	492	10.2	48.6	23	3	US-09-230-944-32	Sequence 32, Appl
c 420	10.4	49.5	47	1	US-08-178-635-2	Sequence 2, Appl	c 493	10.2	48.6	23	3	US-09-142-623-34	Sequence 34, Appl
c 421	10.4	49.5	47	4	US-09-422-978-2163	Sequence 2163, Ap	c 494	10.2	48.6	23	3	US-09-142-623-35	Sequence 35, Appl
c 422	10.4	49.5	49	4	US-09-538-709-945	Sequence 945, App	c 500	10.2	48.6	24	4	US-09-526-992-2	Sequence 2, Appl
c 423	10.4	49.5	49	4	US-09-538-709-945	Sequence 945, App	c 501	10.2	48.6	24	4	US-09-526-992-6	Sequence 6, Appl
c 424	10.4	49.5	50	1	US-08-171-389-335	Sequence 1000, Ap	c 502	10.2	48.6	24	4	US-09-526-992-8	Sequence 8, Appl
c 425	10.4	49.5	50	1	US-08-171-389-335	Sequence 335, App	c 503	10.2	48.6	24	4	US-09-526-992-10	Sequence 10, Appl
c 426	10.4	49.5	50	1	US-08-171-389-406	Sequence 406, App	c 504	10.2	48.6	24	4	US-09-526-992-12	Sequence 12, Appl
c 427	10.4	49.5	50	1	US-08-123-936-335	Sequence 335, App	c 498	10.2	48.6	24	4	US-09-526-992-14	Sequence 14, Appl
c 428	10.4	49.5	50	1	US-08-123-936-406	Sequence 406, App	c 499	10.2	48.6	24	4	US-08-255-892-38	Sequence 38, Appl
c 429	10.4	49.5	50	1	US-08-472-194A-18	Sequence 18, Appl	c 500	10.2	48.6	24	4	US-09-526-992-2	Sequence 2, Appl
c 430	10.4	49.5	50	2	US-08-475-228A-335	Sequence 335, App	c 501	10.2	48.6	24	4	US-09-526-992-6	Sequence 6, Appl
c 431	10.4	49.5	50	2	US-08-475-228A-406	Sequence 406, App	c 502	10.2	48.6	24	4	US-09-526-992-8	Sequence 8, Appl
c 432	10.4	49.5	50	3	US-08-482-080A-335	Sequence 335, App	c 503	10.2	48.6	24	4	US-09-526-992-12	Sequence 12, Appl
c 433	10.4	49.5	50	3	US-08-482-080A-406	Sequence 406, App	c 504	10.2	48.6	24	4	US-09-526-992-14	Sequence 14, Appl
c 434	10.4	49.5	50	3	US-09-262-142-18	Sequence 18, Appl	505	10.2	48.6	25	1	US-08-013-801-12	Sequence 12, Appl
c 435	10.4	49.5	50	3	US-08-849-567A-18	Sequence 18, Appl	506	10.2	48.6	25	1	US-08-430-417-12	Sequence 12, Appl
c 436	10.4	49.5	50	3	US-09-354-947-335	Sequence 335, App	507	10.2	48.6	25	1	US-08-466-822-12	Sequence 12, Appl
c 437	10.4	49.5	50	3	US-09-554-929-119	Sequence 119, App	508	10.2	48.6	25	3	US-09-269-136B-11	Sequence 11, Appl
c 438	10.4	49.5	50	4	US-09-546-934-21	Sequence 21, Appl	509	10.2	48.6	25	4	US-09-425-034A-12	Sequence 12, Appl
c 439	10.4	49.5	50	4	PCT-US93-12388-335	Sequence 335, App	510	10.2	48.6	25	4	US-08-469-260A-111	Sequence 111, App
c 440	10.4	49.5	50	5	PCT-US93-12388-406	Sequence 406, App	511	10.2	48.6	25	4	US-08-488-446-111	Sequence 111, App
c 441	10.2	48.6	16	2	US-08-457-273B-19	Sequence 19, Appl	512	10.2	48.6	25	4	US-08-424-550B-111	Sequence 111, App
c 442	10.2	48.6	17	4	US-09-371-772B-6906	Sequence 6906, Ap	513	10.2	48.6	25	5	PCT-US94-01235-12	Sequence 12, Appl
c 443	10.2	48.6	18	2	US-08-638-323-1	Sequence 1, Appl	c 515	10.2	48.6	26	1	US-08-252-073A-18	Sequence 18, Appl
c 444	10.2	48.6	18	3	US-08-514-542C-8	Sequence 8, Appl	c 516	10.2	48.6	26	3	US-08-936-632B-15	Sequence 15, Appl
c 445	10.2	48.6	18	3	US-09-031-495-1	Sequence 1, Appl	c 517	10.2	48.6	27	4	US-08-749-955-14	Sequence 14, Appl
c 446	10.2	48.6	18	3	US-09-031-237-1	Sequence 1, Appl	c 518	10.2	48.6	27	2	US-08-410-654B-36	Sequence 36, Appl
c 447	10.2	48.6	18	3	US-08-584-040-4499	Sequence 4499, Ap	c 519	10.2	48.6	27	2	US-08-474-851-36	Sequence 36, Appl
c 448	10.2	48.6	18	4	US-09-371-772B-2212	Sequence 2212, Ap	520	10.2	48.6	27	3	US-08-481-560-36	Sequence 36, Appl
c 449	10.2	48.6	19	4	US-09-422-978-9792	Sequence 9792, Ap	521	10.2	48.6	27	3	US-08-584-040-1001	Sequence 1001, Ap
c 450	10.2	48.6	19	4	US-09-696-791-272	Sequence 272, App	c 522	10.2	48.6	27	4	US-08-749-955-15	Sequence 15, Appl
c 451	10.2	48.6	19	4	US-09-696-791-853	Sequence 853, App	c 523	10.2	48.6	27	4	US-08-749-955-15	Sequence 15, Appl
c 452	10.2	48.6	19	4	US-09-696-791-1386	Sequence 1386, Ap	c 524	10.2	48.6	27	4	US-08-749-955-16	Sequence 16, Appl
c 453	10.2	48.6	20	1	US-07-938-334C-20	Sequence 20, Appl	c 525	10.2	48.6	28	4	US-09-216-430C-38	Sequence 38, Appl
c 454	10.2	48.6	20	1	US-08-073-103A-11	Sequence 11, Appl	c 526	10.2	48.6	29	4	US-09-304-232-428	Sequence 428, App
c 455	10.2	48.6	20	1	US-08-107-684B-35	Sequence 35, Appl	c 527	10.2	48.6	30	1	US-07-972-387-58	Sequence 58, Appl
c 456	10.2	48.6	20	1	US-08-299-849B-47	Sequence 47, Appl	528	10.2	48.6	30	1	US-08-349-006-7	Sequence 7, Appl
c 457	10.2	48.6	20	1	US-08-443-341-11	Sequence 11, Appl	529	10.2	48.6	30	1	US-07-977-284A-181	Sequence 181, App
c 458	10.2	48.6	20	3	US-08-967-727-27	Sequence 27, Appl	c 531	10.2	48.6	30	1	US-08-217-210B-14	Sequence 14, Appl
c 459	10.2	48.6	20	3	US-08-354-679C-11	Sequence 11, Appl	c 532	10.2	48.6	30	1	US-08-431-412-58	Sequence 58, Appl
c 460	10.2	48.6	20	3	US-09-249-730-211	Sequence 211, App	c 533	10.2	48.6	30	2	US-08-057-971-58	Sequence 58, Appl
c 461	10.2	48.6	20	3	US-09-418-641-54	Sequence 54, Appl	c 534	10.2	48.6	30	3	US-08-564-100-1	Sequence 1, Appl
c 462	10.2	48.6	20	3	US-09-012-198-3	Sequence 3, Appl	535	10.2	48.6	30	5	PCT-US94-04180-5	Sequence 5, Appl
c 463	10.2	48.6	20	3	US-09-288-461-44	Sequence 44, Appl	c 536	10.2	48.6	31	1	US-08-474-633A-13	Sequence 13, Appl
c 464	10.2	48.6	20	3	US-09-488-671-123	Sequence 123, App	c 537	10.2	48.6	31	4	US-08-823-771-13	Sequence 13, Appl
c 465	10.2	48.6	20	3	US-08-393-273E-11	Sequence 11, Appl	c 538	10.2	48.6	31	5	PCT-US93-02480-13	Sequence 13, Appl

C 539	10.2	48.6	32	3	US-09-234-393-2	Sequence 2, Appli	c 612	10.2	48.6	48	3	US-08-986-659B-13	Sequence 13, Appl
C 540	10.2	48.6	32	3	US-09-865-171-23	Sequence 2, Appli	613	10.2	48.6	49	3	US-09-235-451-13	Sequence 13, Appl
C 541	10.2	48.6	33	4	US-09-043-239-15	Sequence 15, Appl	614	10.2	48.6	49	4	US-09-978-403-13	Sequence 13, Appl
C 542	10.2	48.6	33	3	US-09-080-983-22	Sequence 22, Appl	615	10.2	48.6	50	3	US-09-043-239-7	Sequence 7, Appli
C 543	10.2	48.6	33	4	US-09-495-901-15	Sequence 15, Appl	616	10.2	48.6	50	4	US-08-495-901-7	Sequence 7, Appli
C 544	10.2	48.6	34	2	US-08-381-691-9	Sequence 9, Appli	617	10.2	48.6	50	4	US-08-956-171E-2231	Sequence 2231, Ap
C 545	10.2	48.6	34	4	US-08-468-260A-128	Sequence 128, App	618	10.2	48.6	50	4	US-08-781-986A-2231	Sequence 2231, Ap
C 546	10.2	48.6	34	4	US-08-488-446-128	Sequence 128, App	c 619	10	47.6	14	4	US-07-209-504-1	Sequence 1, Appli
C 547	10.2	48.6	34	4	US-08-467-344A-128	Sequence 128, App	620	10	47.6	17	3	US-09-446-504-28	Sequence 28, Appl
C 548	10.2	48.6	34	4	US-08-424-550B-128	Sequence 128, App	621	10	47.6	17	3	US-09-712-266-38	Sequence 28, Appl
C 549	10.2	48.6	34	4	US-09-971-611-10	Sequence 11, Appl	622	10	47.6	18	1	US-07-702-163B-2	Sequence 2, Appli
C 550	10.2	48.6	34	4	US-09-971-611-11	Sequence 11, Appl	623	10	47.6	18	1	US-08-060-984-2	Sequence 2, Appli
C 551	10.2	48.6	36	4	US-09-371-772B-12820	Sequence 12820, A	624	10	47.6	18	1	US-08-143-219-10	Sequence 10, Appl
C 552	10.2	48.6	37	1	US-08-290-592E-15	Sequence 15, Appl	625	10	47.6	18	1	US-08-383-742-2	Sequence 2, Appli
C 553	10.2	48.6	37	5	PCT-US95-10053-12	Sequence 12, Appl	626	10	47.6	18	2	US-08-532-979-1	Sequence 1, Appli
C 554	10.2	48.6	37	5	PCT-US96-09448-15	Sequence 15, Appl	627	10	47.6	18	2	US-08-532-979-4	Sequence 4, Appli
C 555	10.2	48.6	38	2	US-08-857-946-127	Sequence 127, App	628	10	47.6	18	2	US-08-532-979-6	Sequence 6, Appli
C 556	10.2	48.6	38	3	US-08-970-740-127	Sequence 127, App	629	10	47.6	18	3	US-09-540-699-1	Sequence 1, Appli
C 557	10.2	48.6	38	4	US-09-371-772B-8119	Sequence 8119, Ap	c 630	10	47.6	18	4	US-09-250-609-56	Sequence 56, Appl
C 558	10.2	48.6	39	3	US-09-198-723A-28	Sequence 28, Appl	c 631	10	47.6	18	4	US-09-250-611-56	Sequence 56, Appl
C 559	10.2	48.6	39	3	US-09-198-723A-29	Sequence 29, Appl	632	10	47.6	18	4	US-09-587-934B-20	Sequence 20, Appl
C 560	10.2	48.6	39	3	US-09-198-723A-36	Sequence 36, Appl	633	10	47.6	18	4	US-09-321-249-20	Sequence 20, Appl
C 561	10.2	48.6	39	3	US-09-198-723A-37	Sequence 37, Appl	634	10	47.6	18	4	US-09-375-248-10	Sequence 10, Appl
C 562	10.2	48.6	39	3	US-09-198-723A-44	Sequence 44, Appl	635	10	47.6	18	4	US-08-835-370-39	Sequence 39, Appl
C 563	10.2	48.6	39	3	US-09-198-723A-45	Sequence 45, Appl	636	10	47.6	19	1	US-08-221-579A-48	Sequence 48, Appl
C 564	10.2	48.6	39	3	US-09-198-723A-51	Sequence 51, Appl	637	10	47.6	19	2	US-08-704-701-48	Sequence 48, Appl
C 565	10.2	48.6	39	3	US-09-198-723A-52	Sequence 52, Appl	638	10	47.6	19	2	US-08-979-385B-52	Sequence 52, Appl
C 566	10.2	48.6	39	3	US-09-198-723A-58	Sequence 58, Appl	639	10	47.6	19	3	US-09-321-461-48	Sequence 48, Appl
C 567	10.2	48.6	39	3	US-09-198-723A-59	Sequence 59, Appl	640	10	47.6	19	3	US-08-357-398A-40	Sequence 40, Appl
C 568	10.2	48.6	39	3	US-09-198-723A-61	Sequence 61, Appl	641	10	47.6	19	5	PCT-US95-16206A-40	Sequence 40, Appl
C 569	10.2	48.6	39	3	US-09-198-723A-62	Sequence 62, Appl	642	10	47.6	20	2	US-08-418-848A-43	Sequence 43, Appl
C 570	10.2	48.6	39	3	US-09-198-723A-75	Sequence 75, Appl	c 643	10	47.6	20	2	US-08-418-848A-46	Sequence 46, Appl
C 571	10.2	48.6	39	3	US-09-198-723A-76	Sequence 76, Appl	644	10	47.6	20	2	US-09-167-375-18	Sequence 18, Appl
C 572	10.2	48.6	39	3	US-09-198-723A-81	Sequence 81, Appl	645	10	47.6	20	3	US-09-489-765A-27	Sequence 27, Appl
C 573	10.2	48.6	39	3	US-09-198-723A-82	Sequence 82, Appl	c 646	10	47.6	20	3	US-03-561-497-53	Sequence 53, Appl
C 574	10.2	48.6	39	4	US-09-477-135A-163	Sequence 163, App	647	10	47.6	20	4	US-09-211-823C-13	Sequence 13, Appl
C 575	10.2	48.6	39	4	US-09-684-881-28	Sequence 28, Appl	c 648	10	47.6	21	1	US-08-728-259A-20	Sequence 20, Appl
C 576	10.2	48.6	39	4	US-09-684-881-29	Sequence 29, Appl	649	10	47.6	21	2	US-08-473-486-20	Sequence 20, Appl
C 577	10.2	48.6	39	4	US-09-684-881-36	Sequence 36, Appl	c 650	10	47.6	21	4	US-09-360-545-35	Sequence 35, Appl
C 578	10.2	48.6	39	4	US-09-684-881-37	Sequence 37, Appl	c 651	10	47.6	21	4	US-09-657-472-307	Sequence 307, App
C 579	10.2	48.6	39	4	US-09-684-881-44	Sequence 44, Appl	c 652	10	47.6	22	3	US-09-099-749-3	Sequence 3, Appli
C 580	10.2	48.6	39	4	US-09-684-881-45	Sequence 45, Appl	653	10	47.6	22	3	US-09-341-587-11	Sequence 11, Appl
C 581	10.2	48.6	39	4	US-09-684-881-51	Sequence 51, Appl	c 654	10	47.6	23	3	US-08-964-877-14	Sequence 14, Appl
C 582	10.2	48.6	39	4	US-09-684-881-52	Sequence 52, Appl	655	10	47.6	23	3	US-09-540-699-6	Sequence 6, Appli
C 583	10.2	48.6	39	4	US-09-684-881-58	Sequence 58, Appl	656	10	47.6	23	3	US-09-540-699-10	Sequence 10, Appl
C 584	10.2	48.6	39	4	US-09-684-881-59	Sequence 59, Appl	c 657	10	47.6	24	1	US-08-117-329-2	Sequence 2, Appli
C 585	10.2	48.6	39	4	US-09-684-881-61	Sequence 61, Appl	c 658	10	47.6	24	2	US-08-859-398-776	Sequence 776, App
C 586	10.2	48.6	39	4	US-09-684-881-62	Sequence 62, Appl	659	10	47.6	24	3	US-09-225-928-776	Sequence 776, App
C 587	10.2	48.6	39	4	US-09-684-881-75	Sequence 75, Appl	660	10	47.6	24	3	US-09-540-699-4	Sequence 4, Appli
C 588	10.2	48.6	39	4	US-09-684-881-76	Sequence 76, Appl	661	10	47.6	24	3	US-09-540-699-7	Sequence 7, Appli
C 589	10.2	48.6	39	4	US-09-684-881-81	Sequence 81, Appl	c 662	10	47.6	24	4	US-09-806-354-19	Sequence 19, Appl
C 590	10.2	48.6	39	4	US-09-684-881-82	Sequence 82, Appl	663	10	47.6	24	4	US-09-225-201B-776	Sequence 776, App
C 591	10.2	48.6	40	1	US-07-972-387-57	Sequence 57, Appl	c 664	10	47.6	25	1	US-08-368-281-9	Sequence 9, Appli
C 592	10.2	48.6	40	1	US-08-431-412-57	Sequence 57, Appl	665	10	47.6	25	2	US-08-666-392A-8	Sequence 8, Appli
C 593	10.2	48.6	40	1	US-08-057-971-57	Sequence 57, Appl	c 666	10	47.6	25	3	US-08-737-607-10	Sequence 10, Appl
C 594	10.2	48.6	40	2	US-08-235-515A-53	Sequence 53, Appl	c 667	10	47.6	25	3	US-08-513-974B-213	Sequence 213, App
C 595	10.2	48.6	40	2	US-08-455-968E-45	Sequence 45, Appl	668	10	47.6	25	3	US-09-199-926-8	Sequence 8, Appli
C 596	10.2	48.6	40	3	US-08-929-329-19	Sequence 19, Appl	c 669	10	47.6	25	3	US-09-203-231B-86	Sequence 86, Appl
C 597	10.2	48.6	44	1	US-08-168-917-10	Sequence 10, Appl	670	10	47.6	25	3	US-09-150-766-4	Sequence 4, Appli
C 598	10.2	48.6	44	2	US-08-460-510-10	Sequence 10, Appl	671	10	47.6	25	3	US-09-540-699-8	Sequence 8, Appli
C 599	10.2	48.6	44	2	US-08-460-490-10	Sequence 10, Appl	672	10	47.6	25	3	US-09-540-699-11	Sequence 11, Appl
C 600	10.2	48.6	44	4	US-09-281-851-3	Sequence 3, Appli	673	10	47.6	25	4	US-09-422-936-9	Sequence 9, Appli
C 601	10.2	48.6	44	5	PCT-US92-00730-10	Sequence 5, Appli	674	10	47.6	25	4	US-09-422-936-64	Sequence 64, Appl
C 602	10.2	48.6	44	5	PCT-US92-10430-5	Sequence 13, Appl	675	10	47.6	25	4	US-09-866-108A-12068	Sequence 12068, A
C 603	10.2	48.6	45	2	US-08-687-355A-13	Sequence 12, Appl	676	10	47.6	25	4	US-09-866-108A-12069	Sequence 12069, A
C 604	10.2	48.6	45	3	US-08-986-659B-12	Sequence 12, Appl	677	10	47.6	25	4	US-09-866-108A-12070	Sequence 12070, A
C 605	10.2	48.6	45	4	US-09-407-367-13	Sequence 13, Appl	678	10	47.6	25	4	US-09-866-108A-12071	Sequence 12071, A
C 606	10.2	48.6	45	4	US-09-546-934-32	Sequence 32, Appl	679	10	47.6	25	4	US-09-866-108A-12072	Sequence 12072, A
C 607	10.2	48.6	47	4	US-09-422-978-556	Sequence 556, App	680	10	47.6	25	4	US-09-866-108A-12073	Sequence 12073, A
C 608	10.2	48.6	47	4	US-09-422-978-2239	Sequence 2239, Ap	681	10	47.6	25	4	US-09-866-108A-12074	Sequence 12074, A
C 609	10.2	48.6	47	4	US-09-422-978-2327	Sequence 2327, Ap	682	10	47.6	25	4	US-09-866-108A-12075	Sequence 12075, A
C 610	10.2	48.6	47	4	US-09-422-978-2517	Sequence 2517, Ap	683	10	47.6	25	5	PCT-US94-07659-19	Sequence 19, Appl
C 611	10.2	48.6	47	4	US-09-422-978-3221	Sequence 3221, Ap	684	10	47.6	26	1	US-08-105-483-369	Sequence 369, App

685	10	47.6	26	1	US-08-709-209-369	Sequence 369, App	c 758	10	47.6	36	4	US-09-371-772B-14125	Sequence 14125, A
686	10	47.6	26	1	US-08-458-101-369	Sequence 369, App	c 759	10	47.6	36	4	US-09-371-772B-14130	Sequence 14130, A
687	10	47.6	26	1	US-08-691-563C-82	Sequence 82, Appl	c 760	10	47.6	36	4	US-09-371-772B-14146	Sequence 14146, A
688	10	47.6	26	3	US-09-540-699-9	Sequence 9, Appli	c 761	10	47.6	36	4	US-09-479-005A-541	Sequence 541, App
689	10	47.6	26	4	US-09-374-768-82	Sequence 82, Appl	c 762	10	47.6	36	4	US-09-479-005A-556	Sequence 556, App
690	10	47.6	26	4	US-08-979-847B-76	Sequence 76, Appl	c 763	10	47.6	36	4	US-09-479-005A-562	Sequence 562, App
691	10	47.6	27	1	US-08-375-116A-59	Sequence 59, Appl	c 764	10	47.6	36	4	US-09-479-005A-590	Sequence 590, App
692	10	47.6	27	2	US-08-859-998-905	Sequence 905, App	c 765	10	47.6	36	4	US-09-479-005A-604	Sequence 604, App
693	10	47.6	27	3	US-08-858-111-24	Sequence 24, Appl	c 766	10	47.6	36	4	US-09-479-005A-632	Sequence 632, App
694	10	47.6	27	3	US-09-106-194-7	Sequence 7, Appli	c 767	10	47.6	36	4	US-09-479-005A-662	Sequence 662, App
695	10	47.6	27	3	US-09-223-928-905	Sequence 905, App	c 768	10	47.6	36	4	US-09-479-005A-734	Sequence 734, App
696	10	47.6	27	4	US-09-469-636-3	Sequence 3, Appli	c 769	10	47.6	36	4	US-09-479-005A-753	Sequence 753, App
697	10	47.6	27	4	US-09-225-201B-305	Sequence 305, App	c 770	10	47.6	36	4	US-09-479-005A-794	Sequence 794, App
698	10	47.6	27	4	US-09-470-276-103	Sequence 103, App	c 771	10	47.6	36	4	US-09-479-005A-795	Sequence 795, App
699	10	47.6	27	4	US-09-660-176-2	Sequence 2, Appli	c 772	10	47.6	36	4	US-09-479-005A-797	Sequence 797, App
700	10	47.6	28	1	US-08-290-508-2	Sequence 2, Appli	c 773	10	47.6	36	4	US-09-479-005A-813	Sequence 813, App
701	10	47.6	28	2	US-08-606-144-3	Sequence 3, Appli	c 774	10	47.6	36	4	US-09-479-005A-831	Sequence 831, App
702	10	47.6	28	3	US-08-436-332B-15	Sequence 15, Appl	c 775	10	47.6	36	4	US-09-479-005A-845	Sequence 845, App
703	10	47.6	28	4	US-09-434-840-48	Sequence 48, Appl	c 776	10	47.6	36	4	US-09-479-005A-854	Sequence 854, App
704	10	47.6	28	5	PCT-US94-02174-2	Sequence 2, Appli	c 777	10	47.6	36	4	US-09-479-005A-875	Sequence 875, App
705	10	47.6	29	3	US-08-776-265-13	Sequence 13, Appl	c 778	10	47.6	36	4	US-09-479-005A-884	Sequence 884, App
706	10	47.6	29	3	US-09-225-152A-8	Sequence 8, Appli	c 779	10	47.6	36	4	US-09-479-005A-901	Sequence 901, App
707	10	47.6	29	3	US-09-254-733-40	Sequence 40, Appl	c 780	10	47.6	36	4	US-09-479-005A-909	Sequence 909, App
708	10	47.6	29	3	US-09-339-838-2	Sequence 2, Appli	c 781	10	47.6	36	4	US-09-479-005A-976	Sequence 976, App
709	10	47.6	29	4	US-09-304-232-509	Sequence 509, App	c 782	10	47.6	36	4	US-09-479-005A-998	Sequence 998, App
710	10	47.6	29	4	US-09-398-184-13	Sequence 13, Appl	c 783	10	47.6	36	4	US-09-479-005A-1004	Sequence 1004, Ap
711	10	47.6	30	2	US-08-202-044-27	Sequence 27, Appl	c 784	10	47.6	36	4	US-09-479-005A-1010	Sequence 1010, Ap
712	10	47.6	30	2	US-08-860-882A-23	Sequence 23, Appl	c 785	10	47.6	37	2	US-08-700-670A-45	Sequence 45, Appl
713	10	47.6	30	2	US-08-860-882A-24	Sequence 24, Appl	c 786	10	47.6	37	4	US-09-060-239-121	Sequence 121, App
714	10	47.6	30	3	US-08-751-344B-26	Sequence 26, Appl	c 787	10	47.6	37	4	US-09-402-923A-121	Sequence 121, App
715	10	47.6	30	3	US-09-073-297-7	Sequence 7, Appli	c 788	10	47.6	37	4	US-09-479-005A-1074	Sequence 1074, Ap
716	10	47.6	30	3	US-08-894-818B-33	Sequence 33, Appl	c 789	10	47.6	37	4	US-09-479-005A-1137	Sequence 1137, Ap
717	10	47.6	30	3	US-08-881-450A-19	Sequence 19, Appl	c 790	10	47.6	38	1	US-08-373-124A-953	Sequence 953, App
718	10	47.6	30	3	US-09-445-472-14	Sequence 14, Appl	c 791	10	47.6	38	1	US-08-707-793A-10	Sequence 10, Appl
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726	10	47.6	31	2	US-08-661-479-40	Sequence 40, Appl	c 799	10	47.6	39	1	US-08-318-947A-14	Sequence 14, Appl
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740	10	47.6	35	3	US-09-486-356-21	Sequence 21, Appl	c 813	10	47.6	42	2	US-08-305-764C-66	Sequence 66, Appl
741	10	47.6	35	4	US-09-577-528B-21	Sequence 21, Appl	c 814	10	47.6	42	2	US-08-305-764C-66	Sequence 66, Appl
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743	10	47.6	36	2	US-08-305-764C-50	Sequence 50, Appl	c 816	10	47.6	42	3	US-09-270-751-15	Sequence 15, Appl
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749	10	47.6	36	4	US-09-371-772B-13061	Sequence 13061, A	c 822	10	47.6	45	4	US-09-577-304A-167	Sequence 167, App
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756	10	47.6	36	4	US-09-371-772B-14055	Sequence 14055, A	c 829	10	47.6	47	4	US-09-641-638-1097	Sequence 1097, Ap
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833	10	47.6	47	4	US-09-422-978-1062	Sequence 1062, Ap	9.8	46.7	20	3	US-08-950-779-2	Sequence 8, Appl
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835	10	47.6	47	4	US-09-422-978-2221	Sequence 2221, Ap	9.8	46.7	20	3	US-08-950-779-9	Sequence 73, Appl
836	10	47.6	47	4	US-09-422-978-2376	Sequence 2376, Ap	9.8	46.7	20	3	US-08-950-779-9	Sequence 22, Appl
837	10	47.6	47	4	US-09-422-978-2473	Sequence 2473, Ap	9.8	46.7	20	3	US-09-249-215-84	Sequence 84, Appl
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843	10	47.6	48	3	US-09-012-097A-52	Sequence 52, Appl	9.8	46.7	20	3	US-09-280-805-255	Sequence 255, App
844	10	47.6	48	4	US-09-481-620A-70	Sequence 70, Appl	9.8	46.7	20	3	US-09-313-932-41	Sequence 41, Appl
845	10	47.6	48	4	US-09-781-804-51	Sequence 51, Appl	9.8	46.7	20	3	US-09-177-249-322	Sequence 322, App
846	10	47.6	49	4	US-09-538-709-1076	Sequence 1076, Ap	9.8	46.7	20	3	US-03-409-816-1	Sequence 1, Appl
847	10	47.6	50	1	US-08-171-389-462	Sequence 462, App	9.8	46.7	20	3	US-08-998-416-11	Sequence 11, Appl
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857	9.8	46.7	15	3	US-09-038-073-666	Sequence 666, App	9.8	46.7	20	3	US-09-115-025A-3	Sequence 3, Appl
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871	9.8	46.7	19	3	US-08-701-582D-6	Sequence 20, Appl	9.8	46.7	20	3	US-09-349-659-2	Sequence 1, Appl
872	9.8	46.7	19	3	US-09-306-446C-20	Sequence 6, Appl	9.8	46.7	20	3	US-09-352-058A-1	Sequence 1, Appl
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875	9.8	46.7	19	4	US-08-063-167A-22	Sequence 11, Appl	9.8	46.7	20	3	US-09-343-006-1	Sequence 1, Appl
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882	9.8	46.7	20	1	US-08-333-585-58	Sequence 58, Appl	9.8	46.7	20	3	US-10-318-628-8	Sequence 8, Appl
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885	9.8	46.7	20	1	US-08-339-912-4	Sequence 4, Appl	9.8	46.7	20	3	US-10-318-628-25	Sequence 25, Appl
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891	9.8	46.7	20	2	US-08-440-740A-22	Sequence 22, Appl	9.8	46.7	20	3		
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C 979 9.8 46.7 20 4 US-09-938-642-4 Sequence 4, Appli
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C 981 9.8 46.7 20 4 US-10-029-598-55 Sequence 55, Appl
C 982 9.8 46.7 20 4 US-09-835-370-41 Sequence 41, Appl
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C 984 9.8 46.7 20 5 PCT-US93-08101-22 Sequence 22, Appl
C 985 9.8 46.7 20 6 PCT-US96-08757A-6 Sequence 6, Appli
C 986 9.8 46.7 20 6 5176995-15 Patent No. 5176995
C 987 9.8 46.7 21 1 US-08-531-601-7 Sequence 7, Appli
C 988 9.8 46.7 21 1 US-08-737-597-8 Sequence 8, Appli
C 989 9.8 46.7 21 1 US-08-559-3038-13 Sequence 13, Appli
C 990 9.8 46.7 21 2 US-08-534-479-10 Sequence 10, Appli
C 991 9.8 46.7 21 2 US-08-859-032-7 Sequence 7, Appli
C 992 9.8 46.7 21 3 US-09-175-828-13 Sequence 13, Appl
C 993 9.8 46.7 21 4 US-08-948-113D-18 Sequence 18, Appl
C 994 9.8 46.7 21 4 US-09-657-472-34 Sequence 34, Appl
C 995 9.8 46.7 21 4 US-09-657-472-794 Sequence 794, App
C 996 9.8 46.7 21 4 US-09-657-472-865 Sequence 865, App
C 997 9.8 46.7 21 4 US-09-657-472-1691 Sequence 1691, Ap
C 998 9.8 46.7 21 4 US-09-546-596A-18 Sequence 18, Appl
C 999 9.8 46.7 21 4 US-09-546-596A-26 Sequence 26, Appl
C1000 9.8 46.7 21 4 US-08-117-363A-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
5521093-6/c
; Patent No. 5521093
; APPLICANT: LEMOINE, YVES; NGUYEN, MARTINE; ACHSTETTER, TILMAN
; TITLE OF INVENTION: YEAST VECTOR CODING FOR HETEROLOGOUS
; GENE FUSIONS LINKED VIA KEX2 CLEAVAGE SITE AND CODING FOR
; TRUNCATED KEX2 GENES
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,025
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 191,354
; FILING DATE: 07-FEB-1994
; APPLICATION NUMBER: 26,121
; FILING DATE: 04-MAR-1993
; APPLICATION NUMBER: 500,885
; FILING DATE: 29-MAR-1990
; SEQ ID NO: 6
; LENGTH: 40
5521093-6
Query Match 62.9%; Score 13.2; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GCATGCCAGATTACTGGC 21
DB 22 GCATGCCAATTCATCTGGC 5
RESULT 2
US-09-205-144-29/c
; Sequence 29, Application US/09205144
; Patent No. 5958771
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS
; FILE REFERENCE: RTS-0021
; CURRENT APPLICATION NUMBER: US/09/205,144
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-144-29
Query Match 61.9%; Score 13; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATGCCAGATTACT 18
DB 16 ATGCCAGATTACT 4
RESULT 3
US-09-591-279A-15/c
; Sequence 15, Application US/09591279A
; Patent No. 6770465
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for No. 6770465el Substrate
; FILE REFERENCE: 16516.117
; CURRENT APPLICATION NUMBER: US/09/591,279A
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Oligonucleotide Primer L197A Sense
US-09-591-279A-15
Query Match 61.9%; Score 13; DB 4; Length 32;
Best Local Similarity 76.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AGCGCATGCCAGATTACTGGC 21
DB 27 AACGCCCGCGGAGTACTGGC 7
RESULT 4
US-09-591-279A-16
; Sequence 16, Application US/09591279A
; Patent No. 6770465
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for No. 6770465el Substrate
; FILE REFERENCE: 16516.117
; CURRENT APPLICATION NUMBER: US/09/591,279A
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Oligonucleotide Primer L197A Antisense
US-09-591-279A-16

;
PRIOR APPLICATION DATA:

PLASTID

;; TITLE OF INVENTION: TARGETING POLYPEPTIDES, MANUFACTURE AND
;; TITLE OF INVENTION: USE THEREOF
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PENNIE & EDMONDS LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/029,341
;; FILING DATE: 27-FEB-1998
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9517674.9
;; FILING DATE: 30-AUG-1995
;; APPLICATION NUMBER: PCT/GB96/02129
;; FILING DATE: 28-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 9341-012-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)7909090
;; TELEFAX: (212)8699741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Other
US-09-029-341-5

Query Match 61.0%; Score 12.8; DB 3; Length 28;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GCGCATGCCAGATTAC 17
Db 3 GCGCATGCCAGATTCC 18

RESULT 8
US-08-229-279-17
; Sequence 17, Application US/08229279
; Patent No. 5648211
; GENERAL INFORMATION:
; APPLICANT: Fraiser, Melinda S.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Walker, George T.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM: Diskette
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,279
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-2961
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/229,279
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fugit, Donna R.
;; REGISTRATION NUMBER: 32,135
;; REFERENCE/DOCKET NUMBER: P-2961
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 49 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-229-279-17
Query Match 61.0%; Score 12.8; DB 1; Length 49;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 5 CATGCCAGATTACTGG 20
Db 22 CATGCCCGTTACTGG 37
RESULT 9
US-08-701-269-17
; Sequence 17, Application US/08701269
; Patent No. 5744311
; GENERAL INFORMATION:
; APPLICANT: Fraiser, Melinda S.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Walker, George T.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,279
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-2961
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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US-08-701-269-17
Query Match      61.0%; Score 12.8; DB 1; Length 49;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCGATTACTGG 20
Db 22 CATGCCGTTACTGG 37
|||||
|||||

RESULT 10
US-09-198-452A-3669/c
; Sequence 3669, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3669
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3669

Query Match      60.0%; Score 12.6; DB 4; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCGATTACTG 19
Db 20 AACGCTGCCAAATTACAG 2
|||||
|||||

RESULT 11
US-09-371-772B-12766/c
; Sequence 12766, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12766
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12766

Query Match      60.0%; Score 12.6; DB 4; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCGATTACTG 19
Db 20 AACGCTGCCAAATTACAG 2
|||||
|||||

US-08-701-269-17
Query Match      61.0%; Score 12.8; DB 1; Length 49;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCGATTACTGG 20
Db 22 CATGCCGTTACTGG 37
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|||||

RESULT 12
US-09-179-221D-7
; Sequence 7, Application US/09179221D
; Patent No. 6291168
; GENERAL INFORMATION:
; APPLICANT: Musso, Richard
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES DIAGNOSTIC FOR PATHOGENIC E.
; TITLE OF INVENTION: COLI 0157, METHODS OF IDENTIFICATION AND KIT THEREFOR
; FILE REFERENCE: 922.6496P
; CURRENT APPLICATION NUMBER: US/09/179,221D
; CURRENT FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: No. 6291168epad
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-179-221D-7

Query Match      59.0%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCATGCCGATTAC 17
Db 8 GCATGCCGATTAC 21
|||||
|||||

RESULT 13
US-08-721-979A-71/c
; Sequence 71, Application US/08721979A
; Patent No. 6113911
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Baussant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; STREET: Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
```

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; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "GIV"
; OTHER INFORMATION: /note= "sequence 174-187"
US-08-721-979A-71

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
Db 27 GCATGCAAGATTAC 14

RESULT 14
US-08-721-979A-72/c
; Sequence 72, Application US/08721979A
; Patent No. 6113911
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: N'Guyen, Ngoc Thien
; APPLICANT: Baussant, Thierry
; APPLICANT: Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "GIVdeltaC"
; OTHER INFORMATION: /note= "sequence 174-187"
US-08-721-979A-72

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
Db 27 GCATGCAAGATTAC 14

RESULT 15
US-08-836-501-71/c
; Sequence 71, Application US/08836501
; Patent No. 6149911
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY
; TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
; TITLE OF INVENTION: PREPARATION OF VACCINES
; NUMBER OF SEQUENCES: 78
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,501
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: FR 9413310
; FILING DATE: 07-NOV-1994
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
US-08-836-501-71

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
Db 27 GCATGCAAGATTAC 14

RESULT 16
US-08-836-501-72/c
; Sequence 72, Application US/08836501
; Patent No. 6149911
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY
; TITLE OF INVENTION: OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
; TITLE OF INVENTION: PREPARATION OF VACCINES
; NUMBER OF SEQUENCES: 78
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,501
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9413310
FILING DATE: 07-NOV-1994
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
US-08-836-501-72

Query Match 59.0%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 17
US-09-654-289-71/c
Sequence 71, Application US/09654289
Patent No. 6410030
GENERAL INFORMATION:
APPLICANT: Binz, Hans
APPLICANT: N'Guyen, Ngoc Thien
APPLICANT: Baussant, Thierry
APPLICANT: Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/654,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "GLV"
OTHER INFORMATION: /note= "sequence 174-187"
US-09-654-289-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
|||||
Db 27 GCATGCCAGATTAC 14

RESULT 18
US-09-654-289-72/c
Sequence 72, Application US/09654289
Patent No. 6410030
GENERAL INFORMATION:
APPLICANT: Binz, Hans
APPLICANT: N'Guyen, Ngoc Thien
APPLICANT: Baussant, Thierry
APPLICANT: Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/654,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "GLVdeltaC"
OTHER INFORMATION: /note= "sequence 174-187"

US-09-654-289-72

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17
DB 27 GCATGCCAGATTAC 14

RESULT 19

US-09-582-876-71/c

; Sequence 71, Application US/09582876

; Patent No. 6537556

; GENERAL INFORMATION:

; APPLICANT: Binz, Hans

; N'Guyen, Ngoc Thien

; Baussant, Thierry

; Trudel, Michel

; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

; SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL

; COMPOSITION CONTAINING IT AND PREPARATION PROCESS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gordon W. Hueschen

; STREET: 715 The "H" Bldg., 310 East Michigan

; Avenue

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/582,876

; FILING DATE: 30-Jun-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/721,979

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hueschen, Gordon W.

; REGISTRATION NUMBER: 16,157

; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616-382-0030

; TELEFAX: 616-382-2030

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..42

; OTHER INFORMATION: /product= "G1V"

; /note= "sequence 174-187"

; SEQUENCE DESCRIPTION: SEQ ID NO: 71:

; US-09-582-876-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17

DB 27 GCATGCCAGATTAC 14

RESULT 21

US-09-626-830-71/c

; Sequence 71, Application US/09626830

; Patent No. 6558673

; GENERAL INFORMATION:

Db 27 GCATGCCAGATTAC 14

RESULT 20

US-09-582-876-72/c

; Sequence 72, Application US/09582876

; Patent No. 6537556

; GENERAL INFORMATION:

; APPLICANT: Binz, Hans

; N'Guyen, Ngoc Thien

; Baussant, Thierry

; Trudel, Michel

; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

; SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL

; COMPOSITION CONTAINING IT AND PREPARATION PROCESS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gordon W. Hueschen

; STREET: 715 The "H" Bldg., 310 East Michigan

; Avenue

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/582,876

; FILING DATE: 30-Jun-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/721,979

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Hueschen, Gordon W.

; REGISTRATION NUMBER: 16,157

; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616-382-0030

; TELEFAX: 616-382-2030

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..42

; OTHER INFORMATION: /product= "GIVdeltaC"

; /note= "sequence 174-187"

; SEQUENCE DESCRIPTION: SEQ ID NO: 72:

; US-09-582-876-72

Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTAC 17

DB 27 GCATGCCAGATTAC 14

APPLICANT: ;
TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY ;
OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE ;
PREPARATION OF VACCINES ;
NUMBER OF SEQUENCES: 78 ;
COMPUTER READABLE FORM: ;
MEDIUM TYPE: Floppy disk ;
COMPUTER: IBM PC compatible ;
OPERATING SYSTEM: PC-DOS/MS-DOS ;
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) ;
CURRENT APPLICATION DATA: ;
APPLICATION NUMBER: US/09/626,830 ;
FILING DATE: 27-JULY-2000 ;
CLASSIFICATION: ;
PRIOR APPLICATION DATA: ;
APPLICATION NUMBER: 08/836,501 ;
FILING DATE: 07-NOV-1994 ;
INFORMATION FOR SEQ ID NO: 71: ;
SEQUENCE CHARACTERISTICS: ;
LENGTH: 42 base pairs ;
TYPE: nucleotide ;
STRANDEDNESS: single ;
TOPOLOGY: linear ;
MOLECULE TYPE: cDNA ;
FEATURE: ;
NAME/KEY: CDS ;
LOCATION: 1..42 ;
US-09-626-830-71 ;
Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
||||| |||||
Db 27 GCATGCCAGATTAC 14

RESULT 22
US-09-626-830-72/c
Sequence 72, Application US/09626830
Patent No. 6558673
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROCESS FOR IMPROVING THE IMMUNOGENICITY
OF AN IMMUNOGENIC COMPOUND OR A HAPTEN, AND APPLICATION TO THE
PREPARATION OF VACCINES
NUMBER OF SEQUENCES: 78
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,830
FILING DATE: 27-JULY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,501
FILING DATE: 07-NOV-1994
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
US-09-626-830-72
Query Match 59.0%; Score 12.4; DB 4; Length 42;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
||||| |||||
Db 27 GCATGCCAGATTAC 14

RESULT 23
US-10-091-257-71/c
Sequence 71, Application US/10091257
Patent No. 6616930
GENERAL INFORMATION:
APPLICANT: Binz, Hans
N'Guyen, Ngoc Thien
Bausant, Thierry
Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
(EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/091,257
FILING DATE: 05-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/721,979A
FILING DATE: October 4, 1996
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PFS7PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..42
OTHER INFORMATION: /product= "G1V"
/note= "sequence 174-187"
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-091-257-71

Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GCATGCCAGATTAC 17
||||| |||||
Db 27 GCATGCCAGATTAC 14

RESULT 24
US-10-091-257-72/c
; Sequence 72, Application US/10091257
; Patent No. 6616930
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; N'Guyen, Ngoc Thien
; Baussant, Thierry
; Trudel, Michel
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
; SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
; COMPOSITION CONTAINING IT AND PREPARATION PROCESS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/091,257
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,979A
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: FR 94 04009
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..42
; OTHER INFORMATION: /product= "G1VdeltaC"
; /note= "sequence 174-187"
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-091-257-72
Query Match 59.0%; Score 12.4; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GCATGCCAGATTAC 17
Db 27 GCATGCCAGATTAC 14
RESULT 25
PCT-US93-09070-5
; Sequence 5, Application PC/TUS9309070
; GENERAL INFORMATION:
; APPLICANT: Lee, William T.L.
; Serbin, John J.
; Jolly, Douglas J.
; Barber, Jack R.
; Chada, Sunil
; Chang, Stephen M.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TREATING
; FELINE LEUKEMIA VIRUS AND FELINE
; IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09070
; FILING DATE: N/A
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.415PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; PCT-US93-09070-5
Query Match 59.0%; Score 12.4; DB 5; Length 45;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCGCATGCCAGATT 15
Db 7 GCGCATGCCAGATT 20
RESULT 26
US-08-328-710A-15/c
; Sequence 15, Application US/08328710A
; Patent No. 5795717
; GENERAL INFORMATION:
; APPLICANT: Nakayama, Tomoko
; Tada, Jun
; APPLICANT: Fukushima, Shigeru
; Ohashi, Tetsuo
; TITLE OF INVENTION: Oligonucleotides for detecting bacteria and detection
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: PO Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,710A
; FILING DATE: 25-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; US-08-328-710A-15

Query Match      58.1%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGG 20
Db      17 GAATGTCAGATACTGG 1

RESULT 27
US-08-968-046-15/c
; Sequence 15, Application US/08968046
; Patent No. 6218110
; GENERAL INFORMATION:
; APPLICANT: Nakayama, Tomoko
; APPLICANT: Tada, Jun
; APPLICANT: Fukushima, Shigeru
; APPLICANT: Ohashi, Tetsuo
; TITLE OF INVENTION: Oligonucleotides for detecting bacteria
; TITLE OF INVENTION: and detection process
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: PO Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,046
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/328,710
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S
; REGISTRATION NUMBER: 32,181
```

```
;
; REFERENCE/DOCKET NUMBER: 1422-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; US-08-968-046-15

Query Match      58.1%; Score 12.2; DB 3; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GCATGCCAGATTACTGG 20
Db      17 GAATGTCAGATACTGG 1

RESULT 28
US-07-915-922-9
; Sequence 9, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,922
; FILING DATE: 19920717
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 522-1285
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-915-922-9

Query Match      58.1%; Score 12.2; DB 1; Length 30;
Best Local Similarity 82.4%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTAC 17
          ||| ||| ||| ||| ||| ||| |||
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Query Match
Score 12.2; DB 4; Length 27;
58.1%

Query Match 57.1%; Score 12; DB 4; Length 30;

Query Match 57.1%: Score 12:

Wed Nov 24 08:46:01 2004

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; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,511
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervis, Herbert H.
; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: SBC P50349-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; US-08-776-511-6

Query Match 57.1%; Score 12; DB 3; Length 38;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 9 AGAGCAAGCCACATAGCTGG 28

RESULT 37
US-09-485-737B-29/c
; Sequence 29, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
; US-09-485-737B-29

Query Match 57.1%; Score 12; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 9 AGAGCAAGCCACATAGCTGG 28

RESULT 38
US-09-485-737B-30
; Sequence 30, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
; US-09-485-737B-30

Query Match 57.1%; Score 12; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGG 20
Db 21 ACCGCTGCCAGATTGCTGG 40

RESULT 39
US-09-527-154-13/c
; Sequence 13, Application US/09527154
; Patent No. 6228648
; GENERAL INFORMATION:
; APPLICANT: Thomas P. Condon
; APPLICANT: Shin Cheng Fluoroy
; TITLE OF INVENTION: ANTISENSE MODULATION OF ADAM10 EXPRESSION
; FILE REFERENCE: ISPH-0446
; CURRENT APPLICATION NUMBER: US/09/527,154
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-527-154-13

Query Match 56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 86.7%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACTGG 20
Db 20 ATACCAGATGACTGG 6

RESULT 40
US-08-553-501A-38/c
; Sequence 38, Application US/08553501A
; Patent No. 5856135
```

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAROK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-553-501A-38

Query Match 56.2%; Score 11.8; DB 2; Length 39;
Best Local Similarity 86.7%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACTG 19
||| |
Db 24 CATGCTAAATTACTG 10

Search completed: November 23, 2004, 22:25:58
Job time : 36.3034 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 98.4719 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgtgcccagattactggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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SUMMARIES

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2	21	100.0	21	15	US-10-419-022-1
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4	13.2	62.9	22	18	US-10-813-805-42
5	13.2	62.9	32	17	US-10-250-997-24
6	13.2	62.9	32	17	US-10-250-997-25
7	13.2	62.9	32	17	US-10-250-997-39
8	13.2	62.9	35	17	US-10-641-455A-117
9	13	61.9	18	14	US-10-197-290-29
10	13	61.9	18	15	US-10-388-263-182
11	13	61.9	20	17	US-10-317-278-17
12	13	61.9	20	17	US-10-317-278-51

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c 14	61.9	32	18	US-10-851-894-16	Sequence 16, Appl
c 15	61.9	37	10	US-09-930-423-2899	Sequence 2899, Ap
c 16	61.9	37	10	US-09-745-237A-2899	Sequence 2899, Ap
c 17	61.0	24	9	US-09-780-752-20	Sequence 20, Appl
c 18	61.0	24	10	US-09-940-185-787	Sequence 787, App
c 19	61.0	24	15	US-10-320-231A-8	Sequence 8, Appli
c 20	61.0	25	10	US-09-940-185-4752	Sequence 4752, Ap
c 21	60.0	20	16	US-10-289-762-3669	Sequence 3669, Ap
c 22	60.0	25	10	US-09-754-853A-418	Sequence 418, App
c 23	60.0	36	16	US-10-138-674-15043	Sequence 15043, A
c 24	60.0	36	17	US-10-287-949A-15043	Sequence 15043, A
c 25	59.0	20	16	US-10-318-970-29	Sequence 29, Appl
c 26	59.0	25	15	US-10-098-263B-96896	Sequence 96896, A
c 27	59.0	25	15	US-10-098-263B-105617	Sequence 105617,
c 28	59.0	42	14	US-10-091-257-71	Sequence 71, Appl
c 29	59.0	42	14	US-10-091-257-72	Sequence 72, Appl
c 30	59.0	49	16	US-10-035-833A-2502	Sequence 2502, Ap
c 31	59.0	49	16	US-10-035-833A-4898	Sequence 4898, Ap
c 32	58.1	19	14	US-10-138-381-15	Sequence 15, Appl
c 33	58.1	19	15	US-10-084-839-3754	Sequence 3754, Ap
c 34	58.1	22	15	US-10-085-239A-14	Sequence 14, Appl
c 35	58.1	25	10	US-09-754-853A-786	Sequence 786, App
c 36	58.1	25	15	US-10-098-263B-115941	Sequence 115941,
c 37	58.1	25	15	US-10-098-263B-119516	Sequence 119516,
c 38	58.1	25	15	US-10-084-839-3753	Sequence 3753, Ap
c 39	58.1	26	15	US-10-072-622-26	Sequence 26, Appl
c 40	58.1	27	15	US-10-072-622-25	Sequence 25, Appl
c 41	58.1	32	17	US-10-250-997-31	Sequence 31, Appl
c 42	58.1	32	17	US-10-250-997-45	Sequence 45, Appl
c 43	58.1	41	16	US-10-035-833A-1679	Sequence 1679, Ap
c 44	58.1	41	16	US-10-035-833A-7227	Sequence 7227, Ap
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c 46	58.1	44	15	US-10-170-097-1195	Sequence 1195, Ap
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c 48	57.1	20	15	US-10-113-824-20	Sequence 20, Appl
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c 50	57.1	25	14	US-10-060-756A-3205	Sequence 3205, Ap
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c 52	57.1	25	14	US-10-060-756A-3207	Sequence 3207, Ap
c 53	57.1	25	14	US-10-060-756A-3208	Sequence 3208, Ap
c 54	57.1	25	14	US-10-060-756A-3209	Sequence 3209, Ap
c 55	57.1	25	15	US-10-098-263B-26684	Sequence 26684, A
c 56	57.1	29	15	US-10-336-638-325	Sequence 325, App
c 57	57.1	30	17	US-09-927-046-3574	Sequence 132, App
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c 63	57.1	37	16	US-10-342-902-4096	Sequence 4096, Ap
c 64	57.1	37	16	US-10-342-902-4135	Sequence 4135, Ap
c 65	57.1	37	17	US-10-669-841-8987	Sequence 8987, Ap
c 66	57.1	37	17	US-10-669-841-9026	Sequence 9026, Ap
c 67	57.1	40	14	US-10-071-485-30	Sequence 30, Appl
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c 73	56.2	25	15	US-10-098-263B-81468	Sequence 81468, A
c 74	56.2	25	15	US-10-098-263B-103084	Sequence 103084,
c 75	56.2	25	15	US-10-098-263B-126931	Sequence 126931,
c 76	56.2	35	16	US-10-321-039-598	Sequence 598, App
c 77	56.2	47	16	US-10-349-143-275	Sequence 275, App
c 78	55.2	20	16	US-10-289-762-2720	Sequence 2720, Ap
c 79	55.2	25	14	US-10-060-756A-3210	Sequence 3210, Ap
c 80	55.2	25	14	US-10-060-756A-3211	Sequence 3211, Ap
c 81	55.2	25	15	US-10-098-263B-93920	Sequence 93920, A
c 82	55.2	25	17	US-10-469-552-12	Sequence 12, Appl
c 83	55.2	31	15	US-10-401-343-32	Sequence 32, Appl
c 84	55.2	31	16	US-10-057-475B-10978	Sequence 10978, A
c 85	55.2	31	16	US-10-154-884B-10978	Sequence 10978, A

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c 87	11.6	55.2	36	17	US-10-287-949A-15258	Sequence 15258, A	c 161	11.4	54.3	48	15	US-10-234-671-97	Sequence 97, Appl
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c 89	11.6	55.2	37	16	US-09-877-478-4087	Sequence 4087, Ap	c 162	11.4	54.3	50	15	US-10-341-967-68	Sequence 68, Appl
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c 91	11.6	55.2	37	17	US-10-665-841-8978	Sequence 8978, Ap	c 163	11.2	53.3	18	9	US-09-969-373-3139	Sequence 3139, Ap
c 92	11.6	55.2	45	10	US-09-997-623-24	Sequence 24, Appl	c 165	11.2	53.3	19	9	US-09-909-544-5	Sequence 5, Appl
c 93	11.6	55.2	45	10	US-09-978-917A-24	Sequence 611, App	c 166	11.2	53.3	19	14	US-10-155-785-5	Sequence 5, Appl
c 94	11.6	55.2	46	9	US-09-759-143-611	Sequence 611, App	c 167	11.2	53.3	19	15	US-10-005-956-80	Sequence 80, Appl
c 95	11.6	55.2	46	9	US-09-759-143-615	Sequence 615, App	c 168	11.2	53.3	19	15	US-10-311-907-383	Sequence 383, App
c 96	11.6	55.2	46	9	US-09-780-669-611	Sequence 611, App	c 169	11.2	53.3	20	17	US-10-303-165-20	Sequence 20, Appl
c 97	11.6	55.2	46	9	US-09-780-669-615	Sequence 615, App	c 170	11.2	53.3	20	17	US-10-303-165-97	Sequence 97, Appl
c 98	11.6	55.2	46	9	US-09-822-827-611	Sequence 611, App	c 171	11.2	53.3	20	17	US-10-619-739-45	Sequence 45, Appl
c 99	11.6	55.2	46	9	US-09-822-827-615	Sequence 611, App	c 172	11.2	53.3	21	17	US-10-257-344A-8	Sequence 8, Appl
c 100	11.6	55.2	46	9	US-09-895-793-611	Sequence 611, App	c 173	11.2	53.3	23	9	US-09-753-143-48	Sequence 48, Appl
c 101	11.6	55.2	46	9	US-09-895-793-615	Sequence 615, App	c 174	11.2	53.3	23	15	US-10-401-194-72	Sequence 72, Appl
c 102	11.6	55.2	46	9	US-09-895-814-611	Sequence 611, App	c 175	11.2	53.3	24	10	US-09-940-185-349	Sequence 349, App
c 103	11.6	55.2	46	9	US-09-895-814-615	Sequence 615, App	c 176	11.2	53.3	24	10	US-09-940-185-1528	Sequence 1528, Ap
c 104	11.6	55.2	46	13	US-10-012-896-611	Sequence 611, App	c 177	11.2	53.3	25	10	US-09-940-185-4325	Sequence 4325, Ap
c 105	11.6	55.2	46	13	US-10-012-896-615	Sequence 615, App	c 178	11.2	53.3	25	14	US-10-215-112-4318	Sequence 4318, Ap
c 106	11.6	55.2	46	15	US-10-144-678A-611	Sequence 611, App	c 179	11.2	53.3	25	15	US-10-098-263B-5933	Sequence 5933, Ap
c 107	11.6	55.2	46	15	US-10-144-678A-615	Sequence 615, App	c 180	11.2	53.3	25	15	US-10-098-263B-43709	Sequence 43709, A
c 108	11.6	55.2	46	15	US-10-294-025-611	Sequence 611, App	c 181	11.2	53.3	25	15	US-10-098-263B-43710	Sequence 43710, A
c 109	11.6	55.2	46	15	US-10-294-025-615	Sequence 615, App	c 182	11.2	53.3	25	15	US-10-098-263B-60528	Sequence 60528, A
c 110	11.6	55.2	47	15	US-10-170-037-962	Sequence 962, App	c 183	11.2	53.3	25	15	US-10-098-263B-76272	Sequence 76272, A
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c 114	11.6	55.2	50	16	US-10-131-827-6878	Sequence 6878, Ap	c 187	11.2	53.3	31	9	US-09-801-274-1627	Sequence 1627, Ap
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c 118	11.4	54.3	20	17	US-10-317-278-68	Sequence 68, Appl	c 191	11.2	53.3	34	9	US-09-769-864-49	Sequence 49, Appl
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c 121	11.4	54.3	22	10	US-09-974-149-25	Sequence 25, Appl	c 194	11.2	53.3	36	14	US-10-105-963-18	Sequence 18, Appl
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c 123	11.4	54.3	23	9	US-09-805-761-45	Sequence 45, Appl	c 196	11.2	53.3	36	16	US-10-105-616-14	Sequence 14, Appl
c 124	11.4	54.3	24	10	US-09-940-185-1118	Sequence 1118, Ap	c 197	11.2	53.3	36	16	US-10-138-674-15121	Sequence 15121, A
c 125	11.4	54.3	25	15	US-10-098-263B-19925	Sequence 19925, A	c 198	11.2	53.3	36	17	US-10-287-949A-15121	Sequence 15121, A
c 126	11.4	54.3	25	15	US-10-098-263B-20561	Sequence 20561, A	c 199	11.2	53.3	40	15	US-10-407-352-10	Sequence 10, Appl
c 127	11.4	54.3	26	14	US-10-287-919-541	Sequence 541, App	c 200	11.2	53.3	41	11	US-09-760-897-15	Sequence 15, Appl
c 128	11.4	54.3	33	10	US-09-798-689-31	Sequence 31, Appl	c 201	11.2	53.3	41	15	US-10-005-956-269	Sequence 269, App
c 129	11.4	54.3	33	10	US-09-996-954B-7	Sequence 7, Appl	c 202	11.2	53.3	41	15	US-10-331-329-15	Sequence 15, Appl
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c 131	11.4	54.3	35	16	US-10-422-366-25	Sequence 25, Appl	c 204	11.2	53.3	45	17	US-10-131-827-1143	Sequence 1143, Ap
c 132	11.4	54.3	37	10	US-09-730-289B-2740	Sequence 2740, Ap	c 205	11.2	53.3	50	16	US-10-131-827-4218	Sequence 4218, Ap
c 133	11.4	54.3	37	10	US-09-877-478-4093	Sequence 4093, Ap	c 206	11.2	53.3	50	16	US-10-131-827-5777	Sequence 5777, Ap
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c 138	11.4	54.3	37	10	US-09-930-423-2909	Sequence 2909, Ap	c 211	11	52.4	17	10	US-09-825-805-419	Sequence 419, App
c 139	11.4	54.3	37	10	US-09-745-237A-2777	Sequence 2777, Ap	c 212	11	52.4	17	10	US-09-818-875-427	Sequence 427, App
c 140	11.4	54.3	37	10	US-09-745-237A-2840	Sequence 2840, Ap	c 213	11	52.4	17	10	US-09-818-875-428	Sequence 428, App
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c 156	11.4	54.3	41	15	US-10-224-683-51	Sequence 51, Appl	c 229	11	52.4	21	18	US-10-444-853A-235	Sequence 235, App
c 157	11.4	54.3	46	9	US-09-419-305-14	Sequence 14, Appl	c 230	11	52.4	21	18	US-10-444-853A-236	Sequence 236, App
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C 445	11	52.4	50	10	US-09-999-834A-344	Sequence 344, Appl	517	11	52.4	50	16		
C 446	11	52.4	50	10	US-09-978-423A-344	Sequence 344, Appl	518	11	52.4	50	16		
C 447	11	52.4	50	10	US-09-978-193A-344	Sequence 344, Appl	519	11	52.4	50	16		
C 448	11	52.4	50	10	US-09-999-830A-344	Sequence 344, Appl	520	11	52.4	50	16		
C 449	11	52.4	50	10	US-09-978-757A-344	Sequence 344, Appl	521	11	52.4	50	16		
C 450	11	52.4	50	10	US-09-978-187B-344	Sequence 344, Appl	522	11	52.4	50	16		
							523	10.8	51.4	17	15		

c 524	10.8	51.4	20	14	US-10-005-338B-136	Sequence 136, App	597	10.6	50.5	17	17	US-10-287-949A-7740	Sequence 7740, App
c 525	10.8	51.4	20	14	US-10-005-338B-138	Sequence 138, App	598	10.6	50.5	17	18	US-10-712-633-823	Sequence 823, App
c 526	10.8	51.4	20	14	US-10-032-585-4860	Sequence 4860, App	599	10.6	50.5	17	18	US-10-712-633-4238	Sequence 4238, App
c 527	10.8	51.4	20	15	US-10-159-266-74	Sequence 147, Appl	600	10.6	50.5	18	9	US-09-969-373-2799	Sequence 2799, App
c 528	10.8	51.4	20	15	US-10-159-266-147	Sequence 147, App	601	10.6	50.5	18	17	US-10-182-952A-9	Sequence 9, Appli
c 529	10.8	51.4	20	16	US-10-199-674-41	Sequence 41, Appl	c 602	10.6	50.5	19	16	US-10-280-183A-414	Sequence 414, App
c 530	10.8	51.4	20	16	US-10-199-674-100	Sequence 100, App	603	10.6	50.5	19	17	US-10-665-951-2244	Sequence 2244, App
c 531	10.8	51.4	20	16	US-10-292-337-14	Sequence 14, Appl	604	10.6	50.5	19	17	US-10-665-951-2264	Sequence 2264, App
c 532	10.8	51.4	20	16	US-10-292-337-85	Sequence 85, Appl	605	10.6	50.5	19	17	US-10-665-951-2265	Sequence 2265, App
c 533	10.8	51.4	20	17	US-10-317-500-98	Sequence 98, Appl	c 606	10.6	50.5	20	9	US-09-454-394-70	Sequence 70, Appl
c 534	10.8	51.4	20	17	US-10-619-739-2008	Sequence 2008, App	607	10.6	50.5	20	9	US-09-454-394-71	Sequence 71, Appl
c 535	10.8	51.4	20	18	US-10-741-789A-65	Sequence 65, Appl	608	10.6	50.5	20	9	US-09-969-373-3127	Sequence 3127, App
c 536	10.8	51.4	21	15	US-10-002-623-518	Sequence 518, App	c 609	10.6	50.5	20	9	US-09-969-373-3128	Sequence 3128, App
c 537	10.8	51.4	21	15	US-10-184-085A-43	Sequence 43, Appl	610	10.6	50.5	20	10	US-09-770-107-20	Sequence 20, Appl
c 538	10.8	51.4	21	15	US-10-184-085A-635	Sequence 635, App	611	10.6	50.5	20	10	US-09-846-863-70	Sequence 70, Appl
c 539	10.8	51.4	23	10	US-09-945-943-1	Sequence 1, Appli	612	10.6	50.5	20	10	US-09-846-863-71	Sequence 71, Appl
c 540	10.8	51.4	24	13	US-10-027-632-52767	Sequence 52767, A	613	10.6	50.5	20	15	US-10-181-856-69	Sequence 69, Appl
c 541	10.8	51.4	24	15	US-10-027-632-52767	Sequence 52767, A	614	10.6	50.5	20	15	US-10-370-143-18	Sequence 18, Appl
c 542	10.8	51.4	25	10	US-09-754-835A-748	Sequence 748, App	c 615	10.6	50.5	20	16	US-10-452-510-116	Sequence 116, App
c 543	10.8	51.4	25	14	US-10-215-112-2106	Sequence 2106, App	c 616	10.6	50.5	20	16	US-10-617-334-116	Sequence 116, App
c 544	10.8	51.4	25	15	US-10-098-263B-47551	Sequence 47551, A	617	10.6	50.5	20	16	US-10-298-953-25	Sequence 25, Appl
c 545	10.8	51.4	25	15	US-10-098-263B-65678	Sequence 65678, A	c 618	10.6	50.5	20	16	US-10-298-953-59	Sequence 59, Appl
c 546	10.8	51.4	25	15	US-10-098-263B-81467	Sequence 81467, A	c 619	10.6	50.5	20	17	US-10-360-854-7	Sequence 7, Appli
c 547	10.8	51.4	25	15	US-10-098-263B-85311	Sequence 85311, A	c 620	10.6	50.5	20	17	US-10-744-465-116	Sequence 116, App
c 548	10.8	51.4	25	15	US-10-098-263B-85312	Sequence 85312, A	c 621	10.6	50.5	20	17	US-10-833-679-116	Sequence 116, App
c 549	10.8	51.4	25	15	US-10-098-263B-96895	Sequence 96895, A	c 622	10.6	50.5	20	18	US-10-659-473-72	Sequence 72, Appl
c 550	10.8	51.4	25	15	US-10-098-263B-105618	Sequence 105618, A	623	10.6	50.5	21	8	US-08-987-689A-11	Sequence 11, Appl
c 551	10.8	51.4	25	15	US-10-098-263B-112284	Sequence 112284, A	624	10.6	50.5	21	8	US-08-987-689A-23	Sequence 23, Appl
c 552	10.8	51.4	25	15	US-10-168-771-7	Sequence 7, Appli	625	10.6	50.5	21	15	US-10-292-524-11	Sequence 11, Appl
c 553	10.8	51.4	25	16	US-10-188-186-290	Sequence 290, App	626	10.6	50.5	21	15	US-10-292-524-23	Sequence 23, Appl
c 554	10.8	51.4	25	17	US-10-775-169-827	Sequence 827, App	c 627	10.6	50.5	21	15	US-10-072-622-23	Sequence 23, Appl
c 555	10.8	51.4	25	17	US-10-775-169-3758	Sequence 3758, App	628	10.6	50.5	21	15	US-10-072-622-24	Sequence 24, Appl
c 556	10.8	51.4	26	9	US-09-893-238-74	Sequence 74, Appl	629	10.6	50.5	21	15	US-10-214-670-27	Sequence 27, Appl
c 557	10.8	51.4	26	9	US-10-161-493-271	Sequence 271, App	630	10.6	50.5	21	16	US-10-464-805-11	Sequence 11, Appl
c 558	10.8	51.4	28	9	US-09-971-309-90	Sequence 90, Appl	631	10.6	50.5	21	16	US-10-464-805-23	Sequence 23, Appl
c 559	10.8	51.4	28	15	US-10-435-633-9	Sequence 9, Appli	632	10.6	50.5	21	16	US-10-420-194-427	Sequence 427, App
c 560	10.8	51.4	28	15	US-10-434-837-8	Sequence 8, Appli	633	10.6	50.5	21	16	US-10-420-194-430	Sequence 430, App
c 561	10.8	51.4	28	16	US-10-188-186-308	Sequence 308, App	c 634	10.6	50.5	21	16	US-10-420-194-937	Sequence 937, App
c 562	10.8	51.4	29	10	US-09-374-046A-228	Sequence 228, App	c 635	10.6	50.5	21	16	US-10-420-194-940	Sequence 940, App
c 563	10.8	51.4	29	16	US-10-616-263-228	Sequence 228, App	c 636	10.6	50.5	21	17	US-10-665-951-2275	Sequence 2275, App
c 564	10.8	51.4	30	17	US-10-644-355A-102	Sequence 102, App	c 637	10.6	50.5	21	17	US-10-665-951-2278	Sequence 2278, App
c 565	10.8	51.4	31	9	US-09-746-284-51	Sequence 51, Appl	c 638	10.6	50.5	21	17	US-10-665-951-2373	Sequence 2373, App
c 566	10.8	51.4	32	10	US-09-851-486-129	Sequence 129, App	639	10.6	50.5	21	17	US-10-665-951-2385	Sequence 2385, App
c 567	10.8	51.4	32	15	US-10-339-674-1210	Sequence 1210, App	c 640	10.6	50.5	21	17	US-10-665-951-2386	Sequence 2386, App
c 568	10.8	51.4	33	10	US-09-826-509-112	Sequence 112, App	c 641	10.6	50.5	21	17	US-10-665-951-2386	Sequence 2386, App
c 569	10.8	51.4	35	9	US-09-766-095-38	Sequence 38, Appl	642	10.6	50.5	21	17	US-10-728-491-17	Sequence 17, Appl
c 570	10.8	51.4	35	9	US-09-766-095-118	Sequence 118, App	c 643	10.6	50.5	21	18	US-10-786-720-1231	Sequence 1231, App
c 571	10.8	51.4	36	14	US-09-897-778-444	Sequence 444, App	c 644	10.6	50.5	21	18	US-10-786-720-1232	Sequence 1232, App
c 572	10.8	51.4	36	14	US-10-007-700-444	Sequence 444, App	645	10.6	50.5	21	18	US-10-786-720-1233	Sequence 1233, App
c 573	10.8	51.4	36	15	US-10-117-982-444	Sequence 444, App	646	10.6	50.5	21	18	US-10-786-720-13186	Sequence 13186, A
c 574	10.8	51.4	36	15	US-10-313-986-444	Sequence 444, App	c 647	10.6	50.5	21	18	US-10-786-720-13188	Sequence 13188, A
c 575	10.8	51.4	38	9	US-09-823-829-62	Sequence 62, Appl	c 648	10.6	50.5	21	18	US-10-786-720-13300	Sequence 13300, A
c 576	10.8	51.4	38	9	US-09-823-823-62	Sequence 62, Appl	c 649	10.6	50.5	21	18	US-10-786-720-13302	Sequence 13302, A
c 577	10.8	51.4	38	10	US-09-839-575-42	Sequence 42, Appl	c 650	10.6	50.5	22	16	US-10-114-270-369	Sequence 369, App
c 578	10.8	51.4	38	11	US-10-164-433-8	Sequence 8, Appli	c 651	10.6	50.5	22	16	US-10-262-511-420	Sequence 420, App
c 579	10.8	51.4	39	11	US-09-923-917-6	Sequence 6, Appli	c 652	10.6	50.5	22	16	US-10-287-226-459	Sequence 459, App
c 580	10.8	51.4	41	9	US-09-892-864A-6	Sequence 6, Appli	653	10.6	50.5	23	16	US-10-420-194-1046	Sequence 1046, App
c 581	10.8	51.4	41	9	US-09-996-561-7	Sequence 7, Appli	654	10.6	50.5	23	16	US-10-420-194-1049	Sequence 1049, App
c 582	10.8	51.4	41	9	US-09-884-948-7	Sequence 7, Appli	c 655	10.6	50.5	23	16	US-10-420-194-1155	Sequence 1155, App
c 583	10.8	51.4	41	14	US-10-092-750-149	Sequence 149, App	c 656	10.6	50.5	23	16	US-10-420-194-1158	Sequence 1158, App
c 584	10.8	51.4	41	16	US-10-035-833A-1534	Sequence 1534, App	c 657	10.6	50.5	24	10	US-09-940-185-375	Sequence 375, App
c 585	10.8	51.4	41	16	US-10-035-833A-4031	Sequence 4031, App	c 658	10.6	50.5	24	16	US-10-401-077-3	Sequence 3, Appli
c 586	10.8	51.4	42	11	US-09-923-917-7	Sequence 7, Appli	c 659	10.6	50.5	25	9	US-09-893-238-26	Sequence 26, Appli
c 587	10.8	51.4	42	15	US-10-040-206A-4	Sequence 4, Appli	660	10.6	50.5	25	10	US-09-754-853A-410	Sequence 410, App
c 588	10.8	51.4	42	15	US-10-243-509-4	Sequence 4, Appli	c 661	10.6	50.5	25	10	US-09-940-185-4350	Sequence 4350, App
c 589	10.8	51.4	47	16	US-10-349-143-323	Sequence 323, App	c 662	10.6	50.5	25	14	US-10-060-756A-3212	Sequence 3212, App
c 590	10.8	51.4	47	16	US-10-349-143-2538	Sequence 2538, App	c 663	10.6	50.5	25	15	US-10-098-263B-34248	Sequence 34248, A
c 591	10.8	51.4	47	16	US-10-349-143-3718	Sequence 3718, App	664	10.6	50.5	25	15	US-10-098-263B-51667	Sequence 51667, A
c 592	10.8	51.4	50	16	US-10-131-827-1182	Sequence 1182, App	665	10.6	50.5	25	15	US-10-098-263B-77507	Sequence 77507, A
c 593	10.8	51.4	50	16	US-10-131-827-3481	Sequence 3481, App	c 666	10.6	50.5	25	15	US-10-098-263B-115942	Sequence 115942, A
c 594	10.6	50.5	17	14	US-10-060-756A-1206	Sequence 1206, App	c 667	10.6	50.5	25	15	US-10-098-263B-119515	Sequence 119515, A
c 595	10.6	50.5	17	14	US-10-060-756A-1207	Sequence 1207, App	c 668	10.6	50.5	25	15	US-10-098-263B-130624	Sequence 130624, A
c 596	10.6	50.5	17	16	US-10-138-674A-7740	Sequence 7740, App	c 669	10.6	50.5	25	17	US-10-717-597-762	Sequence 762, App

C 816	10.4	49.5	20	16	US-10-617-334-147	Sequence 147, App	C 889	10.4	49.5	30	10	US-09-854-867-595	Sequence 595, App
C 817	10.4	49.5	20	16	US-10-371-701-46	Sequence 46, App1	C 890	10.4	49.5	30	15	US-10-215-062-20	Sequence 20, App1
C 818	10.4	49.5	20	17	US-10-317-280-75	Sequence 75, App1	C 891	10.4	49.5	30	15	US-10-310-734-58	Sequence 58, App1
C 819	10.4	49.5	20	17	US-10-317-280-147	Sequence 147, App	C 892	10.4	49.5	30	16	US-10-471-171-1	Sequence 1, Appli
C 820	10.4	49.5	20	17	US-10-317-278-35	Sequence 35, App1	C 893	10.4	49.5	30	17	US-10-416-621-49	Sequence 49, Appli
C 821	10.4	49.5	20	17	US-10-317-278-65	Sequence 65, App1	C 894	10.4	49.5	31	9	US-09-801-274-373	Sequence 373, App
C 822	10.4	49.5	20	17	US-10-728-491-4	Sequence 4, Appli1	C 895	10.4	49.5	31	9	US-09-801-274-1125	Sequence 1125, Ap
C 823	10.4	49.5	20	17	US-10-744-465-147	Sequence 147, App	C 896	10.4	49.5	31	9	US-09-801-274-1299	Sequence 1299, Ap
C 824	10.4	49.5	20	17	US-10-833-679-147	Sequence 147, App	C 897	10.4	49.5	31	10	US-09-912-263-297	Sequence 297, App
C 825	10.4	49.5	21	9	US-09-975-408-3	Sequence 3, Appli	C 898	10.4	49.5	31	15	US-10-163-552-1466	Sequence 1466, Ap
C 826	10.4	49.5	21	10	US-09-952-267-66	Sequence 66, App1	C 899	10.4	49.5	31	16	US-10-395-741B-67	Sequence 67, Appli
C 827	10.4	49.5	21	10	US-09-936-008B-18	Sequence 18, App1	C 900	10.4	49.5	31	18	US-10-807-837-24	Sequence 24, Appli
C 828	10.4	49.5	21	13	US-10-075-579-3	Sequence 3, App1	C 901	10.4	49.5	32	14	US-10-221-841-3	Sequence 3, Appli
C 829	10.4	49.5	21	16	US-10-349-143-11666	Sequence 11666, A	C 902	10.4	49.5	32	17	US-10-220-481-175	Sequence 175, App
C 830	10.4	49.5	21	16	US-10-287-971-291	Sequence 291, App	C 903	10.4	49.5	32	17	US-10-220-481-404	Sequence 404, App
C 831	10.4	49.5	22	9	US-09-798-584-11	Sequence 11, App1	C 904	10.4	49.5	33	17	US-10-467-479-5	Sequence 5, Appli
C 832	10.4	49.5	22	15	US-10-209-372-21	Sequence 21, App1	C 905	10.4	49.5	33	14	US-10-121-857-75	Sequence 75, Appli
C 833	10.4	49.5	22	15	US-10-005-041A-172	Sequence 172, App	C 906	10.4	49.5	33	15	US-10-208-018-75	Sequence 75, Appli
C 834	10.4	49.5	22	15	US-10-024-212-233	Sequence 233, App	C 907	10.4	49.5	33	15	US-10-336-566-76	Sequence 76, Appli
C 835	10.4	49.5	22	17	US-10-333-068-142	Sequence 142, App	C 908	10.4	49.5	33	15	US-10-336-566-77	Sequence 77, Appli
C 836	10.4	49.5	23	9	US-09-784-423-47	Sequence 47, App1	C 909	10.4	49.5	33	15	US-10-363-427-25	Sequence 25, Appli
C 837	10.4	49.5	23	17	US-10-465-498-124	Sequence 124, App	C 910	10.4	49.5	33	17	US-10-338-552-14	Sequence 14, App1
C 838	10.4	49.5	24	9	US-09-815-585-21	Sequence 21, App1	C 911	10.4	49.5	33	17	US-10-338-627-14	Sequence 14, App1
C 839	10.4	49.5	24	10	US-09-940-185-221	Sequence 221, App	C 912	10.4	49.5	33	17	US-10-772-227-81	Sequence 81, Appli
C 840	10.4	49.5	24	10	US-09-940-185-507	Sequence 507, App	C 913	10.4	49.5	34	9	US-09-978-758-14	Sequence 14, Appli
C 841	10.4	49.5	24	10	US-09-940-185-2507	Sequence 2507, Ap	C 914	10.4	49.5	34	16	US-10-001-052-50	Sequence 50, Appli
C 842	10.4	49.5	24	10	US-09-841-994-39	Sequence 39, App1	C 915	10.4	49.5	34	17	US-10-766-421-14	Sequence 14, Appli
C 843	10.4	49.5	24	15	US-10-322-138-68	Sequence 68, App1	C 916	10.4	49.5	35	16	US-10-420-194-648	Sequence 648, App
C 844	10.4	49.5	24	15	US-10-317-832-154	Sequence 154, App	C 917	10.4	49.5	35	17	US-10-751-928-12	Sequence 12, Appli
C 845	10.4	49.5	24	16	US-10-336-603A-117	Sequence 117, App	C 918	10.4	49.5	36	9	US-09-010-733-23	Sequence 23, Appli
C 846	10.4	49.5	24	18	US-08-469-172-154	Sequence 154, App	C 919	10.4	49.5	36	9	US-09-996-634-164	Sequence 164, App
C 847	10.4	49.5	25	10	US-09-940-185-4202	Sequence 4202, Ap	C 920	10.4	49.5	36	10	US-09-997-182-164	Sequence 164, App
C 848	10.4	49.5	25	10	US-09-940-185-4477	Sequence 4477, Ap	C 921	10.4	49.5	36	15	US-09-997-181-164	Sequence 164, App
C 849	10.4	49.5	25	14	US-10-060-756A-2785	Sequence 2785, Ap	C 922	10.4	49.5	36	15	US-10-045-674-617	Sequence 617, App
C 850	10.4	49.5	25	14	US-10-060-756A-2786	Sequence 2786, Ap	C 923	10.4	49.5	37	10	US-09-730-289B-2772	Sequence 2772, Ap
C 851	10.4	49.5	25	14	US-10-060-756A-2787	Sequence 2787, Ap	C 924	10.4	49.5	37	10	US-09-780-533A-4319	Sequence 4319, Ap
C 852	10.4	49.5	25	14	US-10-060-756A-2788	Sequence 2788, Ap	C 925	10.4	49.5	37	10	US-09-927-046-3466	Sequence 3466, Ap
C 853	10.4	49.5	25	14	US-10-060-756A-2789	Sequence 2789, Ap	C 926	10.4	49.5	37	10	US-09-927-046-3614	Sequence 3614, Ap
C 854	10.4	49.5	25	14	US-10-060-756A-2790	Sequence 2790, Ap	C 927	10.4	49.5	37	10	US-09-927-046-3617	Sequence 3617, Ap
C 855	10.4	49.5	25	15	US-10-060-756A-2796	Sequence 2796, Ap	C 928	10.4	49.5	37	10	US-09-877-478-4112	Sequence 4112, Ap
C 856	10.4	49.5	25	15	US-10-098-263B-2476	Sequence 2476, Ap	C 929	10.4	49.5	37	10	US-09-877-478-4144	Sequence 4144, Ap
C 857	10.4	49.5	25	15	US-10-098-263B-10614	Sequence 10614, A	C 930	10.4	49.5	37	10	US-09-877-478-4146	Sequence 4146, Ap
C 858	10.4	49.5	25	15	US-10-098-263B-26683	Sequence 26683, A	C 931	10.4	49.5	37	10	US-09-877-478-4151	Sequence 4151, Ap
C 859	10.4	49.5	25	15	US-10-098-263B-35494	Sequence 35494, A	C 932	10.4	49.5	37	10	US-09-776-474-1952	Sequence 1952, Ap
C 860	10.4	49.5	25	15	US-10-098-263B-56690	Sequence 56690, A	C 933	10.4	49.5	37	10	US-09-930-423-2740	Sequence 2740, Ap
C 861	10.4	49.5	25	15	US-10-098-263B-87196	Sequence 87196, A	C 934	10.4	49.5	37	10	US-09-930-423-2796	Sequence 2796, Ap
C 862	10.4	49.5	25	15	US-10-098-263B-114687	Sequence 114687, A	C 935	10.4	49.5	37	10	US-09-930-423-2802	Sequence 2802, Ap
C 863	10.4	49.5	25	15	US-10-098-263B-114688	Sequence 114688, A	C 936	10.4	49.5	37	10	US-09-930-423-2885	Sequence 2885, Ap
C 864	10.4	49.5	25	15	US-10-098-263B-126636	Sequence 126636, A	C 937	10.4	49.5	37	10	US-09-930-423-2896	Sequence 2896, Ap
C 865	10.4	49.5	25	15	US-10-098-263B-129144	Sequence 129144, A	C 938	10.4	49.5	37	10	US-09-930-423-2902	Sequence 2902, Ap
C 866	10.4	49.5	25	15	US-10-231-115-18	Sequence 18, App1	C 939	10.4	49.5	37	10	US-09-780-164-1790	Sequence 1790, Ap
C 867	10.4	49.5	25	15	US-10-331-285-21	Sequence 21, App1	C 940	10.4	49.5	37	10	US-09-792-818-1423	Sequence 1423, Ap
C 868	10.4	49.5	25	17	US-10-717-597-2160	Sequence 10, App1	C 941	10.4	49.5	37	10	US-09-792-818-1447	Sequence 1447, Ap
C 869	10.4	49.5	25	17	US-10-788-779-10	Sequence 10, App1	C 942	10.4	49.5	37	10	US-09-745-237A-2740	Sequence 2740, Ap
C 870	10.4	49.5	25	17	US-10-716-029-80	Sequence 80, App1	C 943	10.4	49.5	37	10	US-09-745-237A-2796	Sequence 2796, Ap
C 871	10.4	49.5	25	17	US-10-716-029-95	Sequence 95, App1	C 944	10.4	49.5	37	10	US-09-745-237A-2802	Sequence 2802, Ap
C 872	10.4	49.5	26	17	US-10-775-169-3937	Sequence 3937, Ap	C 945	10.4	49.5	37	10	US-09-745-237A-2885	Sequence 2885, Ap
C 873	10.4	49.5	26	9	US-09-985-694A-3	Sequence 3, Appli	C 946	10.4	49.5	37	10	US-09-745-237A-2896	Sequence 2896, Ap
C 874	10.4	49.5	26	13	US-10-176-079-3	Sequence 3, Appli	C 947	10.4	49.5	37	10	US-09-745-237A-2902	Sequence 2902, Ap
C 875	10.4	49.5	26	15	US-10-281-673-28	Sequence 28, App1	C 948	10.4	49.5	37	16	US-10-342-902-4112	Sequence 4112, Ap
C 876	10.4	49.5	26	15	US-10-232-544-2	Sequence 2, App1	C 949	10.4	49.5	37	16	US-10-342-902-4144	Sequence 4144, Ap
C 877	10.4	49.5	26	15	US-10-232-544-137	Sequence 137, App	C 950	10.4	49.5	37	16	US-10-342-902-4146	Sequence 4146, Ap
C 878	10.4	49.5	26	16	US-10-600-389-18	Sequence 18, App1	C 951	10.4	49.5	37	16	US-10-342-902-4151	Sequence 4151, Ap
C 879	10.4	49.5	27	15	US-10-076-047A-73	Sequence 73, App1	C 952	10.4	49.5	37	17	US-10-669-841-9003	Sequence 9003, Ap
C 880	10.4	49.5	27	15	US-10-182-033-7	Sequence 7, App1	C 953	10.4	49.5	37	17	US-10-669-841-9035	Sequence 9035, Ap
C 881	10.4	49.5	28	9	US-09-764-619-6	Sequence 6, App1	C 954	10.4	49.5	37	17	US-10-669-841-9037	Sequence 9037, Ap
C 882	10.4	49.5	28	13	US-10-038-001-9	Sequence 9, App1	C 955	10.4	49.5	37	17	US-10-669-841-9042	Sequence 9042, Ap
C 883	10.4	49.5	28	13	US-10-174-654-12	Sequence 12, App1	C 956	10.4	49.5	38	15	US-10-408-878-13	Sequence 13, Appli
C 884	10.4	49.5	28	17	US-10-220-481-245	Sequence 245, App	C 957	10.4	49.5	38	15	US-10-149-736-49	Sequence 49, Appli
C 885	10.4	49.5	28	17	US-10-220-481-270	Sequence 270, App	C 958	10.4	49.5	38	15	US-10-149-736-50	Sequence 50, Appli
C 886	10.4	49.5	29	10	US-09-746-783-199	Sequence 199, App	C 959	10.4	49.5	39	13	US-10-027-075-16	Sequence 16, Appli
C 887	10.4	49.5	29	15	US-10-258-073-15	Sequence 15, App1	C 960	10.4	49.5	39	13	US-10-027-075-17	Sequence 17, Appli
C 888	10.4	49.5	30	9	US-09-953-052-30	Sequence 30, App1	C 961	10.4	49.5	39	15	US-10-134-645-6	Sequence 6, Appli

Publication No. US20040191902A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; APPLICANT: Hambor, John E.
; APPLICANT: Roach, Marsha L.
; TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS
; FILE REFERENCE: PC25028A
; CURRENT APPLICATION NUMBER: US/10/813,805
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US 60/459,449
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-813-805-42

Query Match 62.9%; Score 13.2; DB 18; Length 22;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGATGCCAGATTACTG 19
| ||||| |||||
Db 21 GAGCATGCCAAATTAGT 4

RESULT 5
US-10-250-997-24/c
; Sequence 24, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 24
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-24

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCG 21
| ||||| |||||
Db 26 GAATGTCAGATAACTGCG 9

RESULT 6
US-10-250-997-25/c
; Sequence 25, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08

; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 25
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-25

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCG 21
| ||||| |||||
Db 26 GAATGTCAGATAACTGCG 9

RESULT 7
US-10-250-997-39
; Sequence 39, Application US/10250997
; Publication No. US20040110251A1
; GENERAL INFORMATION:
; APPLICANT: Grabowski et al.
; TITLE OF INVENTION: DETECTION OF PATHOGENIC BACTERIA
; FILE REFERENCE: 223374
; CURRENT APPLICATION NUMBER: US/10/250,997
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/EP01/11901
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: DE 10100493.1
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 39
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-250-997-39

Query Match 62.9%; Score 13.2; DB 17; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCG 21
| ||||| |||||
Db 7 GAATGTCAGATAACTGCG 24

RESULT 8
US-10-641-455A-117/c
; Sequence 117, Application US/10641455A
; Publication No. US20040171566A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; APPLICANT: McKay, Robert
; APPLICANT: Popoff, Ian
; APPLICANT: Wong, Wai Shiu Fred
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of p38 Mitogen
; TITLE OF INVENTION: Activated Protein Kinase Expression
; FILE REFERENCE: ISPH-0762
; CURRENT APPLICATION NUMBER: US/10/641,455A
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/238,442
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/640,101
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 09/286,904
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117

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; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-641-455A-117

Query Match          62.9%; Score 13.2; DB 17; Length 35;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
Db 34 GCATACCAGATTACAGCC 17

RESULT 9
US-10-197-290-29/c
; Sequence 29, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/857,299
; PRIOR FILING DATE: 2001-20-04
; PRIOR APPLICATION NUMBER: PCT/US99/22083
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-29

Query Match          61.9%; Score 13; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACT 18
Db 16 ATGCCAGATTACT 4

RESULT 10
US-10-388-263-182/c
; Sequence 182, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-182

Query Match          61.9%; Score 13; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGCCAGATTACT 18
Db 16 ATGCCAGATTACT 4

RESULT 11
US-10-317-278-17
; Sequence 17, Application US/10317278
; Publication No. US20040110702A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MAGE-D1 EXPRESSION
; FILE REFERENCE: HTS-0041
; CURRENT APPLICATION NUMBER: US/10/317,278
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-278-17

Query Match          61.9%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGCCAGATTACTG 19
Db 8 TGCCAGATTACTG 20

RESULT 12
US-10-317-278-51/c
; Sequence 51, Application US/10317278
; Publication No. US20040110702A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MAGE-D1 EXPRESSION
; FILE REFERENCE: HTS-0041
; CURRENT APPLICATION NUMBER: US/10/317,278
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-317-278-51

Query Match          61.9%; Score 13; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGCCAGATTACTG 19
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Db      13 TGCCAGATTACTG 1
|||||
RESULT 13
US-10-851-894-15/c
; Sequence 15, Application US/10851894
; Publication No. US20040216185A1
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for Novel Substrate Specific
; FILE REFERENCE: 16518.137
; CURRENT APPLICATION NUMBER: US/10/851,894
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 09/591,279
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Oligonucleotide Primer L197A Sense
US-10-851-894-15
Query Match      61.9%; Score 13; DB 18; Length 32;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      27 AACGCCCGCGAGTACTGGC 7
|||||

RESULT 14
US-10-851-894-16
; Sequence 16, Application US/10851894
; Publication No. US20040216185A1
; GENERAL INFORMATION:
; APPLICANT: DEHESH et al.
; TITLE OF INVENTION: Engineering Beta Ketoacyl ACP Synthase for Novel Substrate Specific
; FILE REFERENCE: 16518.137
; CURRENT APPLICATION NUMBER: US/10/851,894
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 09/591,279
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/138,308
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Oligonucleotide Primer L197A Antisense
US-10-851-894-16
Query Match      61.9%; Score 13; DB 18; Length 32;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      6 AACGCCCGCGAGTACTGGC 26
|||||
```

```
RESULT 15
US-09-930-423-2899/c
; Sequence 2899, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2899
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2899
Query Match      61.9%; Score 13; DB 10; Length 37;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      22 AGTGCATGCCATCATGCTGGC 2
|||||

RESULT 16
US-09-745-237A-2899/c
; Sequence 2899, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2899
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2899
Query Match      61.9%; Score 13; DB 10; Length 37;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 AGCGCATGCCAGATTACTGGC 21
|||||
Db      22 AGTGCATGCCATCATGCTGGC 2
|||||

RESULT 17
US-09-780-752-20
; Sequence 20, Application US/09780752
; Patent No. US20020019349A1
; GENERAL INFORMATION:
; APPLICANT: Conrad, Kirk P.
; APPLICANT: Martyn Lewis
; APPLICANT: Elaine N. Unemori
; APPLICANT: Xinfan Huang
; APPLICANT: Carol A. Tozzi
```

; TITLE OF INVENTION: Use of Relaxin to Treat Diseases Related
; TITLE OF INVENTION: to Vasoconstriction
; FILE REFERENCE: CONN-001
; CURRENT APPLICATION NUMBER: US/09/780,752
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,408
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/200,284
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/242,216
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-752-20

Query Match 61.0%; Score 12.8; DB 9; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGGC 21
||| . ||||| |||||
Db 9 ATGGAGATTACTGGC 24

RESULT 18
US-09-940-185-787/c
; Sequence 787, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 787
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-787

Query Match 61.0%; Score 12.8; DB 10; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACT 18
||| ||||| ||||| |||||
Db 20 CGCATGCCAAATTCCT 5

RESULT 19
US-10-320-231A-8/c
; Sequence 8, Application US/10320231A
; Publication No. US20030194403A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163

; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-8

Query Match 61.0%; Score 12.8; DB 15; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
||| ||||| |||||
Db 19 GCATACCAGAACTAG 4

RESULT 20
US-09-940-185-4752/c
; Sequence 4752, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4752
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4752

Query Match 61.0%; Score 12.8; DB 10; Length 25;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACT 18
||| ||||| ||||| |||||
Db 21 CGCATGCCAAATTCCT 6

RESULT 21
US-10-289-762-3669/c
; Sequence 3669, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3669
; LENGTH: 20
; TYPE: DNA

ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
(EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/091,257

FILING DATE: 05-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/721,979A

FILING DATE: October 4, 1996

APPLICATION NUMBER: FR 94 04009

FILING DATE: 06-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hueschen, Gordon W.

REGISTRATION NUMBER: 16,157

REFERENCE/DOCKET NUMBER: PF57PCTUS/dln

TELECOMMUNICATION INFORMATION:

TELEPHONE: 616-382-0030

TELEFAX: 616-382-2030

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..42

OTHER INFORMATION: /product= "GivdeltaC"

/note= "sequence 174-187"

SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-10-091-257-72

Query Match 59.0%; Score 12.4; DB 14; Length 42;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTAC 17

Db 27 GCATGCCAGATTAC 14

RESULT 30

US-10-035-833A-2502

Sequence 2502, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho

APPLICANT: Sekine, Akihiro

APPLICANT: Iida, Aritoshi

APPLICANT: Saito, Osamu

TITLE OF INVENTION: Detection of Genetic Polymorphisms

FILE REFERENCE: FORS-06904

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT FILING DATE: 2001-12-27

NUMBER OF SEQ ID NOS: 7669

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2502

LENGTH: 49

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (29)..(29)

OTHER INFORMATION: t is present or absent.

US-10-035-833A-2502

Query Match 59.0%; Score 12.4; DB 16; Length 49;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACT 18
Db 30 CTTGCCAGATTACT 43

RESULT 31

US-10-035-833A-4898

Sequence 4898, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho

APPLICANT: Sekine, Akihiro

APPLICANT: Iida, Aritoshi

APPLICANT: Saito, Osamu

TITLE OF INVENTION: Detection of Genetic Polymorphisms

FILE REFERENCE: FORS-06904

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT FILING DATE: 2001-12-27

NUMBER OF SEQ ID NOS: 7669

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4898

LENGTH: 49

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (29)..(29)

OTHER INFORMATION: t is present or absent.

US-10-035-833A-4898

Query Match 59.0%; Score 12.4; DB 16; Length 49;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CATGCCAGATTACT 18

Db 30 CTTGCCAGATTACT 43

RESULT 32

US-10-138-381-15/c

Sequence 15, Application US/10138381

Publication No. US20030064388A1

GENERAL INFORMATION:

APPLICANT: NAKAYAMA, Tomoko

APPLICANT: TADA, Jun

APPLICANT: FUKUSHIMA, Shigeru

APPLICANT: OHASHI, Tetsuo

TITLE OF INVENTION: Oligonucleotides for Detecting Bacteria and

TITLE OF INVENTION: Detection Process

FILE REFERENCE: 1422-0430P

CURRENT APPLICATION NUMBER: US/10/138,381

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: US/09/614,681

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: 08/968,046

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 08/328,710

PRIOR FILING DATE: 1994-10-25

PRIOR APPLICATION NUMBER: 6-48174 JAPAN

PRIOR FILING DATE: 1994-03-18

PRIOR APPLICATION NUMBER: 6-30277 JAPAN

PRIOR FILING DATE: 1994-02-28

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 19

TYPE: DNA

ORGANISM: Escherichia coli

US-10-138-381-15

Query Match 58.1%; Score 12.2; DB 14; Length 19;

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; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer antisense 1257-1278 used to make probe against K10
US-10-085-239A-14

Query Match      58.1%; Score 12.2; DB 15; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGATGCCAGATTACTG 19
Db 21 CGAGTCCAGAACTACTG 5

RESULT 35
US-09-754-853A-786
; Sequence 786, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754.853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 786
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 318013_region_A3_140551_15_Reverse_Primer_Seq
US-09-754-853A-786

Query Match      58.1%; Score 12.2; DB 10; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGATGCCAGATTAC 17
Db 3 AACGCATACCAGATGAC 19

RESULT 36
US-10-098-263B-115941/c
; Sequence 115941, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115941

; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer antisense 1257-1278 used to make probe against K10
US-10-085-239A-14

Query Match      58.1%; Score 12.2; DB 15; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGG 20
Db 17 GAATGTCAGATAACTGG 1

RESULT 33
US-10-084-839-3754/c
; Sequence 3754, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Teetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3754
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3754

Query Match      58.1%; Score 12.2; DB 15; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCGATGCCAGATTACT 18
Db 19 GCGCAGCAGACAGATCT 3

RESULT 34
US-10-085-239A-14/c
; Sequence 14, Application US/10085239A
; Publication No. US2003019715A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Ward, Simon
; APPLICANT: Bavik, Claes
; APPLICANT: Corrk, Michael
; APPLICANT: Tazi-aahini, Rachid
; TITLE OF INVENTION: Treatment of Hyperproliferative Diseases
; FILE REFERENCE: 674569-2001
; CURRENT APPLICATION NUMBER: US/10/085,239A
```



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Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATGCCGATTACTGGC 21
Db 23 CTTGACAGATTACTGCC 7

RESULT 37
US-10-098-263B-119516
; Sequence 119516, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098.263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-119516

Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACT 18
Db 3 GAGAAATGTCAGATTACT 19

RESULT 38
US-10-084-839-3753
; Sequence 3753, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chenak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: IP, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Teetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084.839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004

Query Match      58.1%; Score 12.2; DB 15; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACT 18
Db 7 GCGCACGACAGATTTCCT 23

RESULT 39
US-10-072-622-26
; Sequence 26, Application US/10072622
; Publication No. US20030158102A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; APPLICANT: Bajorath, Jorgen
; TITLE OF INVENTION: ICOS Mutants
; FILE REFERENCE: 07039-331001
; CURRENT APPLICATION NUMBER: US/10/072.622
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-072-622-26

Query Match      58.1%; Score 12.2; DB 15; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGG 20
Db 9 GCATGCTAAATTTGCTGG 25

RESULT 40
US-10-072-622-25/c
; Sequence 25, Application US/10072622
; Publication No. US20030158102A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; APPLICANT: Bajorath, Jorgen
; TITLE OF INVENTION: ICOS Mutants
; FILE REFERENCE: 07039-331001
; CURRENT APPLICATION NUMBER: US/10/072.622
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-072-622-25

Query Match      58.1%; Score 12.2; DB 15; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Oy 4 GCATGCCAGATTACTGG 20
|||
Db 19 GCATGCTAAATTGCTGG 3
|||

Search completed: November 24, 2004, 03:41:54
Job time : 113.572 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-1

Perfect score: 21

Sequence: 1 agcgatgccagattactggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hlc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gssi:*

9: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	61.9	34	9	BX547835 Arabidops
C 2	12.8	61.0	38	9	DR10119T
C 3	12.6	60.0	37	1	AL182864 uc66g08.r
C 4	12.6	60.0	46	1	AI182864 qt72d04.x
C 5	12.2	58.1	37	1	AI561150
C 6	12.2	58.1	48	9	AG203065 Pan. trogl
C 7	12	57.1	39	9	CG709763 1119014G1
C 8	12	57.1	43	1	AI182198 uc64f11.r
C 9	12	57.1	43	8	BH635056 1008002C1
C 10	12	57.1	45	2	BE907096 601500842
C 11	12	57.1	48	9	CL423735 01S0749-0
C 12	12	57.1	50	1	AI102389 AU02389
C 13	11.8	56.2	36	9	TA329D01Q
C 14	11.8	56.2	44	9	CR358600 Arabidops
C 15	11.8	56.2	50	9	CG711376 1119021B0
C 16	11.8	56.2	50	9	AG215560 Drosophil
C 17	11.6	55.2	28	1	AU255721 AU255721
C 18	11.6	55.2	31	6	CD036166 mgmt009XB
C 19	11.6	55.2	32	8	AZ828889 2M0106L07
C 20	11.6	55.2	41	8	AZ471345 1M0285119
C 21	11.6	55.2	42	9	TA92F10Q
C 22	11.6	55.2	49	8	AZ503905 1M0343820
C 23	11.6	55.2	50	9	AB082362 Drosophil
C 24	11.4	54.3	31	9	BX651219 Arabidops

C	25	11.4	54.3	34	1	AV857727	AV857727
C	26	11.4	54.3	35	6	CD533621	32M9 Arab
C	27	11.4	54.3	41	8	AZ804337	2M0065805
C	28	11.4	54.3	47	8	AZ369672	1M0120821
C	29	11.4	54.3	48	9	CL302431	G058B11 G
C	30	11.4	54.3	50	1	AU104945	AU104945
C	31	11.2	53.3	34	1	AA641303	nr78d09.8
C	32	11.2	53.3	35	1	AU040922	AU040922
C	33	11.2	53.3	35	1	AU040926	AU040926
C	34	11.2	53.3	35	9	DR4J11T	AL736749 Danio rer
C	35	11.2	53.3	37	8	AZ821751	2M0094H09
C	36	11.2	53.3	40	9	AL760654	Arabidops
C	37	11.2	53.3	41	8	AZ471345	1M0285119
C	38	11	52.4	32	6	CA853264	B06C01.se
C	39	11	52.4	41	1	AU746715	AJ746715
C	40	11	52.4	43	8	AZ447897	1M0245G17
C	41	11	52.4	43	8	AZ872071	2M0185B13
C	42	11	52.4	44	9	CNS07F95	AL608171 Anopheles
C	43	11	52.4	50	1	AU106987	AU106987
C	44	10.8	51.4	28	8	AZ502451	1M0341D17
C	45	10.8	51.4	29	8	AZ948785	2M0211F21
C	46	10.8	51.4	31	8	AZ596685	1M0410A07
C	47	10.8	51.4	33	9	DR13K9T	AL745568 Danio rer
C	48	10.8	51.4	34	9	DR43K2T	AL975040 Danio rer
C	49	10.8	51.4	35	1	AJ655516	AJ655516
C	50	10.8	51.4	36	8	AZ353586	1M0092105
C	51	10.8	51.4	37	8	BH910433	BH910433 SALK 0596
C	52	10.8	51.4	38	8	AZ779310	2M0015M05
C	53	10.8	51.4	38	9	TA170E05Q	AL474182 T. brucei
C	54	10.8	51.4	43	7	D19557	D19557 MUSGS00957
C	55	10.8	51.4	43	8	BH850810	BH850810 SALK_0718
C	56	10.8	51.4	43	8	BH910174	BH910174 SALK_0581
C	57	10.8	51.4	45	9	CG719990	1119060A1
C	58	10.8	51.4	47	8	BH740833	KG04903-3
C	59	10.8	51.4	50	1	AU103992	AU103992
C	60	10.8	51.4	50	1	AU107439	AU107439
C	61	10.6	50.5	25	1	AA880161	AA880161 vv98h04.r
C	62	10.6	50.5	33	9	TA61D02P	AL456624 T. brucei
C	63	10.6	50.5	34	1	AA630482	AA630482 ab98f09.8
C	64	10.6	50.5	37	9	DR43D23T	AL984974 Danio rer
C	65	10.6	50.5	39	2	BE732614	BE732614 601571185
C	66	10.6	50.5	39	4	BJ524497	BJ524497 603051689
C	67	10.6	50.5	39	8	AZ372602	1M0124J02
C	68	10.6	50.5	39	9	CG72J167	CG72J167 1119075A0
C	69	10.6	50.5	40	8	BH852184	BH852184 SALK_0742
C	70	10.6	50.5	40	8	BZ764204	BZ764204 SALK_1241
C	71	10.6	50.5	42	7	N74525	N74525 za06c08.s1
C	72	10.6	50.5	42	8	BH906566	BH906566 SALK_0339
C	73	10.6	50.5	43	1	AA780094	AA780094 af36509.s
C	74	10.6	50.5	43	7	N71938	N71938 y295a03.s1
C	75	10.6	50.5	46	9	TA316D03P	AL491175 T. brucei
C	76	10.6	50.5	47	1	AV842025	AV842025 AV842025
C	77	10.6	50.5	48	2	AW497611	AW497611 RARG5B34
C	78	10.6	50.5	48	1	CG721564	CG721564 1119067H1
C	79	10.6	50.5	49	1	AA871018	AA871018 vq23c04.r
C	80	10.6	50.5	50	1	AU102221	AU102221
C	81	10.6	50.5	50	1	AU106993	AU106993
C	82	10.4	49.5	23	6	CF317783	CF317783 HD--07-J1
C	83	10.4	49.5	25	9	AJ587447	AJ587447 Arabidops
C	84	10.4	49.5	29	8	AZ310013	AZ310013 1M018B12
C	85	10.4	49.5	31	8	AZ849227	AZ849227 2M0150N02
C	86	10.4	49.5	35	9	AG189387	AG189387 Pan. trogl
C	87	10.4	49.5	37	8	AZ643581	AZ643581 1M0507B10
C	88	10.4	49.5	39	4	BJ055437	BJ055437 BJ055437
C	89	10.4	49.5	40	1	AJ749535	AJ749535 at30b05.x
C	90	10.4	49.5	40	8	AZ480737	AZ480737 1M0302A06
C	91	10.4	49.5	41	4	BI596584	BI596584 603243143
C	92	10.4	49.5	41	4	BI602229	BI602229 603244161
C	93	10.4	49.5	42	8	CC025121	CC025121 3591.1.42
C	94	10.4	49.5	42	9	BX650299	BX650299 Arabidops
C	95	10.4	49.5	43	9	BX287314	BX287314 Arabidops
C	96	10.4	49.5	45	1	AA683880	AA683880 vr06c09.r
C	97	10.4	49.5	47	8	CC020084	CC020084 3591.1.18

98	10.4	49.5	48	9	CL423502	CL423502 01S0557-0	C 171	10	47.6	49	1	AA122130	AA122130 zn82f09.r
99	10.4	49.5	49	1	AI671091	AI671091 wb13a05.x	C 172	10	47.6	49	1	AI966717	AI966717 sc56b04.v
100	10.4	49.5	49	8	BH636470	BH636470 1008011E0	C 173	10	47.6	49	8	AZ784737	AZ784737 2M0027L14
101	10.4	49.5	49	8	BH755942	BH755942 SALK_0525	C 174	10	47.6	49	8	AZ817223	AZ817223 2M0086N19
102	10.4	49.5	50	1	AI102514	AI102514 AU102514	C 175	10	47.6	49	9	BX131909	BX131909 Danilo rer
103	10.4	49.5	50	1	AI102516	AI102516 AU102516	C 176	10	47.6	50	1	AI103679	AI103679 AU103679
104	10.4	49.5	50	1	AI103904	AI103904 AU103904	C 177	10	47.6	50	1	AI104966	AI104966 AU104966
105	10.4	49.5	50	1	AI104912	AI104912 AU104912	C 178	10	47.6	50	1	AI104967	AI104967 AU104967
106	10.4	49.5	50	1	AI104927	AI104927 AU104927	C 179	10	47.6	50	1	AI105067	AI105067 AU105067
107	10.4	49.5	50	1	AI106996	AI106996 AU106996	C 180	10	47.6	50	1	AI105077	AI105077 AU105077
108	10.4	49.5	50	1	AI107003	AI107003 AU107003	C 181	10	47.6	50	1	AI105973	AI105973 AU105973
109	10.4	49.5	22	9	AG202039	AG202039 Fan trogl	C 182	10	47.6	50	1	AI106349	AI106349 AU106349
110	10.2	48.6	26	8	AZ827167	AZ827167 2M0103N22	C 183	10	47.6	50	1	AA406919	AA406919 MBAFCZ6G1
111	10.2	48.6	27	1	AJ789439	AJ789439 AJ789439	C 184	10	47.6	50	7	CO578886	CO578886 tai59f10.
112	10.2	48.6	29	8	AZ650214	AZ650214 1M0520G15	C 185	10	47.6	50	8	AZ510728	AZ510728 1M0355I20
113	10.2	48.6	29	8	AZ784520	AZ784520 2M027H10	C 186	10	47.6	50	8	BH856729	BH856729 SALK_0792
114	10.2	48.6	31	9	CG723474	CG723474 1119076E1	C 187	10	47.6	19	8	AZ482658	AZ482658 1M0307L16
115	10.2	48.6	33	6	CA795338	CA795338 cac BL_23	C 188	9.8	46.7	21	8	AZ313684	AZ313684 1M0303D08
116	10.2	48.6	33	8	BZ770289	BZ770289 SALK_1432	C 189	9.8	46.7	24	9	TA386G12P	TA386G12P T. brucei
117	10.2	48.6	33	8	BZ770290	BZ770290 SALK_1432	C 190	9.8	46.7	26	9	TA157A01Q	TA157A01Q T. brucei
118	10.2	48.6	33	9	DR7G2T	DR7G2T Danilo rer	C 191	9.8	46.7	27	8	AZ404641	AZ404641 1M0173G08
119	10.2	48.6	33	9	TA131H12P	TA131H12P T. brucei	C 192	9.8	46.7	28	8	AZ647786	AZ647786 1M0514P23
120	10.2	48.6	34	4	BJ055330	BJ055330 BJ055330	C 193	9.8	46.7	29	9	TA174H12P	TA174H12P T. brucei
121	10.2	48.6	36	8	AZ867774	AZ867774 2M0178D15	C 194	9.8	46.7	29	9	TA300E08Q	TA300E08Q T. brucei
122	10.2	48.6	37	8	BZ380454	BZ380454 SALK_1151	C 195	9.8	46.7	30	4	BI763468	BI763468 603047483
123	10.2	48.6	39	9	CL524306	CL524306 SAO7D11 F	C 196	9.8	46.7	31	4	BG432088	BG432088 602496951
124	10.2	48.6	40	1	AI1218856	AI1218856 GG75G08.x	C 197	9.8	46.7	31	9	AL767632	AL767632 Arabidops
125	10.2	48.6	40	1	AA137304	AA137304 mg80b07.r	C 198	9.8	46.7	32	8	AZ494703	AZ494703 1M0330F08
126	10.2	48.6	40	7	W88034	W88034 mf68d04.r1	C 199	9.8	46.7	32	9	DR43118T	DR43118T Danilo rer
127	10.2	48.6	40	8	AZ788205	AZ788205 2M0035H09	C 200	9.8	46.7	33	2	BE275474	BE275474 601121496
128	10.2	48.6	43	1	AJ655037	AJ655037 AJ655037	C 201	9.8	46.7	33	8	AZ433514	AZ433514 1M0219I22
129	10.2	48.6	43	9	TA102809Q	TA102809Q T. brucei	C 202	9.8	46.7	33	9	AG196275	AG196275 Pan trogl
130	10.2	48.6	44	8	AZ588580	AZ588580 1M0397F04	C 203	9.8	46.7	34	1	AI035901	AI035901 ub49b03.r
131	10.2	48.6	45	8	AZ649699	AZ649699 1M0519Q24	C 204	9.8	46.7	34	1	AI762091	AI762091 wi53e10.x
132	10.2	48.6	45	8	AZ666398	AZ666398 1M0548G21	C 205	9.8	46.7	34	9	DR1J12T	DR1J12T Danilo rer
133	10.2	48.6	45	8	AZ782306	AZ782306 2M0222A05	C 206	9.8	46.7	34	9	DR3F10T	DR3F10T Danilo rer
134	10.2	48.6	45	9	CG720647	CG720647 1119063C0	C 207	9.8	46.7	34	9	TA294F06P	TA294F06P T. brucei
135	10.2	48.6	45	9	CL001730	CL001730 01S0456-0	C 208	9.8	46.7	36	8	AZ468285	AZ468285 1M0281O12
136	10.2	48.6	48	8	AZ923360	AZ923360 4908_gf20	C 209	9.8	46.7	36	8	AZ635152	AZ635152 1M0491B19
137	10.2	48.6	48	8	BH846418	BH846418 SALK_0078	C 210	9.8	46.7	36	8	AZ841045	AZ841045 2M0138B19
138	10.2	48.6	49	9	DR13307T	DR13307T Danilo rer	C 211	9.8	46.7	36	9	AL952164	AL952164 Arabidops
139	10.2	48.6	50	1	AI102397	AI102397 AU102397	C 212	9.8	46.7	37	1	AI240580	AI240580 qh52e10.x
140	10.2	48.6	50	1	AI104025	AI104025 AU104025	C 213	9.8	46.7	37	1	AI240580	AI240580 qh52e10.x
141	10.2	48.6	50	1	AI104026	AI104026 AU104026	C 214	9.8	46.7	37	4	BJ015204	BJ015204 BJ015204
142	10.2	48.6	50	1	AI105307	AI105307 AU105307	C 215	9.8	46.7	37	8	AZ769896	AZ769896 1M0571E03
143	10.2	48.6	50	1	AI107672	AI107672 AU107672	C 216	9.8	46.7	37	8	AZ766530	AZ766530 1M0564K08
144	10	47.6	21	8	AZ383946	AZ383946 1M0141114	C 217	9.8	46.7	38	8	AZ768339	AZ768339 1M0568E19
145	10	47.6	23	8	AZ629873	AZ629873 1M0483E10	C 218	9.8	46.7	38	8	AL770066	AL770066 Arabidops
146	10	47.6	25	8	BZ596571	BZ596571 SALK_0927	C 219	9.8	46.7	38	8	AZ624746	AZ624746 1M0463E14
147	10	47.6	28	8	AZ494158	AZ494158 1M0329D16	C 220	9.8	46.7	39	8	BZ291057	BZ291057 SALK_1123
148	10	47.6	29	6	CF315943	CF315943 HD--05-A2	C 221	9.8	46.7	40	1	AA990168	AA990168 ua60e08.r
149	10	47.6	29	8	AZ799034	AZ799034 2M0056K09	C 222	9.8	46.7	41	1	AI596178	AI596178 uk23a03.x
150	10	47.6	31	1	AI240510	AI240510 qh12g08.x	C 223	9.8	46.7	41	8	AZ873114	AZ873114 2M0186B15
151	10	47.6	31	1	AI394304	AI394304 t909g12.x	C 224	9.8	46.7	41	9	AL756737	AL756737 Arabidops
152	10	47.6	31	4	BG18864	BG18864 602819370	C 225	9.8	46.7	42	8	CC042159	CC042159 3591_1_14
153	10	47.6	31	8	AZ764843	AZ764843 1M0561N21	C 226	9.8	46.7	42	8	CC042159	CC042159 3591_1_14
154	10	47.6	33	8	AZ766467	AZ766467 1M0564M05	C 227	9.8	46.7	42	9	TA297B12Q	TA297B12Q T. brucei
155	10	47.6	33	9	CL639656	CL639656 P028B07 G	C 228	9.8	46.7	42	9	AL489567	AL489567 T. brucei
156	10	47.6	34	1	AA909241	AA909241 0108e11.s	C 229	9.8	46.7	43	1	AA059057	AA059057 zf63b10.s
157	10	47.6	34	8	AZ482387	AZ482387 1M030700J2	C 230	9.8	46.7	43	1	AI747484	AI747484 ul18b11.x
158	10	47.6	36	9	CL639626	CL639626 P028C08 G	C 231	9.8	46.7	43	6	CA901093	CA901093 PCSC07959
159	10	47.6	38	7	TA66847	TA66847 yb94a12.r1	C 232	9.8	46.7	43	7	R08919	R08919 yf25e05.s1
160	10	47.6	38	8	AZ665949	AZ665949 1M0547L09	C 233	9.8	46.7	43	9	BX170734	BX170734 Danilo rer
161	10	47.6	40	9	AJ600030	AJ600030 Arabidops	C 234	9.8	46.7	44	7	CO780747	CO780747 BL010C.B0
162	10	47.6	40	9	BX959583	BX959583 Arabidops	C 235	9.8	46.7	44	8	AZ656465	AZ656465 1M0532G02
163	10	47.6	41	9	TA126G07Q	TA126G07Q T. brucei	C 236	9.8	46.7	45	8	AZ780685	AZ780685 2M018D06
164	10	47.6	42	4	BI819090	BI819090 603033449	C 237	9.8	46.7	45	9	TA88D07Q	TA88D07Q T. brucei
165	10	47.6	42	9	TA38A10P	TA38A10P T. brucei	C 238	9.8	46.7	46	1	AA576353	AA576353 nh10g03.s
166	10	47.6	43	1	AA869977	AA869977 vq10a08.r	C 239	9.8	46.7	46	9	BX293225	BX293225 Arabidops
167	10	47.6	44	9	CG708578	CG708578 1119009H0	C 240	9.8	46.7	46	9	CG805059	CG805059 1119056H1
168	10	47.6	45	8	BH790044	BH790044 SALK_0543	C 241	9.8	46.7	46	9	CL523052	CL523052 SAP1A08.F
169	10	47.6	47	9	TA120G01P	TA120G01P T. brucei	C 242	9.8	46.7	47	1	AV858479	AV858479
170	10	47.6	49	1	AA929668	AA929668 vy75b04.r	C 243	9.8	46.7	47	7	CO790279	CO790279 NT009B_A0

244	9.8	46.7	47	8	BH810032	BH810032 SALK 0404	317-	9.6	45.7	48	8	AZ801292	AZ801292 2M059M10
245	9.8	46.7	47	8	BH857538	BH857538 SALK 0473	c 318	9.6	45.7	48	8	BH902004	BH902004 SALK 0911
246	9.8	46.7	47	8	BH863999	BH863999 SALK 0951	319	9.6	45.7	48	9	BX242824	BX242824 Danilo rer
247	9.8	46.7	47	1	TA195A08P	TA195A08P	320	9.6	45.7	48	9	CL436088	CL436088 PST2288-N
248	9.8	46.7	47	1	AI168820	AI168820 ox67d03.s	321	9.6	45.7	49	1	AI938114	AI938114 sc43a01.x
249	9.8	46.7	48	8	A2659192	A2659192 1M0536J20	c 322	9.6	45.7	49	1	AJ796516	AJ796516 AJ796516
250	9.8	46.7	48	8	A2847830	A2847830 2M0148M01	c 323	9.6	45.7	49	6	CA996330	CA996330 T938d03.y
251	9.8	46.7	48	8	BH909833	BH909833 SALK 0561	c 324	9.6	45.7	49	8	BH752880	BH752880 SALK 0194
252	9.8	46.7	48	8	BZ595002	BZ595002 SALK 0855	c 325	9.6	45.7	49	9	BX151075	BX151075 Danilo rer
253	9.8	46.7	49	1	AA975152	AA975152 om99C07.s	326	9.6	45.7	49	9	AG215173	AG215173 Drosophil
254	9.8	46.7	49	4	BI450422	BI450422 kt25d08.y	327	9.6	45.7	50	1	AU102620	AU102620 AU102620
255	9.8	46.7	49	4	BI450714	BI450714 kt73g09.y	328	9.6	45.7	50	1	AU102908	AU102908 AU102908
256	9.8	46.7	49	6	CF276937	CF276937 14ETL--02	c 329	9.6	45.7	50	1	AU103909	AU103909 AU103909
257	9.8	46.7	50	1	AU103043	AU103043 AU103043	330	9.6	45.7	50	1	AU104006	AU104006 AU104006
258	9.8	46.7	50	1	AU103046	AU103046 AU103046	331	9.6	45.7	50	1	AU105700	AU105700 AU105700
259	9.8	46.7	50	1	AU103047	AU103047 AU103047	c 332	9.6	45.7	50	1	AU106310	AU106310 AU106310
260	9.8	46.7	50	1	AU103641	AU103641 AU103641	333	9.6	45.7	50	1	AU106560	AU106560 AU106560
261	9.8	46.7	50	1	AU103719	AU103719 AU103719	c 334	9.6	45.7	50	1	AU107002	AU107002 AU107002
262	9.8	46.7	50	1	AU103722	AU103722 AU103722	335	9.6	45.7	50	1	AU107447	AU107447 AU107447
263	9.8	46.7	50	1	AU105888	AU105888 AU105888	c 336	9.6	45.7	50	8	AZ619247	AZ619247 1M0451C05
264	9.8	46.7	50	1	AU107277	AU107277 AU107277	337	9.6	45.7	50	9	CC203941	CC203941 Forward s
265	9.8	46.7	50	1	AU107374	AU107374 AU107374	338	9.6	45.7	50	9	CC476388	CC476388 CH240_302
266	9.8	46.7	50	4	BG315187	BG315187 PO1_0.161	c 339	9.4	44.8	23	1	AJ648209	AJ648209 AJ648209
267	9.8	46.7	50	6	CB360725	CB360725 ZF001-P00	340	9.4	44.8	23	1	DI8743	DI8743 MUSGS01805
268	9.8	46.7	50	9	AG242574	AG242574 Lotus cor	c 341	9.4	44.8	23	8	AZ493087	AZ493087 1M0327L24
269	9.6	45.7	26	8	AZ309743	AZ309743 1M0016N05	c 342	9.4	44.8	24	8	AZ307995	AZ307995 1M0010F06
270	9.6	45.7	27	8	AZ347928	AZ347928 1M0084D14	343	9.4	44.8	25	8	AZ240657	AZ240657 1M0198P02
271	9.6	45.7	29	8	AZ663335	AZ663335 1M0542J20	c 344	9.4	44.8	25	8	AZ595654	AZ595654 1M0408J22
272	9.6	45.7	30	9	AL759587	AL759587 Arabidops	345	9.4	44.8	25	9	AG201639	AG201639 Pan trogl
273	9.6	45.7	31	8	AZ71947	AZ71947 1M0286A22	346	9.4	44.8	26	8	AZ592727	AZ592727 1M0403B22
274	9.6	45.7	31	9	TA157C09P	TA157C09P	347	9.4	44.8	26	1	TA24G03P	TA24G03P T. brucei
275	9.6	45.7	32	2	BH909898	BH909898 601674114	c 348	9.4	44.8	27	1	AJ648985	AJ648985 AJ648985
276	9.6	45.7	33	8	AZ30767	AZ30767 1M0056N08	c 349	9.4	44.8	27	1	AJ681094	AJ681094 AJ681094
277	9.6	45.7	33	8	AZ807552	AZ807552 2M0070A02	350	9.4	44.8	27	8	AZ422212	AZ422212 1M0200K21
278	9.6	45.7	34	1	AI738615	AI738615 willb02.x	c 351	9.4	44.8	28	8	BH610052	BH610052 KG00330-5
279	9.6	45.7	35	2	FI136704	FI136704 601780470	c 352	9.4	44.8	30	8	AZ582016	AZ582016 1M0374C01
280	9.6	45.7	35	7	H67588	H67588 Y*61D03.r1	c 353	9.4	44.8	31	1	AI183733	AI183733 qe15f07.x
281	9.6	45.7	35	8	BH851743	BH851743 SALK 0734	354	9.4	44.8	31	9	TA239G12P	TA239G12P T. brucei
282	9.6	45.7	35	8	BZ353610	BZ353610 SALK 1205	c 355	9.4	44.8	32	6	CD531922	CD531922 12J07 Ara
283	9.6	45.7	35	8	AZ836165	AZ836165 2M0130E23	356	9.4	44.8	32	8	AZ581120	AZ581120 1M0369E02
284	9.6	45.7	36	8	AZ836757	AZ836757 2M0136H03	c 357	9.4	44.8	32	8	BH901742	BH901742 SALK 0859
285	9.6	45.7	37	7	TS1409	TS1409 YP20G08.r1	c 358	9.4	44.8	32	9	CL436724	CL436724 PST3687-N
286	9.6	45.7	38	9	CL438605	CL438605 PST7841-N	c 359	9.4	44.8	33	1	AV845578	AV845578 AV845578
287	9.6	45.7	39	9	TA99A07Q	TA99A07Q	c 360	9.4	44.8	33	8	AZ834737	AZ834737 2M0117006
288	9.6	45.7	40	1	AI093634	AI093634 ou83d06.s	c 361	9.4	44.8	33	8	BZ665773	BZ665773 KG10504-5
289	9.6	45.7	41	7	TA1581	TA1581 YD44B01.s1	c 362	9.4	44.8	33	9	AG201498	AG201498 Pan trogl
290	9.6	45.7	42	1	AA553224	AA553224 VK89C09.s	c 363	9.4	44.8	34	9	TA174F10Q	TA174F10Q T. brucei
291	9.6	45.7	42	2	AW246483	AW246483 2821543.3	c 364	9.4	44.8	35	1	AJ651156	AJ651156 AJ651156
292	9.6	45.7	42	4	B1855685	B1855685 603383215	c 365	9.4	44.8	35	4	BI668131	BI668131 603295966
293	9.6	45.7	42	7	H14364	H14364 Yml8e07.s1	366	9.4	44.8	35	8	BH846699	BH846699 SALK 0098
294	9.6	45.7	43	1	AA103211	AA103211 mo22a07.r	c 367	9.4	44.8	36	1	AL046065	AL046065 DKF2P434F
295	9.6	45.7	43	7	CO789466	CO789466 NT007A.A0	c 368	9.4	44.8	36	9	AJ597380	AJ597380 Arabidops
296	9.6	45.7	43	8	AZ365276	AZ365276 1M0111C24	c 369	9.4	44.8	37	1	AA948700	AA948700 Oq44G09.s
297	9.6	45.7	43	8	AH866395	AH866395 SALK 1012	c 370	9.4	44.8	37	1	AV956951	AV956951 AV956951
298	9.6	45.7	43	9	AL953361	AL953361 Arabidops	c 371	9.4	44.8	37	8	AZ589066	AZ589066 1M0397K16
299	9.6	45.7	43	9	DR35H17T	DR35H17T	372	9.4	44.8	37	8	AZ591849	AZ591849 1M0402B13
300	9.6	45.7	44	8	AZ778971	AZ778971 Danilo rer	c 373	9.4	44.8	37	8	AZ601975	AZ601975 1M0420F01
301	9.6	45.7	44	8	B07611	B07611 CDC1004 Cri	374	9.4	44.8	37	8	AZ662400	AZ662400 1M0541A02
302	9.6	45.7	44	9	AJ591011	AJ591011 Arabidops	375	9.4	44.8	37	9	AG203441	AG203441 Pan trogl
303	9.6	45.7	44	9	CG708578	CG708578 1119009H0	376	9.4	44.8	38	4	BU063802	BU063802 BU063802
304	9.6	45.7	45	8	AZ802142	AZ802142 2M0061L05	c 377	9.4	44.8	38	7	TE1852	TE1852 YP29G06.s1
305	9.6	45.7	45	8	BH171689	BH171689 SALK 0046	c 378	9.4	44.8	38	8	AZ370459	AZ370459 1M0121D03
306	9.6	45.7	45	8	BH848994	BH848994 SALK_0691	c 379	9.4	44.8	38	8	AZ489446	AZ489446 1M0321P10
307	9.6	45.7	45	9	AG025506	AG025506 Oryza sat	c 380	9.4	44.8	38	8	AZ492049	AZ492049 1M0325N19
308	9.6	45.7	46	1	AA244435	AA244435 nc07f09.s	381	9.4	44.8	38	8	AZ593583	AZ593583 1M0405N09
309	9.6	45.7	46	8	AZ826374	AZ826374 2M0102K06	c 382	9.4	44.8	38	8	AZ939810	AZ939810 2M0198P20
310	9.6	45.7	46	8	BH612763	BH612763 SALK 0332	c 383	9.4	44.8	38	9	AL944937	AL944937 Arabidops
311	9.6	45.7	46	9	CHS07827	CHS07827	c 384	9.4	44.8	39	8	AZ779704	AZ779704 2M0016N20
312	9.6	45.7	46	9	CL528749	CL528749 ASV7G03.f	385	9.4	44.8	39	9	CG171918	CG171918 1119056F0
313	9.6	45.7	47	7	RS2627	RS2627 Y982C02.s1	c 386	9.4	44.8	40	1	AA068300	AA068300 mm61h03.r
314	9.6	45.7	47	7	R94759	R94759 Yt71F05.s1	c 387	9.4	44.8	40	4	BG330536	BG330536 602430418
315	9.6	45.7	47	8	AZ802676	AZ802676 2M0061I11	388	9.4	44.8	40	8	AZ778876	AZ778876 2M0014D03
316	9.6	45.7	47	8	AZ802676	AZ802676 2M0061I11	c 389	9.4	44.8	40	8	AZ823569	AZ823569 2M0097M01

390	9.4	44.8	40	8	AZ949468	2M0213A08	C 463	9.2	43.8	19	8	AZ947788	2M0210D11
391	9.4	44.8	40	8	BH865369	SALK 0983	C 464	9.2	43.8	20	9	CL668826	PR10158d
C 392	9.4	44.8	40	8	BH902530	SALK 0919	C 465	9.2	43.8	22	9	AJ590743	Arabidops
C 393	9.4	44.8	40	9	AL760347	Arabidops	C 466	9.2	43.8	25	9	AZ864042	2M0173K19
C 394	9.4	44.8	41	2	BE371184	601218901	C 467	9.2	43.8	23	9	TA330D07P	T. brucei
C 395	9.4	44.8	41	4	BJ050988	BJ050988	C 468	9.2	43.8	25	8	AZ495794	1M0331C21
C 396	9.4	44.8	41	7	T64715	YC25b11.r1	C 469	9.2	43.8	27	8	BH792557	SALK 0647
C 397	9.4	44.8	41	8	AZ584174	1M0388G02	C 470	9.2	43.8	27	9	TA346G04Q	T. brucei
C 398	9.4	44.8	42	1	AJ649217	AJ649217	C 471	9.2	43.8	28	4	BG925479	HNC5-1-B1
C 399	9.4	44.8	42	7	T71216	Yd34h11.s1	C 472	9.2	43.8	28	8	CC057404	SALK 1412
C 400	9.4	44.8	42	8	AZ433972	1M0220E11	C 473	9.2	43.8	29	1	AJ795646	AJ795646
C 401	9.4	44.8	42	8	AZ779593	2M0016B13	C 474	9.2	43.8	30	8	BH854506	KG01921-3
C 402	9.4	44.8	42	9	AG023665	OrYZa sat	C 475	9.2	43.8	31	1	AA890609	ak12G01.s
C 403	9.4	44.8	43	1	AI048043	Wt21F12.r	C 476	9.2	43.8	31	8	AZ487266	1M0316F16
C 404	9.4	44.8	43	1	AJ666356	AJ666356	C 477	9.2	43.8	32	8	AZ306035	1M0006W23
C 405	9.4	44.8	43	7	H62069	YU37h05.r1	C 478	9.2	43.8	32	8	BH758925	P[5'why]1
C 406	9.4	44.8	43	8	CC455427	CC455427	C 479	9.2	43.8	33	1	AU255073	AU255073
C 407	9.4	44.8	44	4	BJ050556	BJ050556	C 480	9.2	43.8	33	5	BX626406	EX626406
C 408	9.4	44.8	44	4	AZ874461	2M0188P06	C 481	9.2	43.8	33	8	BX892689	Arabidops
C 409	9.4	44.8	44	9	AJ595690	Arabidops	C 482	9.2	43.8	33	9	BX894791	Arabidops
C 410	9.4	44.8	44	9	AG023352	Oryza sat	C 483	9.2	43.8	33	1	AA390119	mr37C04.r
C 411	9.4	44.8	45	1	AA812181	ca97r05.s	C 484	9.2	43.8	34	8	AZ626294	1M0466A04
C 412	9.4	44.8	45	7	CF660851	CCLM09A32	C 485	9.2	43.8	34	8	AZ829250	2M0106K17
C 413	9.4	44.8	45	8	AZ452257	1M0252C01	C 486	9.2	43.8	34	8	AQ254767	EP(X)1346
C 414	9.4	44.8	45	8	BZ596472	SALK 0926	C 487	9.2	43.8	34	8	BH406304	RPCI-23-3
C 415	9.4	44.8	45	9	BX651841	Arabidops	C 488	9.2	43.8	34	9	AJ597693	Arabidops
C 416	9.4	44.8	45	9	TA54E07Q	Arabidops	C 489	9.2	43.8	34	9	TA82G11P	Arabidops
C 417	9.4	44.8	46	1	AJ950926	wx61b06.x	C 490	9.2	43.8	35	6	CA913569	PCSC09477
C 418	9.4	44.8	46	1	AJ650474	AJ650474	C 491	9.2	43.8	35	7	N94609	ZB79D03.s1
C 419	9.4	44.8	46	1	AA622161	rq56f10.s	C 492	9.2	43.8	35	8	AZ823097	2M0096K19
C 420	9.4	44.8	46	2	BF682270	602117413	C 493	9.2	43.8	35	9	TA129B11P	AJ633987 T. brucei
C 421	9.4	44.8	46	8	AZ436091	1M0233C08	C 494	9.2	43.8	36	8	AZ658185	AZ658185
C 422	9.4	44.8	46	8	AZ436091	1M0233C08	C 495	9.2	43.8	36	8	AZ817178	2M0086C21
C 423	9.4	44.8	46	8	AZ831992	2M0112L06	C 496	9.2	43.8	36	8	AZ817178	2M0086C21
C 424	9.4	44.8	46	9	TA1000F12P	Arabidops	C 497	9.2	43.8	37	1	AL591377	ts10G07.x
C 425	9.4	44.8	46	9	CC884049	SALK 1028	C 498	9.2	43.8	37	1	AZ644324	1M0508A13
C 426	9.4	44.8	47	6	CF107684	Shultzomi	C 499	9.2	43.8	37	9	TA371B02Q	AJ495897 T. brucei
C 427	9.4	44.8	47	8	AZ663255	1M0542K15	C 500	9.2	43.8	38	1	AJ652946	AJ652946
C 428	9.4	44.8	47	8	AZ801261	2M0059H08	C 501	9.2	43.8	38	8	AZ339876	1M0071J03
C 429	9.4	44.8	47	9	AL760555	Arabidops	C 502	9.2	43.8	38	8	AZ662464	1M0541003
C 430	9.4	44.8	47	9	AB082006	Drosophila	C 503	9.2	43.8	38	8	BZ664429	BZ664429
C 431	9.4	44.8	48	8	AZ603425	1M0422P01	C 504	9.2	43.8	39	7	N75693	YW52A01.r1
C 432	9.4	44.8	48	8	AZ810742	2M0076C06	C 505	9.2	43.8	39	8	AZ360831	1M0104F14
C 433	9.4	44.8	48	8	BH910369	SALK 0591	C 506	9.2	43.8	39	8	AZ834606	2M017G22
C 434	9.4	44.8	48	9	CL265882	03F3660-0	C 507	9.2	43.8	39	8	BH811161	SALK 0575
C 435	9.4	44.8	49	1	AI148915	QC59G08.x	C 508	9.2	43.8	39	9	BX654933	BX654933
C 436	9.4	44.8	49	1	AA232796	2r47a03.r	C 509	9.2	43.8	40	1	AA138030	mq02f11.r
C 437	9.4	44.8	49	1	AA400193	zu64e08.s	C 510	9.2	43.8	40	1	AI493269	tc09c08.x
C 438	9.4	44.8	49	6	CA935081	sau64b02	C 511	9.2	43.8	40	1	AI766423	wh49h03.x
C 439	9.4	44.8	49	7	W30135	mc27e11.r1	C 512	9.2	43.8	40	6	CF299766	7LEAF--03
C 440	9.4	44.8	49	9	BI179896	Danio rer	C 513	9.2	43.8	40	7	D19133	MUGS01349
C 441	9.4	44.8	49	9	CR402501	Arabidops	C 514	9.2	43.8	40	8	BH846353	BH846353
C 442	9.4	44.8	49	9	CC797907	SALK 1455	C 515	9.2	43.8	40	9	CG713594	1119032E0
C 443	9.4	44.8	49	9	CL300934	Q3S0679-0	C 516	9.2	43.8	40	9	CL653498	PR10118c
C 444	9.4	44.8	49	9	CL694976	PR10165C-	C 517	9.2	43.8	41	4	BG614845	602642382
C 445	9.4	44.8	50	1	AL932753	AL932753	C 518	9.2	43.8	41	9	AG189043	Pan trogl
C 446	9.4	44.8	50	1	AU102518	AU102518	C 519	9.2	43.8	42	6	CD743540	IRB14.B02
C 447	9.4	44.8	50	1	AU103816	AU103816	C 520	9.2	43.8	42	8	AZ606691	1M0428C15
C 448	9.4	44.8	50	1	AU104251	AU104251	C 521	9.2	43.8	42	6	CF281213	14ETL--08
C 449	9.4	44.8	50	1	AU105592	AU105592	C 522	9.2	43.8	43	8	AZ834960	2M0117L19
C 450	9.4	44.8	50	1	AU105973	AU105973	C 523	9.2	43.8	43	1	AV956799	AV956799
C 451	9.4	44.8	50	1	AU106018	AU106018	C 524	9.2	43.8	44	8	AZ434899	1M0074D10
C 452	9.4	44.8	50	1	AU106020	AU106020	C 525	9.2	43.8	44	8	AZ419512	1M0196W02
C 453	9.4	44.8	50	1	AU106985	AU106985	C 526	9.2	43.8	44	8	BH864323	SALK 0957
C 454	9.4	44.8	50	1	AU107581	AU107581	C 527	9.2	43.8	44	9	CG711064	1119020A0
C 455	9.4	44.8	50	4	BM319246	ki70c02.y	C 528	9.2	43.8	45	1	AA861335	AA861335
C 456	9.4	44.8	50	5	BX628742	BX628742	C 529	9.2	43.8	45	8	AZ588295	1M0396G03
C 457	9.4	44.8	50	6	CB046639	NISC_gf05	C 530	9.2	43.8	45	9	AJ593903	Arabidops
C 458	9.4	44.8	50	8	AZ330881	1M056101	C 531	9.2	43.8	45	9	EX229715	Danio rer
C 459	9.4	44.8	50	8	AZ466564	1M0277B23	C 532	9.2	43.8	45	9	CL436746	PS13730-N
C 460	9.4	44.8	50	9	CG785978	98F0079-0	C 533	9.2	43.8	46	1	AA782439	AA782439
C 461	9.4	44.8	50	9	CL265883	03F3660-0	C 534	9.2	43.8	46	1	AA834374	of67e02.s
C 462	9.2	43.8	19	8	AZ336303	1M0666G03	C 535	9.2	43.8	46	1	AA501996	ne53q01.s

C 536	9.2	43.8	46	4	B1646968	603278737	609	9	42.9	33	8	AZ607132	1M0429J22
C 537	9.2	43.8	46	8	AZ991900	2M0276P17	C 610	9	42.9	34	1	AA530516	VJ39E05.r
C 538	9.2	43.8	46	8	BZ291224	SALK 1125	611	9	42.9	34	7	N57329	Yw81Q01.r
C 539	9.2	43.8	46	9	BZ769984	SALK 1429	C 612	9	42.9	34	7	N77004	VY50F05.r
C 540	9.2	43.8	46	9	BX290413	Arabidops	C 613	9	42.9	34	8	AZ345514	1M0080J05
C 541	9.2	43.8	46	9	TA123H08P	AL465246	C 614	9	42.9	34	8	AZ462629	1M0269E10
C 542	9.2	43.8	46	9	CL436498	FST3118-N	C 615	9	42.9	34	8	AZ648259	1M0517M11
C 543	9.2	43.8	47	1	AJ789432	AJ789432	616	9	42.9	34	8	AZ877651	BG00655-3
C 544	9.2	43.8	47	8	AQ097186	GSSTC0919	C 617	9	42.9	34	8	CC057359	SALK 1408
C 545	9.2	43.8	47	8	AZ779546	2M0016C09	618	9	42.9	34	8	AL940060	Arabidops
C 546	9.2	43.8	47	8	BZ288624	SALK 0220	C 619	9	42.9	35	7	CF861066	PSZ0003iH
C 547	9.2	43.8	47	9	BX658828	Arabidops	C 620	9	42.9	35	8	AZ371076	1M0122A01
C 548	9.2	43.8	47	9	CL256760	XS0700 Sa	C 621	9	42.9	35	9	AL944678	Arabidops
C 549	9.2	43.8	47	9	CL519316	CL519316	622	9	42.9	36	4	BI246232	602958773
C 550	9.2	43.8	48	8	AZ471910	1M0243N19	623	9	42.9	36	4	BI697010	6032348471
C 551	9.2	43.8	48	8	AZ830212	2M0109M16	C 624	9	42.9	36	6	CA797391	Cac BL 44
C 552	9.2	43.8	48	8	BH851849	SALK 0736	C 625	9	42.9	36	8	AZ423700	1M0202H22
C 553	9.2	43.8	48	8	BZ765762	SALK_1342	C 626	9	42.9	36	8	AZ4739941	1M0301104
C 554	9.2	43.8	49	1	CA456314	CA456314	C 627	9	42.9	36	8	AZ794093	2M0047012
C 555	9.2	43.8	49	1	AA648244	ns07H03.r	C 628	9	42.9	36	8	AZ796083	AG296083
C 556	9.2	43.8	49	1	AA798166	AA798166	629	9	42.9	36	8	BH852549	SALK 0751
C 557	9.2	43.8	49	1	AA109169	mp38f04.r	630	9	42.9	36	8	BH852550	SALK 0751
C 558	9.2	43.8	49	1	AA500776	vg01b11.r	631	9	42.9	36	8	BH853541	SALK 0771
C 559	9.2	43.8	49	2	BF203474	601865731	632	9	42.9	36	8	BZ764686	SALK_1261
C 560	9.2	43.8	49	6	C20872	HUMGS000493	633	9	42.9	36	9	DR746862	SSG14 RPC
C 561	9.2	43.8	49	8	AZ451557	AZ451557	C 634	9	42.9	36	9	AG194334	Pan trogl
C 562	9.2	43.8	49	9	BX182587	Danio rer	C 635	9	42.9	36	9	AG194334	Pan trogl
C 563	9.2	43.8	49	9	CC889041	SALK 1527	636	9	42.9	37	1	AA680722	LmFrAm022
C 564	9.2	43.8	49	9	AG188180	AG188180	C 637	9	42.9	37	1	AI1140898	qa55912.s
C 565	9.2	43.8	50	1	AU103166	AU103166	638	9	42.9	37	1	AA112707	zn70H11.s
C 566	9.2	43.8	50	1	AU103852	AU103852	C 639	9	42.9	37	1	AI667553	fc41G05.x
C 567	9.2	43.8	50	1	AU103860	AU103860	640	9	42.9	37	1	AA233522	cz30b02.r
C 568	9.2	43.8	50	1	AU103861	AU103861	C 641	9	42.9	37	1	AA611583	vo93b03.r
C 569	9.2	43.8	50	1	AU103862	AU103862	C 642	9	42.9	37	2	BE407487	601300314
C 570	9.2	43.8	50	1	AU106594	AU106594	C 643	9	42.9	37	4	BJ034112	BJ034112
C 571	9.2	43.8	50	1	AU107049	AU107049	644	9	42.9	37	7	R70733	Y146d12.r
C 572	9.2	43.8	50	1	AU108052	AU108052	645	9	42.9	37	7	T92129	ye02h11.r
C 573	9.2	43.8	50	1	AU108092	AU108092	646	9	42.9	37	8	AZ480603	1M0302F18
C 574	9.2	43.8	50	4	BM253047	kf01 K.P1	C 647	9	42.9	37	8	AZ658024	1M0534N03
C 575	9.2	43.8	50	5	BP134996	BP134996	648	9	42.9	37	9	BX660247	Arabidops
C 576	9.2	43.8	50	6	CB832519	CB832519	649	9	42.9	38	1	AJ652144	Arabidops
C 577	9.2	43.8	50	6	CD028941	mgn5002xJ	650	9	42.9	38	7	N34814	YV44c12.sl
C 578	9.2	43.8	50	8	BH791926	BH791926	C 651	9	42.9	38	8	AZ483597	1M0309K20
C 579	9.2	43.8	50	9	BX225007	Danio rer	C 652	9	42.9	38	8	AZ662729	1M0542C04
C 580	9.2	43.8	50	9	CR167367	Forward s	C 653	9	42.9	38	8	AZ769958	1M0571G07
C 581	9.2	43.8	50	9	CR198849	Reverse s	C 654	9	42.9	38	8	BH85421	Arabidops
C 582	9.2	43.8	50	9	TA130807P	AL465435	655	9	42.9	38	9	DME547594	Drosophila
C 583	9	42.9	21	8	AZ410517	AZ410517	656	9	42.9	38	9	TA195B01P	Arabidops
C 584	9.2	43.8	22	8	AZ309394	AZ309394	657	9	42.9	39	1	AV851903	AV851903
C 585	9.2	43.8	22	8	AZ479594	AZ479594	658	9	42.9	39	8	AZ499836	1M037C21
C 586	9.2	43.8	22	8	AZ812710	AZ812710	659	9	42.9	39	9	CC887781	SALK 1507
C 587	9.2	43.8	23	8	AZ361811	AZ361811	C 660	9	42.9	40	1	AA769281	nz22H09.s
C 588	9.2	43.8	23	8	AZ433756	AZ433756	C 661	9	42.9	40	1	AA969885	059a10.x
C 589	9.2	43.8	23	8	AZ762598	1M0219J18	C 662	9	42.9	40	1	AI200247	qf57e12.s
C 590	9.2	43.8	24	8	AZ489445	AZ489445	663	9	42.9	40	1	AJ664162	AJ664162
C 591	9.2	43.8	24	8	AZ761439	1M0321P09	C 664	9	42.9	40	1	AA290676	zt19e11.s
C 592	9.2	43.8	24	9	TA39F07Q	AL455326	665	9	42.9	40	1	AV834221	AV834221
C 593	9.2	43.8	25	8	AZ817511	AZ817511	666	9	42.9	40	4	BM36033	5009-0-15
C 594	9.2	43.8	27	1	AJ651227	AJ651227	C 667	9	42.9	40	7	D74285	CELK079A9F
C 595	9.2	43.8	27	1	AJ655548	AJ655548	668	9	42.9	40	7	H55146	CHR220085
C 596	9.2	43.8	27	8	AZ438274	AZ438274	C 669	9	42.9	40	7	H87885	Yw16004.r
C 597	9.2	43.8	28	6	CF305592	CF305592	C 670	9	42.9	40	7	N91653	za20H02.r
C 598	9.2	43.8	28	6	CF305592	CF305592	671	9	42.9	40	7	R89723	ym99c12.r
C 599	9.2	43.8	28	8	AZ810360	AZ810360	672	9	42.9	40	8	BH251215	SALK_0112
C 600	9.2	43.8	28	8	AZ835848	AZ835848	673	9	42.9	40	8	BH909406	Arabidops
C 601	9.2	43.8	29	7	D21044	HUMGS02029	C 674	9	42.9	40	8	AJ600768	SALK_0534
C 602	9.2	43.8	29	8	AZ610133	1M0435F16	675	9	42.9	41	1	BA737623	oa52b06.s
C 603	9.2	43.8	29	8	BH901129	BH901129	C 676	9	42.9	41	8	BZ354052	SALK 1225
C 604	9.2	43.8	30	8	AZ439292	1M0229F19	C 677	9	42.9	41	9	CR662958	Arabidops
C 605	9.2	43.8	31	9	CR399375	CR399375	678	9	42.9	41	9	CR399139	Arabidops
C 606	9.2	43.8	32	6	CO1986	CO1986	679	9	42.9	41	9	HSMC36D01	Arabidops
C 607	9.2	43.8	32	6	AZ625072	1M0464111	680	9	42.9	41	9	AB082397	Drosophila
C 608	9.2	43.8	33	6	CD532323	26K5 Arab	C 681	9	42.9	42	4	B1855685	603383215

C 682	9	42.9	9	42.9	49	1	AI168783	AI168783 ox7ld05.s
683	9	42.9	755	9	49	1	AA110365	AA110365 m195f03.r
684	9	42.9	756	9	49	1	AI457977	AI457977 t154d07.x
C 685	9	42.9	C 757	9	49	1	AI638467	AI638467 t107d10.x
C 686	9	42.9	758	9	49	1	AI760072	AI760072 w57h11.x
C 687	9	42.9	759	9	49	1	AI933401	AI933401 w57d06.x
C 688	9	42.9	C 760	9	49	1	AA501452	AA501452 ne7f107.s
C 689	9	42.9	C 761	9	49	1	AA600891	AA600891 np56e06.s
C 690	9	42.9	C 762	9	49	6	C02336	C02336 HUMG000683
C 691	9	42.9	C 763	9	49	7	H53725	H53725 yu38f12.r1
C 692	9	42.9	C 764	9	49	7	R55033	R55033 v176f02.r1
C 693	9	42.9	C 765	9	49	8	AZ397630	AZ397630 1M0162012
C 694	9	42.9	C 766	9	49	8	BH791685	BH791685 SALK_0608
C 695	9	42.9	C 767	9	49	8	CC040486	CC040486 3591_1_13
C 696	9	42.9	C 768	9	49	9	EX654661	EX654661 Arabidops
C 697	9	42.9	C 769	9	49	9	CR402038	CR402038 Arabidops
C 698	9	42.9	C 770	9	49	9	CG847063	CG847063 01S0596-0
C 699	9	42.9	C 771	9	49	9	CL436086	CL436086 PST2286-N
700	9	42.9	C 772	9	49	50	AU006595	AU006595 AU006595
701	9	42.9	C 773	9	49	50	AU102381	AU102381 AU102381
702	9	42.9	C 774	9	49	50	AU102534	AU102534 AU102534
703	9	42.9	C 775	9	49	50	AU102863	AU102863 AU102863
C 704	9	42.9	C 776	9	49	50	AU103384	AU103384 AU103384
C 705	9	42.9	C 777	9	49	50	AU103838	AU103838 AU103838
C 706	9	42.9	C 778	9	49	50	AU104425	AU104425 AU104425
C 707	9	42.9	C 779	9	49	50	AU104431	AU104431 AU104431
C 708	9	42.9	C 780	9	49	50	AU104436	AU104436 AU104436
C 709	9	42.9	C 781	9	49	50	AU104438	AU104438 AU104438
C 710	9	42.9	C 782	9	49	50	AU104466	AU104466 AU104466
C 711	9	42.9	C 783	9	49	50	AU105701	AU105701 AU105701
C 712	9	42.9	C 784	9	49	50	AU105788	AU105788 AU105788
C 713	9	42.9	C 785	9	49	50	AU105956	AU105956 AU105956
C 714	9	42.9	C 786	9	49	50	AU106897	AU106897 AU106897
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C 716	9	42.9	C 788	9	49	50	AU107342	AU107342 AU107342
C 717	9	42.9	C 789	9	49	50	AU107343	AU107343 AU107343
C 718	9	42.9	C 790	9	49	50	AU107344	AU107344 AU107344
C 719	9	42.9	C 791	9	49	50	BG702400	BG702400 602683696
C 720	9	42.9	C 792	9	49	50	BH439945	BH439945 604143432
C 721	9	42.9	C 793	9	49	50	CF299460	CF299460 7LEAF--03
C 722	9	42.9	C 794	9	49	50	BH232798	BH232798 1006169F1
C 723	9	42.9	C 795	9	49	50	AZ345690	AZ345690 1M0080006
C 724	9	42.9	C 796	9	49	50	BH909964	BH909964 SALK_0567
C 725	9	42.9	C 797	9	49	50	BH910136	BH910136 SALK_0579
C 726	9	42.9	C 798	9	49	50	AJ622759	AJ622759 Drosophila
C 727	9	42.9	C 799	9	49	50	CR002456	CR002456 Reverse.s
C 728	9	42.9	C 800	9	49	50	CG774054	CG774054 1123017A0
C 729	9	42.9	C 801	9	49	50	CL519940	CL519940 DAH6B05.F
C 730	9	42.9	C 802	9	49	50	AZ805949	AZ805949 2M0067F07
C 731	9	42.9	C 803	9	49	50	AZ828387	AZ828387 2M0105P13
C 732	9	42.9	C 804	9	49	20	BX556581	BX556581 BX556581
C 733	9	42.9	C 805	9	49	21	AZ321399	AZ321399 1M0041G24
C 734	9	42.9	C 806	9	49	22	AZ307652	AZ307652 1M0009P20
C 735	9	42.9	C 807	9	49	22	AZ482848	AZ482848 1M0308E10
C 736	9	42.9	C 808	9	49	22	AZ482848	AZ482848 1M0308E10
C 737	9	42.9	C 809	9	49	23	AZ307822	AZ307822 1M0010J11
C 738	9	42.9	C 810	9	49	23	AZ370626	AZ370626 1M0121A16
C 739	9	42.9	C 811	9	49	23	AZ372664	AZ372664 1M0124E09
C 740	9	42.9	C 812	9	49	23	AZ400856	AZ400856 1M0167N17
C 741	9	42.9	C 813	9	49	23	AZ485104	AZ485104 T. brucei
C 742	9	42.9	C 814	9	49	24	AZ502999	AZ502999 1M0368C02
C 743	9	42.9	C 815	9	49	25	CL437569	CL437569 PST5870-N
C 744	9	42.9	C 816	9	49	26	CF329639	CF329639 NACL--05-
C 745	9	42.9	C 817	9	49	26	CF329848	CF329848 NACL--05-
C 746	9	42.9	C 818	9	49	26	AI473394	AI473394 T. brucei
C 747	9	42.9	C 819	9	49	26	CG711323	CG711323 1119020H1
C 748	9	42.9	C 820	9	49	26	CG711323	CG711323 mth2-126G
C 749	9	42.9	C 821	9	49	26	CF312555	CF312555 HD--05-G1
C 750	9	42.9	C 822	9	49	27	CF316215	CF316215 HD--06-E1
C 751	9	42.9	C 823	9	49	27	CF316817	CF316817 HUMXP519A.H
C 752	9	42.9	C 824	9	49	27	L32053	L32053 HUMXP519A.H
C 753	9	42.9	C 825	9	49	27	AZ367484	AZ367484 1M0117H11
C 754	9	42.9	C 826	9	49	27	AZ961301	AZ961301 2M0229L08
C 755	9	42.9	C 827	9	49	27	BZ380146	BZ380146 SALK_1146
							AL466796	AL466796 T. brucei

828	8.8	41.9	28	1	AL118404	AL118404 ue36c02.x	901	8.8	41.9	32	9	DR5N3T	AL738957	Danio rer
c 829	8.8	41.9	28	6	CF278412	CF278412 14ETL--04	902	8.8	41.9	32	9	TA207C02Q	AL475834	T. brucei
c 830	8.8	41.9	28	6	CF315658	CF315658 HD--04-K1	c 903	8.8	41.9	32	6	CF316372	HD--05-K0	
c 831	8.8	41.9	28	6	CF316663	CF316663 HD--06-A2	c 904	8.8	41.9	33	8	AZ785987	2M0030G18	
c 832	8.8	41.9	28	6	CF316792	CF316792 HD--06-D1	c 905	8.8	41.9	33	8	AZ822129	2M0095004	
c 833	8.8	41.9	28	6	CF317075	CF317075 HD--06-K0	c 906	8.8	41.9	33	8	BH856433	SALK_0797	
c 834	8.8	41.9	28	6	CF318998	CF318998 HD--10-J0	c 907	8.8	41.9	33	8	BH856436	SALK_0797	
c 835	8.8	41.9	28	6	CF327928	CF327928 NACL--02	c 908	8.8	41.9	33	9	DR11H23T	BH856436	SALK_0797
c 836	8.8	41.9	28	8	AQ073606	AQ073606 EP(2)2460	c 909	8.8	41.9	33	9	DR15G6T	AL736291	Danio rer
c 837	8.8	41.9	28	8	AQ257938	AQ257938 1M0363B22	c 910	8.8	41.9	33	9	DR19P8T	AL732377	Danio rer
c 838	8.8	41.9	28	8	BH864082	BH864082 SALK_0952	c 911	8.8	41.9	33	9	DR104T	AL744203	Danio rer
c 839	8.8	41.9	28	9	AG191782	AG191782 Pan trogl	c 912	8.8	41.9	33	9	DR43C9T	AL981006	Danio rer
c 840	8.8	41.9	29	6	CF316615	CF316615 HD--05-F1	c 913	8.8	41.9	33	9	DR43F16T	AL975436	Danio rer
c 841	8.8	41.9	29	6	CF316869	CF316869 HD--06-F1	c 914	8.8	41.9	33	9	DR43K14T	AL978734	Danio rer
c 842	8.8	41.9	29	6	CF317167	CF317167 HD--06-M0	c 915	8.8	41.9	33	9	TA152C04P	AL467190	T. brucei
c 843	8.8	41.9	29	6	CF327123	CF327123 NACL--01-	c 916	8.8	41.9	33	9	TA193D02P	AL478361	T. brucei
c 844	8.8	41.9	29	6	CF327275	CF327275 NACL--01-	c 917	8.8	41.9	33	9	CC883904	SALK_1022	
c 845	8.8	41.9	29	7	HL5932	HL5932 Y127903.s1	c 918	8.8	41.9	33	9	CL670049	PR10161a	
c 846	8.8	41.9	29	9	CG724617	CG724617 1119082A0	c 919	8.8	41.9	34	4	BJ064029	BJ064029	
c 847	8.8	41.9	29	9	CG729336	CG729336 1119110H0	c 920	8.8	41.9	34	4	CO578297	TVEST091D	
c 848	8.8	41.9	30	1	AV833957	AV833957 AV833957	c 921	8.8	41.9	34	7	D19569	MUSGS00974	
c 849	8.8	41.9	30	6	CA794646	CA794646 Cac BL 11	c 922	8.8	41.9	34	8	AZ486062	1M0313P14	
c 850	8.8	41.9	30	6	CF301322	CF301322 7L5AF--06	c 923	8.8	41.9	34	8	BH846925	SALK_0119	
c 851	8.8	41.9	30	6	CF311738	CF311738 ABF--07-C	c 924	8.8	41.9	34	9	BZ761684	SALK_0750	
c 852	8.8	41.9	30	6	CF313400	CF313400 HD--01-I0	c 925	8.8	41.9	34	9	AJ596322	Arabidops	
c 853	8.8	41.9	30	6	CF314025	CF314025 HD--02-G0	c 926	8.8	41.9	34	9	AJ601221	Arabidops	
c 854	8.8	41.9	30	6	CF314237	CF314237 HD--02-K2	c 927	8.8	41.9	34	9	DMES45069	AJ601221	Arabidops
c 855	8.8	41.9	30	6	CF314484	CF314484 HD--03-A1	c 928	8.8	41.9	34	9	TA48H05Q	AJ601221	Arabidops
c 856	8.8	41.9	30	6	CF316772	CF316772 HD--06-D0	c 929	8.8	41.9	35	1	AJ655516	AJ655516	
c 857	8.8	41.9	30	6	CF317266	CF317266 HD--06-O1	c 930	8.8	41.9	35	4	BI834797	BI834797	603090235
c 858	8.8	41.9	30	6	CF317281	CF317281 HD--06-O1	c 931	8.8	41.9	35	8	AZ371114	1M0122J03	
c 859	8.8	41.9	30	6	CF337208	CF337208 JMT--07-J	c 932	8.8	41.9	35	8	AZ417198	1M0192H13	
c 860	8.8	41.9	30	8	AZ759753	AZ759753 1M0552O13	c 933	8.8	41.9	35	8	AZ511217	1M0356H11	
c 861	8.8	41.9	30	8	AX001445	AX001445 Arabidops	c 934	8.8	41.9	35	8	AZ610544	1M0435F24	
c 862	8.8	41.9	30	9	AL978971	AL978971 Danio rer	c 935	8.8	41.9	35	8	BH128269	BH128269	G-2p13.f
c 863	8.8	41.9	30	9	AL975331	AL975331 Danio rer	c 936	8.8	41.9	35	8	BH846699	SALK_0098	
c 864	8.8	41.9	30	9	AL984425	AL984425 Danio rer	c 937	8.8	41.9	35	8	DR10P1T	DR10P1T	Danio rer
c 865	8.8	41.9	30	9	TA272C09Q	TA272C09Q	c 938	8.8	41.9	35	9	DR7M21T	CL737464	Danio rer
c 866	8.8	41.9	30	9	CG708764	CG708764 T. brucei	c 939	8.8	41.9	35	9	CL529717	HIV42F05	
c 867	8.8	41.9	31	1	AA999756	AA999756 os93e04.s	c 940	8.8	41.9	36	4	BI761983	BI761983	603048930
c 868	8.8	41.9	31	1	AL582089	AL582089 ar96c09.x	c 941	8.8	41.9	36	7	H97116	H97116	YV89h06.r1
c 869	8.8	41.9	31	1	AV845243	AV845243 AV845243	c 942	8.8	41.9	36	7	T64414	T64414	Yc48e08.s1
c 870	8.8	41.9	31	6	CF313407	CF313407 HD--01-I1	c 943	8.8	41.9	36	7	T65804	T65804	Yc11h12.s1
c 871	8.8	41.9	31	6	CF313473	CF313473 HD--01-J2	c 944	8.8	41.9	36	8	BH810737	BH810737	SALK_0511
c 872	8.8	41.9	31	6	CF313764	CF313764 HD--02-A0	c 945	8.8	41.9	36	9	AL752038	AL752038	Arabidops
c 873	8.8	41.9	31	6	CF316529	CF316529 HD--05-N1	c 946	8.8	41.9	36	9	DR43H15T	DR43H15T	Danio rer
c 874	8.8	41.9	31	6	CF319713	CF319713 HD--10-F0	c 947	8.8	41.9	36	9	DR43L19T	DR43L19T	Danio rer
c 875	8.8	41.9	31	6	CF336854	CF336854 JMT--07-B	c 948	8.8	41.9	36	9	DR43M4T	DR43M4T	Danio rer
c 876	8.8	41.9	31	6	CF337032	CF337032 JMT--07-F	c 949	8.8	41.9	36	9	TA127A09P	TA127A09P	
c 877	8.8	41.9	31	6	CF337142	CF337142 JMT--07-H	c 950	8.8	41.9	36	9	CL213621	CL213621	W126B07.G
c 878	8.8	41.9	31	8	AZ596685	AZ596685 1M0410A07	c 951	8.8	41.9	36	9	AG203210	AG203210	Pan trogl
c 879	8.8	41.9	31	8	AZ815238	AZ815238 2M0083B23	c 952	8.8	41.9	37	1	AA871389	AA871389	vq34g05.r
c 880	8.8	41.9	31	8	AZ832018	AZ832018 2M0112B11	c 953	8.8	41.9	37	1	AA103225	AA103225	mo22g08.r
c 881	8.8	41.9	31	9	DR1567T	DR1567T	c 954	8.8	41.9	37	1	AA1565790	AA1565790	tn20d12.x
c 882	8.8	41.9	31	9	DR43B24T	DR43B24T	c 955	8.8	41.9	37	1	AA190625	AA190625	mp86e08.s
c 883	8.8	41.9	31	9	DR43B2T	DR43B2T	c 956	8.8	41.9	37	1	AA231248	AA231248	mp38h11.r
c 884	8.8	41.9	31	9	DR43J7T	DR43J7T	c 957	8.8	41.9	37	1	AA457896	AA457896	vt34e07.s
c 885	8.8	41.9	31	9	DR43O8T	DR43O8T	c 958	8.8	41.9	37	1	AA482567	AA482567	vt34e07.s
c 886	8.8	41.9	31	9	DR48D10T	DR48D10T	c 959	8.8	41.9	37	1	AA625732	AA625732	ad10h09.s
c 887	8.8	41.9	31	9	DR48K10T	DR48K10T	c 960	8.8	41.9	37	8	AZ460879	AZ460879	1M0266022
c 888	8.8	41.9	31	9	CC887244	CC887244 SALK_1498	c 961	8.8	41.9	37	8	BH759504	BH759504	KG04663-s-5
c 889	8.8	41.9	32	4	B1223057	B1223057 602942007	c 962	8.8	41.9	37	9	DR21K7T	DR21K7T	Danio rer
c 890	8.8	41.9	32	6	CF313280	CF313280 HD--01-F1	c 963	8.8	41.9	38	1	AU008661	AU008661	AU008661
c 891	8.8	41.9	32	6	CF313422	CF313422 HD--01-I1	c 964	8.8	41.9	38	1	AV833104	AV833104	AV833104
c 892	8.8	41.9	32	6	CF313772	CF313772 HD--02-A1	c 965	8.8	41.9	38	4	BU082600	BU082600	BU082600
c 893	8.8	41.9	32	6	CF316885	CF316885 HD--06-F2	c 966	8.8	41.9	38	4	BU082600	BU082600	BU082600
c 894	8.8	41.9	32	8	AZ597602	AZ597602 1M0411P03	c 967	8.8	41.9	38	6	CF297975	CF297975	7LEAF--01
c 895	8.8	41.9	32	8	AZ660571	AZ660571 1M0538C13	c 968	8.8	41.9	38	7	T73578	T73578	Yc36d06.s1
c 896	8.8	41.9	32	8	AZ772645	AZ772645 1M0583N09	c 969	8.8	41.9	38	8	AZ346775	AZ346775	1M0082J08
c 897	8.8	41.9	32	8	AZ779073	AZ779073 2M0014N20	c 970	8.8	41.9	38	8	AZ596174	AZ596174	1M0409115
c 898	8.8	41.9	32	8	AZ989128	AZ989128 2M0272D24	c 971	8.8	41.9	38	8	BZ287177	BZ287177	SALK_0205
c 899	8.8	41.9	32	9	DR1009T	DR1009T	c 972	8.8	41.9	38	9	DR43C7T	DR43C7T	Danio rer
c 900	8.8	41.9	32	9	DR14123T	DR14123T	c 973	8.8	41.9	38	9	DR48J2T	DR48J2T	Danio rer

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974 8.8 41.9 38 9 CC885168
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976 8.8 41.9 39 4 BJ047458
977 8.8 41.9 39 7 H26408
978 8.8 41.9 39 8 AZ416776
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980 8.8 41.9 39 9 DR1L3T
981 8.8 41.9 39 9 DR43P11T
982 8.8 41.9 39 9 TAJ31D02Q
983 8.8 41.9 39 9 CL661996
984 8.8 41.9 39 9 AG198761
985 8.8 41.9 40 1 AA666796
986 8.8 41.9 40 1 AA980528
987 8.8 41.9 40 1 AA983363
988 8.8 41.9 40 1 AI089080
989 8.8 41.9 40 1 AI140587
990 8.8 41.9 40 1 AI174290
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992 8.8 41.9 40 1 AI219362
993 8.8 41.9 40 1 AA199222
994 8.8 41.9 40 1 AV851328
995 8.8 41.9 40 1 AV967687
996 8.8 41.9 40 4 BI158571
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998 8.8 41.9 40 7 CO786949
999 8.8 41.9 40 8 AZ433386
1000 8.8 41.9 40 8 AZ438011

ALIGNMENTS

RESULT 1
BX547835/c 34 bp DNA linear GSS 04-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-548F05-020587,
DEFINITION genomic survey sequence.
ACCESSION BX547835.1 GI:32440655
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
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High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE
4 (bases 1 to 34)
Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

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COMMENT
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At2g40320.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
Location/Qualifiers
1..34
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-548F05-020587"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 61.9%; Score 13; DB 9; Length 34;
Best Local Similarity 76.2%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGATGCCAGATTACTGGC 21
| ||||| ||||| |||||
DB 22 AACGCATGCCAAGTAGTGAC 2

RESULT 2
DR10119T 38 bp DNA linear GSS 26-NOV-2002
LOCUS Danio rerio genomic clone DKEY-10119, genomic survey sequence.
DEFINITION
ACCESSION AL741198
VERSION AL741198.1 GI:21335922
KEYWORDS GSS
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 38)
Humphray, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 10119. 10119 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
Location/Qualifiers
1..38
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-10119"
/tissue_type="Testis"
/notes="vector pindigoBAC-536"

ORIGIN
Query Match 61.0%; Score 12.8; DB 9; Length 38;
Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTG 19
| ||||| ||||| |||||

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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1275 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES

Location/Qualifiers
 1..37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2210966"
 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Utl1"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 58.1%; Score 12.2; DB 1; Length 37;
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTAC 17
 Db 21 AGCGCATGCTGATTAC 5

RESULT 6

AG203065/c
 LOCUS 48 bp DNA linear GSS 06-MAR-2004
 DEFINITION Pan troglodytes DNA, clone: RP43-087A19.TJ, genomic survey sequence.
 AG203065
 VERSION AG203065.1 GI:45233240
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 48)

AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krribb.re.kr, URL: <http://phs.grc.krribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: TJ
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcorI
 R.Site 2 : EcorI
 Location/Qualifiers

FEATURES

source

1..48
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-087A19.TJ"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 58.1%; Score 12.2; DB 9; Length 48;
 Best Local Similarity 82.4%; Pred. No. 1.7e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATGCCAGATTACTGGC 21
 Db 23 CATGCCGTGCTGCTGGC 7

RESULT 7

CG709763/c
 LOCUS 39 bp DNA linear GSS 20-OCT-2003
 DEFINITION 1119014G12.1EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG709763
 VERSION CG709763.1 GI:37735669
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE 1
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1119014 row: G column: 12
 Class: transposon-tagged.

FEATURES

source

1..39
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescueMu Grid AA"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu,' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 57.1%; Score 12; DB 9; Length 39;
 Best Local Similarity 75.0%; Pred. No. 2.1e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGGC 21
 Db 33 GCGCATACCTGATGATGAC 14

RESULT 8

Al182198/c
 LOCUS
 DEFINITION uc64f11.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
 IMAGE:1430445 5' similar to TR:Q90574 Q90574 FILAMIN. ;, mRNA
 sequence.

ACCESSION

Al182198

VERSION

Al182198.1 GI:3732836

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 43)
 Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE

The WashU-HHMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:914513

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .43

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:1430445"

/sex="male"

/tissue_type="mammary gland"

/dev_stages="4 weeks"

/lab_host="DH10B"

/clone_lib="Soares_mammary_gland NbMMG"

/note="Organ: mammary Gland; Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

constructed and normalized by Bento Soares and M.Fatima

Bonaldo."

ORIGIN

Query Match

Best Local Similarity 57.1%; Score 12; DB 1; Length 43;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGGC 21

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Db 34 GCACTTACCAGATTCTTGGC 15

RESULT 9

LOCUS

DEFINITION

BH635056 43 bp DNA linear GSS 14-FEB-2002
 1008002C10.2EL_xl 1008 - RescueMu Grid I Zea mays genomic, genomic
 survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008002 row: 36

Class: transposon-tagged.

Location/Qualifiers

1. .43

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1008 - RescueMu Grid I"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site www.zmdb.iastate.edu and follow the links for

'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was

extracted from leaf punches, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

ORIGIN

Query Match

Best Local Similarity 57.1%; Score 12; DB 8; Length 43;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTGGC 21

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RESULT 10

LOCUS

DEFINITION

BE907096 45 bp mRNA linear EST 20-OCT-2000
 601500842F1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3902555 5',
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
JOURNAL        1 (bases 1 to 45)
COMMENT        NIH-MGC http://mgc.nci.nih.gov/.
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs-r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM9705 row: d column: 12
                High quality sequence stop: 45.
FEATURES       Location/Qualifiers
                1..45
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3902555"
                /tissue_type="epithelioid carcinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 70"
                /note="Organ: Pancreas; Vector: pCMV-SPORT6; Site: 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.1 Kb. Library constructed by Life
                Technologies."
ORIGIN
Query Match      57.1%; Score 12; DB 2; Length 45;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 AGCGCATGCCAGATTACTGG 20
      ||| ||| ||| ||| ||| ||| |||
Db      5 AGTCATCGCAGATGCTGG 24

RESULT 11
CL423735
LOCUS      CL423735      48 bp      DNA      linear      GSS 16-MAR-2004
DEFINITION      01S0749-01C1-F01 UniformMu MutAIL Library Zea mays genomic clone
ACCESSION      01S0749-01C1-F01, genomic survey sequence.
VERSION        CL423735
KEYWORDS       GSS.
SOURCE        Zea mays
ORGANISM      Zea mays
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                Clade; Panicoideae; Andropogoneae; Zea.
TITLE          1 (bases 1 to 48)
JOURNAL        Latschew.S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
COMMENT        Sequence tagged transposon insertions from the UniformMu maize
                population
                Unpublished (2003)
                Contact: Donald R. McCarty
                Plant Molecular and Cellular Biology Program
                University of Florida
                PO 110690 Gainesville, FL 32611-0690, USA
                Tel: 352-392-1928 x322
                Email: drmc@ufl.edu
                Sequence flanking probable Mu insertion site in UniformMu
                line: 01S0749-01, Primer set: C
                Class: transposon insertion site.
FEATURES       Location/Qualifiers
                1..48
                /organism="Zea mays"
                /mol_type="genomic DNA"

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/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0749-01C1-F01"
/clone_lib="UniformMu MutAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
ORIGIN
Query Match      57.1%; Score 12; DB 9; Length 48;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 GCGCATGCCAGATTACTGGC 21
      ||| ||| ||| ||| ||| ||| |||
Db      4 GCGCATGCCAGTAATGGGC 23

RESULT 12
AUI02389/c
LOCUS      AUI02389      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION      AUI02389 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION      ADSH01565, mRNA sequence.
VERSION        AUI02389
KEYWORDS       EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
                1 (bases 1 to 50)
TITLE          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
                Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
                Sakaki,Y., Nakamura,Y., Sugama,A. and Sugano,S.
                Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
JOURNAL        EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE        21270072
PUBMED         11375929
COMMENT        Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: yusuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                Sugano,S. Construction and characterization of a full
                length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                149-156 (1997).
FEATURES       Location/Qualifiers
                1..50
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="ADSH01565"
                /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      57.1%; Score 12; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AGCGCATGCCAGATTACTGGC 21
      ||| ||| ||| ||| ||| ||| |||
Db      34 AGCCGTCGCTGATCNCITGGC 14

RESULT 13
TA329D01Q

```

LOCUS TA329D01Q 36 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 329d01, reverse sequence,
 genomic survey sequence.
 ACCESSION AL492403
 VERSION AL492403.1 GI:11868665
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
 Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
 Melville S.E., Rajandream M.A. and Barrell B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The V + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..36
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="329d01"
 ORIGIN
 Query Match 56.2%; Score 11.8; DB 9; Length 36;
 Best Local Similarity 86.7%; Pred. No. 2.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GCGCATGCCAGATTA 16
 |||||
 Db 19 GCCCATGCCAGACTA 33
 RESULT 14
 CR358600/c
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-729F02-025222,
 genomic survey sequence.
 ACCESSION CR358600
 VERSION CR358600.1 GI:45541522
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22755829
 PUBMED 12874060
 REFERENCE 2
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14756321
 REFERENCE 3
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weissshaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 44)
 AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weissshaar, B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 TSK6. Details on the protocols used for generation of the sequence
 are described in References 1-3. The sequences are generated at the
 MPI for Plant Breeding Research in the context of the GABI-Kat
 project. GABI-Kat is part of the German Plant Genomics program
 designated 'GABI'. Information on line availability can be found
 at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 Location/Qualifiers
 1..44
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-729F02-025222"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (Ti) which were transformed with the T-DNA from
 vector pGAB1 (GenBank accession number: AY529716). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."
 ORIGIN
 Query Match 56.2%; Score 11.8; DB 9; Length 44;
 Best Local Similarity 86.7%; Pred. No. 2.7e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 AGCGCATGCCAGATT 15
 |
 Db 18 ATCCGATGCCACATT 4
 RESULT 15
 CG711376/c
 LOCUS 1119021B09.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION CG711376
 VERSION CG711376.1 GI:37737282
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

TITLE
JOURNAL COMMENT
 Bhatteai, K. and Dean, R.A.
 Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
 Unpublished (2002)
 Contact: Ebbolle DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebbole@tamu.edu
 Chromatogram file of this sequence is available, see contact person;
 PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgmt009 row: B column: 10
 Seq primer: T3.

FEATURES
 source

1. .31
 /location/Qualifiers
 /organism="Magnaporthe grisea"
 /mol_type="mRNA"
 /strain="4091-5-8 X 4136-4-3"
 /db_xref="taxon:148305"
 /clone="mgmt009xB10"
 /sex="Mat1-2 and Mat1-1 mixed culture"
 /cell_type="mixed sexual development"
 /dev_stage="asci, ascospores, perithecia, mycelium"
 /clone_lib="Mated culture"
 /note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI; Two mating types were co-cultivated over a filter paper on oatmeal agar medium. After three days at 25 C plates were transferred to 21 C. Perithecia with asci and ascospores formed at the beginning of the third week. Material was collected by scraping tissue from the filter paper. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN

Query Match 55.2%; Score 11.6; DB 6; Length 31;
 Best Local Similarity 77.8%; Pred. No. 3.2e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCG 21
 |||||
 Db 26 GCATGCCAGTGATCATGC 9

RESULT 19
AZ828889
LOCUS
DEFINITION
 2M0106L07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0106L07 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 32)
REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss

REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0106 row: L column: 07
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES
 source

1. .32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0106L07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.2%; Score 11.6; DB 8; Length 32;
 Best Local Similarity 77.8%; Pred. No. 3.2e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGCATGCCAGATTACTG 19
 |||||
 Db 1 GCGAATGCCAGGTCATG 18

RESULT 20
AZ471345
LOCUS
DEFINITION
 1M0285I119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0285I19 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 41)
REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss

REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0285 row: 1 column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
 1. 41
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0285119"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 55.2%; Score 11.6; DB 8; Length 41;
 Best Local Similarity 77.8%; Pred. No. 3.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
 |||||
 Db 20 GTATGCCAGAAACTGGC 37

RESULT 21
 TA92F10Q/c
 LOCUS
 DEFINITION
 T. brucei sheared genomic DNA clone 92f10, reverse sequence, genomic survey sequence.
 ACCESSION
 AL462451
 VERSION
 AL462451.1 GI:11862749
 KEYWORDS
 GSS.
 SOURCE
 Trypanosoma brucei
 ORGANISM
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 42)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajadream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0285 row: 1 column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers
 1. 42
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="92f10"

Query Match 55.2%; Score 11.6; DB 9; Length 42;
 Best Local Similarity 77.8%; Pred. No. 3.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCATGCCAGATTACTGGC 21
 |||||
 Db 23 GCAGCCAGATAGGGGC 6

RESULT 22
 AZ503905
 LOCUS
 DEFINITION
 1M0343E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0343E20 R, genomic survey sequence.
 ACCESSION
 AZ503905
 VERSION
 AZ503905.1 GI:10685221
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0343 row: E column: 20
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 49.
 Location/Qualifiers
 1. 49
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0343E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

COMMENT
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.2%; Score 11.6; DB 8; Length 49;
Best Local Similarity 77.8%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTGCC 21
|||||
Db 14 GCCTGCTGTTACTGCC 31

RESULT 23
AB082362
LOCUS Drosophila melanogaster DNA, clone:1(2)SH2 1052, genomic survey
DEFINITION sequence.
ACCESSION AB082362
VERSION AB082362.1 GI:23307398
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Oh,S.W., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X., Wang,H., Ruan,P., Moody,M. and Hou,S.X.
TITLE A p-element insertion screen identified mutations in 455 novel essential genes in Drosophila

JOURNAL Genetics 163 (1), 195-201 (2003)
MEDLINE 22474228
PUBMED 12586707
REFERENCE 2 (bases 1 to 50)
AUTHORS Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2002) Suan Oh, The Laboratory of Immunobiology, National Institutes of Health, National Cancer Institute, Frederick, 1050 Boyles st., Frederick, Maryland 21702-1201, USA (E-mail:ohsuan@mail.ncifcrf.gov, Tel:1-301-846-7314, Fax:1-301-846-6145)

FEATURES
source Location/Qualifiers
1..50
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="1(2)SH2 1052"

ORIGIN

Query Match 55.2%; Score 11.6; DB 9; Length 50;
Best Local Similarity 73.7%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCGATCCGATTACTG 19
|||||

Db 32 AGACTGGCCATTACTG 50

RESULT 24
BX651219/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-555H12-021706,
DEFINITION genomic survey sequence.
ACCESSION BX651219
VERSION BX651219.1 GI:37607607
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2

AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3

AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE 14682050
PUBMED

REFERENCE 4 (bases 1 to 31)
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g48830. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source Location/Qualifiers
1..31
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-555H12-021706"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 54.3%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.1e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 41;
Best Local Similarity 92.3%; Pred. No. 4.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCCAGATTACTG 19
| | | | |
Db 23 TGCCATATTACTG 35

RESULT 28

AZ3369672

LOCUS

DEFINITION MW120E21F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0120E21 F, genomic survey sequence.

ACCESSION

AZ3369672

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0120 row: E column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 47.

FEATURES
source
1. 47

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0120E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 47;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCGCATGCCAGATTACTGGC 21
| | | | |
Db 7 ATCGCGTGCACACAGACTGTC 27

RESULT 29

CL302431

LOCUS

DEFINITION G058B11 GGTc Gene Trap Library GV07C05 Mus musculus cDNA clone G058B11, mRNA sequence.

ACCESSION

CL302431

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

On Jun 30, 2004 this sequence version replaced gi:42743260.
Contact: GGTc
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
USCEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G058B11', ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 17086
Class: Gene Trap.

FEATURES
source
1. 48

/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G058B11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"

```

ORIGIN
Query Match      54.3%; Score 11.4; DB 9; Length 48;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
    ||||| ||||| ||||| ||||| |||||
Db 3 ACTGGATCTCACATTCTGGC 23

RESULT 30
AA641303/c
LOCUS      34 bp mRNA linear EST 28-JAN-2004
DEFINITION Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION   HRC05721, mRNA sequence.
VERSION     AU104945
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isoqai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PubMed      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).

FEATURES
source
1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="HRC05721"
    /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 4.4e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCGCATGCCAGATTACTGGC 21
    ||||| ||||| ||||| ||||| |||||
Db 27 AGCGCTCGCAGCAGATGGC 47

RESULT 31
AA641303/c
LOCUS      34 bp mRNA linear EST 27-OCT-1997
DEFINITION nr78d09.s1 NCI CGAP Pr24 Homo sapiens cDNA clone IMAGE:1174097 3,
            similar to TR:G440389 G440399 EPSILON-COP., mRNA sequence.
ACCESSION   AA641303
VERSION     AA641303.1 GI:2566653
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 34)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..34
source
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="IMAGE:1174097"
    /tissue_type="invasive tumor (cell line)"
    /lab_host="SOLR (kanamycin resistant)"
    /clone_lib="NCI CGAP Pr24"
    /note="Organ: prostate; Vector: Bluescript SK-; Site:1:
    EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
    Oligo dr. Invasive prostate tumor cell line (HPV
    immortalized). 5' adaptor sequence: 5' GAATTCGGCAGAG 3'
    3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
    Average insert size: 1.0 kb."

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 34;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGCGATGCCAGATTAC 17
    ||||| ||||| ||||| ||||| |||||
Db 33 CGCGTGCACATTGC 18

RESULT 32
AU040922/c
LOCUS      35 bp mRNA linear EST 04-DEC-1998
DEFINITION AU040922 Mouse four-cell-embryo cDNA Mus musculus cDNA clone
ACCESSION   J0820609 3', mRNA sequence.
VERSION     AU040922
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 35)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
            Ko,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T.,
            DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Lim,M.K. and
            Doi,H.
            Systematic analyses of genes expressed in 4-cell mouse embryo (The
            ERATO/Doi Project at Wayne State University)
            Unpublished (1998)
            Contact: Hirofumi Doi
            Doi Biosymmetry Project, ERATO
            Japan Science and Technology Corporation (JST)
            WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
            Email: hd@bioa.jst.go.jp.
            Location/Qualifiers
            1..35
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6J"

```

```

/db_xref="taxon:10090"
/clone="J0820609"
/dev_stage="four-cell-embryo"
/clone_lib="Mouse four-cell-embryo cDNA"

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGCG 21
    ||| ||||| |||||
Db 16 ATGTCAGATCACTGAC 1

RESULT 33
AU040926/c
LOCUS AU040926 35 bp mRNA linear EST 04-DEC-1998
DEFINITION AU040926 Mouse four-cell-embryo cDNA Mus musculus cDNA clone
ACCESSION J0820609 3', mRNA sequence.
VERSION AU040926
KEYWORDS AU040926.1 GI:3955091
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T.,
DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K. and
Doi, H.
Systematic analyses of genes expressed in 4-cell mouse embryo (The
ERATO/Doi Project at Wayne State University)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdo@bioa.jst.go.jp.

FEATURES
source
1. .35
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="J0820609"
/dev_stage="four-cell-embryo"
/clone_lib="Mouse four-cell-embryo cDNA"

ORIGIN
Query Match      53.3%; Score 11.2; DB 1; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGCG 21
    ||| ||||| |||||
Db 16 ATGTCAGATCACTGAC 1

RESULT 34
DR4J11T
LOCUS DR4J11T 35 bp DNA linear GSS 27-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-4J11, genomic survey sequence.
ACCESSION AL736749
VERSION AL736749.1 GI:21350789
KEYWORDS GSS
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 35)
Humphray, S.J., Huckle, E. and Hunt, S.E.

Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 4J11. 4J11 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
1. .35
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-4J11"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN
Query Match      53.3%; Score 11.2; DB 9; Length 35;
Best Local Similarity 81.2%; Pred. No. 5.3e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCATGCCAGATTACTG 19
    ||| ||||| |||||
Db 20 GCATGCCAGCTTATTG 35

RESULT 35
AZ821751/c
LOCUS AZ821751 37 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0094H09 R, genomic survey sequence.
ACCESSION AZ821751
VERSION AZ821751.1 GI:12991659
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: H column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

FEATURES
source
1. .37
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="UUGC2M0094H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 37;
Best Local Similarity 81.2%; Pred. No. 5.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCGATGCCAGATTA 16
||| ||||| |||||
Db 16 AGGAATGCCAGATTA 1

RESULT 36
AL760654/c
LOCUS
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-200F07-014483,
genomic survey sequence.

ACCESSION AL760654
VERSION AL760654.1 GI:21499948
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
MEDLINE
PUBMED
22753829
12874060

REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics

JOURNAL
MEDLINE
PUBMED
23117147
14756321

REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

JOURNAL
PUBMED
14682050

REFERENCE 4
(bases 1 to 40)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.

TITLE Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At3g14440.

DETAILS on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source

Location/Qualifiers
1..40
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clones="GK-200F07-014483"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 40;
Best Local Similarity 81.2%; Pred. No. 5.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCATGCCAGATTACT 18
||| ||||| |||||

Db 34 CGCTTGGCGTTACT 19
||| ||||| |||||

RESULT 37
AZ471345/c

LOCUS
DEFINITION AZ471345
1M0285119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0285119 R, genomic survey sequence.

ACCESSION AZ471345
VERSION AZ471345.1 GI:10629470
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0285 row: 1 column: 19

Seq primer: CACACAGGAAACAGTCATGACC

Class: plasmid ends

High quality sequence stop: 41.

FEATURES
source

Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0285119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 41;
Best Local Similarity 81.2%; Pred. No. 5.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATGCCAGATTACTGGC 21
||||| ||| |||
Db 39 ATGCCAGTTTCTGCC 24

RESULT 38

CA853264/c
LOCUS 32 bp mRNA linear EST 01-AUG-2003
DEFINITION B06C01.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
B06C01.5', mRNA sequence.

CA853264
B06C01.5', mRNA sequence.

CA853264.1 GI:33390057

EST.

KEYWORDS Glycine max (soybean)

SOURCE Glycine max

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 32)

Akharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Akharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ars.usda.gov.

Location/Qualifiers

1..32

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clones="B06C01"

/tissue_type="Roots"

/dev_stages="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: phluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN

Unpublished (2000)

Query Match 52.4%; Score 11; DB 6; Length 32;
Best Local Similarity 73.7%; Pred. No. 6.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCGCATCCAGATTACTGGC 20

||||| ||| ||| |||

Db 21 GTGCGTCGAGATTACTGGC 3

RESULT 39

AJ746715
LOCUS 41 bp mRNA linear EST 07-JUL-2004
DEFINITION AJ746715 muscle - muscle minus alveolar macrophage Sus scrofa cDNA clone ap03_6_D02, mRNA sequence.

ACCESSION AJ746715

VERSION AJ746715.1 GI:49916774

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 41)

AUTHORS Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.

and Dixon, L.

Development of a porcine cDNA microarray

Unpublished (2004)

Contact: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES

source

1..41

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="ap03_6_D02"

/tissue_type="muscle"

/cell_type="macrophage"

/clone_lib="muscle - muscle minus alveolar macrophage"

ORIGIN

Query Match 52.4%; Score 11; DB 1; Length 41;
Best Local Similarity 73.7%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CGCATGCCAGATTACTGGC 21

||||| ||| ||| |||

Db 12 CGCACCCAGCTTGCTGTC 30

RESULT 40

AZ447897/c
LOCUS 43 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0245G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0245G17 F, genomic survey sequence.

ACCESSION AZ447897

VERSION AZ447897.1 GI:10600152

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 43)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Rielly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 378.157 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21
Sequence: 1 tcgcgtacgggtctaatgacgc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
c	1	21	100.0	21	6	BD181363		BD181363 A method
	2	21	100.0	21	6	BD181378		BD181378 A method
	3	21	100.0	21	6	AX523943		AX523943 Sequence
c	4	21	100.0	21	6	AX524841		AX524841 Sequence
	5	21	100.0	21	6	AX524856		AX524856 Sequence
	6	13.6	64.8	29	6	BD227377		BD227377 Secreted
c	7	12.8	61.0	30	6	AX752106		AX752106 Sequence
	8	12.6	60.0	20	6	AX295474		AX295474 Sequence
	9	12.6	60.0	24	6	AX290841		AX290841 Sequence
c	10	12.6	60.0	26	6	BD260345		BD260345 Methods.
	11	12.6	60.0	26	6	AX044390		AX044390 Sequence
	12	12.6	60.0	31	6	AR168721		AR168721 Sequence
c	13	12.6	60.0	33	6	AR047950		AR047950 Sequence
	14	12.6	60.0	38	6	AR334533		AR334533 Sequence
	15	12.6	60.0	38	6	AR335779		AR335779 Sequence
c	16	12.6	60.0	38	6	AR336409		AR336409 Sequence
	17	12.6	60.0	38	6	AR455837		AR455837 Sequence
	18	12.6	60.0	38	6	AX219207		AX219207 Sequence
c	19	12.6	60.0	38	6	AX219231		AX219231 Sequence

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c	21	12.6	38	6	AX424618	AX424618 Sequence
c	22	12.6	38	6	AX424731	AX424731 Sequence
c	23	12.6	38	6	AX581188	AX581188 Sequence
c	24	12.6	38	6	AX581359	AX581359 Sequence
c	25	12.6	42	6	AX5234	AX5234 Sequence
c	26	12.4	20	6	AX295733	AX295733 Sequence
c	27	12.4	24	6	AX291100	AX291100 Sequence
c	28	12.4	34	6	AX464504	AX464504 Sequence
c	29	12.4	38	6	AR046887	AR046887 Sequence
c	30	12.4	38	6	IS3939	IS3939 Sequence
c	31	12.4	38	6	AX220204	AX220204 Sequence
c	32	12.2	20	6	AR314417	AR314417 Sequence
c	33	12.2	21	6	AR364921	AR364921 Sequence
c	34	12.2	22	6	AX392054	AX392054 Sequence
c	35	12.2	32	6	AX755148	AX755148 Sequence
c	36	12.2	32	6	AX755156	AX755156 Sequence
c	37	12.2	37	6	AX351239	AX351239 Sequence
c	38	12.2	37	6	AX581788	AX581788 Sequence
c	39	12.2	37	6	AX581793	AX581793 Sequence
c	40	12.2	37	6	AX581826	AX581826 Sequence
c	41	12.2	40	6	CQ759972	CQ759972 Sequence
c	42	12.2	41	6	AR238615	AR238615 Sequence
c	43	12	21	6	AR1179	AR1179 Sequence
c	44	12	25	6	AS1919	AS1919 Sequence
c	45	12	25	6	AR085879	AR085879 Sequence
c	46	12	29	6	AR474494	AR474494 Sequence
c	47	12	29	6	AX259926	AX259926 Sequence
c	48	12	29	6	AX260008	AX260008 Sequence
c	49	12	29	6	AX262370	AX262370 Sequence
c	50	12	37	6	AX581813	AX581813 Sequence
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c	53	12	38	6	AR330702	AR330702 Sequence
c	54	12	38	6	AR330939	AR330939 Sequence
c	55	12	38	6	AR331990	AR331990 Sequence
c	56	12	38	6	AR332379	AR332379 Sequence
c	57	12	38	6	AR332572	AR332572 Sequence
c	58	12	38	6	AR332919	AR332919 Sequence
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c	60	12	38	6	AR333110	AR333110 Sequence
c	61	12	38	6	AX580628	AX580628 Sequence
c	62	12	41	11	BV108924	BV108924 PZA01577
c	63	12	45	6	BD096959	BD096959 Delivery
c	64	11.8	15	6	BD208648	BD208648 Enzymatic
c	65	11.8	21	6	BD014023	BD014023 Plant gen
c	66	11.8	28	6	A56797	A56797 Sequence
c	67	11.8	29	6	BD198088	BD198088 Method an
c	68	11.6	20	6	E30584	E30584 Neurogesi
c	69	11.6	20	6	AR268852	AR268852 Sequence
c	70	11.6	20	6	AX295529	AX295529 Sequence
c	71	11.6	24	6	AX290896	AX290896 Sequence
c	72	11.6	24	6	AX291942	AX291942 Sequence
c	73	11.6	25	6	BD225557	BD225557 Assay for
c	74	11.6	26	6	BD260282	BD260282 Methods.
c	75	11.6	26	6	BD260303	BD260303 Methods.
c	76	11.6	26	6	AX044227	AX044227 Sequence
c	77	11.6	26	6	AX044248	AX044248 Sequence
c	78	11.6	36	6	BD259716	BD259716 Regulatio
c	79	11.6	36	6	BD259812	BD259812 Regulatio
c	80	11.6	37	6	AR492124	AR492124 Sequence
c	81	11.6	37	6	AX581783	AX581783 Sequence
c	82	11.6	37	6	AX581844	AX581844 Sequence
c	83	11.6	37	6	BD095159	BD095159 Novel met
c	84	11.6	38	6	AR334011	AR334011 Sequence
c	85	11.6	38	6	AR334672	AR334672 Sequence
c	86	11.6	38	6	AR334753	AR334753 Sequence
c	87	11.6	38	6	AR334978	AR334978 Sequence
c	88	11.6	38	6	AR334994	AR334994 Sequence
c	89	11.6	38	6	AR335787	AR335787 Sequence
c	90	11.6	38	6	AR336048	AR336048 Sequence
c	91	11.6	38	6	AX219110	AX219110 Sequence
c	92	11.6	38	6	AX219178	AX219178 Sequence

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C 94	11.6	55.2	38	6	AX219192	Sequence	AR437607	Sequence
C 95	11.6	55.2	38	6	AX219200	Sequence	AR437607	Sequence
C 96	11.6	55.2	38	6	AX219271	Sequence	AR437607	Sequence
C 97	11.6	55.2	38	6	AX219280	Sequence	AR437607	Sequence
C 98	11.6	55.2	38	6	AX219292	Sequence	AR437607	Sequence
C 99	11.6	55.2	38	6	AX219431	Sequence	AR437607	Sequence
C 100	11.6	55.2	38	6	AX219808	Sequence	AR437607	Sequence
C 101	11.6	55.2	38	6	AX219850	Sequence	AR437607	Sequence
C 102	11.6	55.2	38	6	AX273715	Sequence	AR437607	Sequence
C 103	11.6	55.2	38	6	AX273790	Sequence	AR437607	Sequence
C 104	11.6	55.2	38	6	AX424283	Sequence	AR437607	Sequence
C 105	11.6	55.2	38	6	AX424348	Sequence	AR437607	Sequence
C 106	11.6	55.2	38	6	AX424517	Sequence	AR437607	Sequence
C 107	11.6	55.2	38	6	AX424549	Sequence	AR437607	Sequence
C 108	11.6	55.2	38	6	AX424598	Sequence	AR437607	Sequence
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C 111	11.6	55.2	38	6	AX424661	Sequence	AR437607	Sequence
C 112	11.6	55.2	38	6	AX581097	Sequence	AR437607	Sequence
C 113	11.6	55.2	38	6	AX581155	Sequence	AR437607	Sequence
C 114	11.6	55.2	38	6	AX581516	Sequence	AR437607	Sequence
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C 116	11.6	55.2	39	6	AR205071	Sequence	AR437607	Sequence
C 117	11.6	55.2	39	6	AR452254	Sequence	AR437607	Sequence
C 118	11.4	54.3	15	6	BD208647	Sequence	AR437607	Sequence
C 119	11.4	54.3	22	6	BD103836	Sequence	AR437607	Sequence
C 120	11.4	54.3	24	6	AX289153	Sequence	AR437607	Sequence
C 121	11.4	54.3	24	6	AX445926	Sequence	AR437607	Sequence
C 122	11.4	54.3	27	6	AR477047	Sequence	AR437607	Sequence
C 123	11.4	54.3	27	6	AR203477	Sequence	AR437607	Sequence
C 124	11.4	54.3	28	6	AX034693	Sequence	AR437607	Sequence
C 125	11.4	54.3	28	6	AR034103	Sequence	AR437607	Sequence
C 126	11.4	54.3	37	6	AR009624	Sequence	AR437607	Sequence
C 127	11.4	54.3	44	6	AR009625	Sequence	AR437607	Sequence
C 128	11.4	54.3	44	6	AX672014	Sequence	AR437607	Sequence
C 129	11.2	53.3	17	6	AX761422	Sequence	AR437607	Sequence
C 130	11.2	53.3	17	6	AX718842	Sequence	AR437607	Sequence
C 131	11.2	53.3	18	6	AX718872	Sequence	AR437607	Sequence
C 132	11.2	53.3	18	6	BD107270	Nucleic a	AR437607	Sequence
C 133	11.2	53.3	24	6	BD107270	Sequence 14	AR437607	Sequence
C 134	11.2	53.3	28	6	A63970	Sequence	AR437607	Sequence
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C 136	11.2	53.3	29	6	BD176654	Promoter.	AR437607	Sequence
C 137	11.2	53.3	30	6	BD184212	Method an	AR437607	Sequence
C 138	11.2	53.3	30	6	AX742388	Sequence	AR437607	Sequence
C 139	11.2	53.3	31	6	AR195923	Sequence	AR437607	Sequence
C 140	11.2	53.3	31	6	AX248728	Sequence	AR437607	Sequence
C 141	11.2	53.3	34	6	AR175461	Sequence	AR437607	Sequence
C 142	11.2	53.3	34	6	BD234326	Determina	AR437607	Sequence
C 143	11.2	53.3	37	6	AX581827	Sequence	AR437607	Sequence
C 144	11.2	53.3	38	6	AR455819	Sequence	AR437607	Sequence
C 145	11.2	53.3	38	6	AX351230	Sequence	AR437607	Sequence
C 146	11.2	53.3	42	6	A36511	Sequence 52	AR437607	Sequence
C 147	11.2	53.3	42	6	AR080144	Sequence	AR437607	Sequence
C 148	11.2	53.3	45	6	AX232635	Sequence	AR437607	Sequence
C 149	11.2	53.3	48	6	AR363852	Sequence	AR437607	Sequence
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C 151	11.2	53.3	48	6	AX583392	Sequence	AR437607	Sequence
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C 156	11.2	53.3	17	6	AR326427	Sequence	AR437607	Sequence
C 157	11.2	53.3	17	6	AR326428	Sequence	AR437607	Sequence
C 158	11.2	53.3	20	6	AR295140	Sequence	AR437607	Sequence
C 159	11.2	53.3	20	6	AR314966	Sequence	AR437607	Sequence
C 160	11.2	53.3	21	6	C0798984	Sequence	AR437607	Sequence
C 161	11.2	53.3	24	6	AR084197	Sequence	AR437607	Sequence
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C 163	11.2	53.3	24	6	AR211660	Sequence	AR437607	Sequence
C 164	11.2	53.3	24	6	AR252691	Sequence	AR437607	Sequence
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C 304	11	52.4	38	6	AX219343	Sequence	AX219343	Sequence	C 377	11	52.4	38	6	AX424913	Sequence
C 305	11	52.4	38	6	AX219382	Sequence	AX219382	Sequence	C 378	11	52.4	38	6	AX424922	Sequence
C 306	11	52.4	38	6	AX219420	Sequence	AX219420	Sequence	C 379	11	52.4	38	6	AX580655	Sequence
C 307	11	52.4	38	6	AX219429	Sequence	AX219429	Sequence	C 380	11	52.4	38	6	AX580944	Sequence
C 308	11	52.4	38	6	AX219511	Sequence	AX219511	Sequence	C 381	11	52.4	38	6	AX580980	Sequence
C 309	11	52.4	38	6	AX219521	Sequence	AX219521	Sequence	C 382	11	52.4	38	6	AX580995	Sequence
C 310	11	52.4	38	6	AX219523	Sequence	AX219523	Sequence	C 383	11	52.4	38	6	AX581018	Sequence
C 311	11	52.4	38	6	AX219543	Sequence	AX219543	Sequence	C 384	11	52.4	38	6	AX581093	Sequence

C 385	11	52.4	38	6	AX581157	Sequence	C 458	10.6	50.5	18	6	BD250577	Identific
C 386	11	52.4	38	6	AX581200	Sequence	C 459	10.6	50.5	18	6	AR215579	Sequence
C 387	11	52.4	38	6	AX581242	Sequence	C 460	10.6	50.5	18	6	AR293681	Sequence
C 388	11	52.4	38	6	AX581278	Sequence	C 461	10.6	50.5	18	6	AX498002	Sequence
C 389	11	52.4	38	6	AX581286	Sequence	C 462	10.6	50.5	19	6	CQ798895	Sequence
C 390	11	52.4	38	6	AX581302	Sequence	C 463	10.6	50.5	20	6	AX295232	Sequence
C 391	11	52.4	38	6	AX581352	Sequence	C 464	10.6	50.5	20	6	AX296546	Sequence
C 392	11	52.4	38	6	AX581365	Sequence	C 465	10.6	50.5	21	6	AX963392	Sequence
C 393	11	52.4	38	6	AX581446	Sequence	C 466	10.6	50.5	22	6	AX922710	Sequence
C 394	11	52.4	38	6	AX581446	Sequence	C 467	10.6	50.5	24	6	AX56684	Sequence
C 395	11	52.4	40	6	AR095875	Sequence	C 468	10.6	50.5	24	6	BD260387	Methods.
C 396	11	52.4	40	6	AR167230	Sequence	C 469	10.6	50.5	24	6	AR261951	Sequence
C 397	11	52.4	40	6	AR361064	Sequence	C 470	10.6	50.5	24	6	AX044332	Sequence
C 398	11	52.4	40	6	AX767184	Sequence	C 471	10.6	50.5	24	6	AX181781	Sequence
C 399	11	52.4	40	6	AX767190	Sequence	C 472	10.6	50.5	24	6	AX290523	Sequence
C 400	11	52.4	42	6	AR007099	Sequence	C 473	10.6	50.5	24	6	AX290599	Sequence
C 401	11	52.4	42	6	AR034923	Sequence	C 474	10.6	50.5	24	6	AX231913	Sequence
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ACCESSION BD181363
VERSION BD181363.1 GI:30792281
KEYWORDS JP 2002335981-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 2 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2002335981-A/2
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/566,G01N33/58,
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SOURCE synthetic construct
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REFERENCE 1 (bases 1 to 21)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 17 26-NOV-2002;
COMMENT F HOFFMANN LA ROCHE AG
PN JP 2002335981-A/17
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/69,G01N33/50,G01N33/566,G01N33/58,
PC C12N15/00
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ACCESSION AX523943
VERSION AX523943.1 GI:25168874
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 2 04-SEP-2002;
FEATURES Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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DEFINITION Sequence 2 from Patent EP1236805.
ACCESSION AX524841
VERSION AX524841.1 GI:25169935
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Jaeger,S.
AUTHORS
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 2 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES
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/morganism="synthetic construct"
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/db_xref="taxon:32630"
/note="artificial sequence to exemplify principle"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 21; DB 6; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 21
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Db 1 TCGGTACGGTCTAATGACC 21
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RESULT 5
AX524856/c
LOCUS AX524856 21 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 17 from Patent EP1236805.
ACCESSION AX524856
VERSION AX524856.1 GI:25169950
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Jaeger,S.
AUTHORS
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 17 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial sequence to exemplify principle"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 21; DB 6; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 21
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Db 1 TCGGTACGGTCTAATGACC 21
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21 TCGGTACGGTCTAATGACC 1
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RESULT 6
BD227377/c
LOCUS BD227377 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD227377
VERSION BD227377.1 GI:33037147
KEYWORDS JP 2002522062-A/138.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 29)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,
Merberg,D., Treacy,M., Agostino,M.J., Ii,R.J.S., Spaulding,V.,
Wong,G.G., Clark,H.F. and Fechtel,K.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2002522062-A 138 23-JUL-2002;
GENETICS INSTITUTE INC
COMMENT OS Artificial Sequence
PN JP 2002522062-A/138
PD 23-JUL-2002
PF 13-AUG-1999 JP 2000565001
PR 14-AUG-1998 US 60/096622,17-AUG-1998 US 60/096815 PR
04-SEP-1998 US 60/099229,23-OCT-1998 US 60/105368 PR
08-JAN-1999 US 60/115234,12-FEB-1999 US 60/119931 PR
18-FEB-1999 US 60/120575,30-APR-1999 US 60/132020 PR
11-AUG-1999 US 60/148424
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS
PI RACIE,
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,
PI ROBERT J STEININGER II,VIKKI SPAULDING,GORDON G WONG,HILARY F
PI CLARK,
PI KIM FECHTEL
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
PC A61P7/00,
PC A61P7/02,A61P7/04,A61P7/06,A61P13/00,A61P29/00,A61P35/00, PC
A61P37/02,
PC A61P43/00,A61P43/00,C07K14/47,C12N5/10,C12P21/02,G01N33/15, PC
G01N33/50,
PC C12N15/00,C12N5/00,A61K37/02
CC oligonucleotide
CC biotinylated phosphoramidite residue
FH Key Location/Qualifiers
FT misc feature (2).
Location/Qualifiers
source
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/morganism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Best Local Similarity 80.0%; Pred.No.2.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
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Db 24 TGGAGTACTGCTTATGACC 5
|||||

RESULT 7
AX752106
LOCUS AX752106 30 bp DNA linear PAT 20-JUN-2003
DEFINITION Sequence 5 from Patent WO03035876.
ACCESSION AX752106
VERSION AX752106.1 GI:32134216
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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REFERENCE 1 Hepacivirus.
AUTHORS Krebs,A., John,M., Schuppan,D., Limmer,S. and Kreutzer,R.
TITLE Use of a double strand ribonucleic acid for treating an infection with a positive-strand rna-virus
JOURNAL Patent: WO 03035876-A 5 01-MAY-2003;
Ribopharma AG (DE)
FEATURES
source
1. .30
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"
ORIGIN
Query Match 61.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 8.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CGGTACGGTCTAATGAC 19
Db 15 CGGACGGTCTAATGAC 30
RESULT 8
AX295474 20 bp DNA linear PAT 21-NOV-2001
LOCUS
DEFINITION Sequence 7236 from Patent WO0179548.
ACCESSION AX295474
VERSION AX295474.1 GI:17057163
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7236 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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Query Match 60.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGGTACGGTCTAATGACCG 21
Db 2 CGGTCTGGTCTAGTGACGG 20
RESULT 9
AX290841 24 bp DNA linear PAT 21-NOV-2001
LOCUS
DEFINITION Sequence 2603 from Patent WO0179548.
ACCESSION AX290841
VERSION AX290841.1 GI:17052524
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 2603 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
Location/Qualifiers

1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGGTACGGTCTAATGACCG 21
Db 2 CGGTCTGGTCTAGTGACGG 20
RESULT 10
BD260345 26 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Methods.
ACCESSION BD260345
VERSION BD260345.1 GI:33070115
KEYWORDS JP 2002542803-A/102.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Windass,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S., Gibson,N.J., Theaker,J. and Stanger,C.P.
TITLE Methods
JOURNAL Patent: JP 2002542803-A 102 17-DEC-2002;
SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002542803-A/102
PD 17-DEC-2002
PF 26-APR-2000 JP 2000615395
PR 30-APR-1999 GB 9910100.8,13-MAR-2000 GB 0006004.6 PR
31-MAR-2000 GB 0007901.2
PI JOHN DAVID WINDASS,STEPHEN PAUL HEANEY,ANNABEL RENWICK, PI
DAVID MARK WHITCOMBE,STEPHEN LITTLE,NEIL JAMES GIBSON,JANE PI
THEAKER.
PI CAROLE PATRICIA STANGER
PC C12N15/09,C07K14/37,C12Q1/68,G01N33/566,G01N33/569,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
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Location/Qualifiers
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1. .26
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Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGGTACGGTCTAATGACC 20
Db 2 CGGTATGGTCAATGACC 20
RESULT 11
AX044290 26 bp DNA linear PAT 24-NOV-2000
LOCUS
DEFINITION Sequence 102 from Patent WO0066773.
ACCESSION AX044290
VERSION AX044290.1 GI:11343168
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

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REFERENCE
AUTHORS      Windass,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S.,
              Gibson,N.J., Theaker,J. and Stanger,C.P.
TITLE        Method of detection of cytochrome b mutations in fungi leading to
              resistance against anti-fungal agents
JOURNAL      Patent: WO 0066773-A 102 09-NOV-2000;
              ZENECA LIMITED (GB)
FEATURES
source       Location/Qualifiers
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              /note="Primer"

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Query Match      60.0%; Score 12.6; DB 6; Length 26;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Qy 2 CGCGTACGGTCTAATGACC 20
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Db 2 CGTGTATGGTCAAAATGAGC 20
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RESULT 12
AR168721
LOCUS         AR168721
DEFINITION   Sequence 17 from patent US 6287866.
ACCESSION    AR168721
VERSION      AR168721.1 GI:17904788
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.

REFERENCE
AUTHORS      Mukerji,P., Lemmel,S.A., Leonard,A.Eun.-Yeong. and Chaudhary,S.
TITLE        .beta.-casein expressing constructs
JOURNAL      Patent: US 6287866-A 17 11-SEP-2001;
              Location/Qualifiers
FEATURES
source       1..31
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Qy 3 CGGTACGGTCTTAATGACCG 21
    |||||
Db 12 GAGTACTGTCTCATGAGCG 30
    |||||

RESULT 13
AR047950
LOCUS         AR047950
DEFINITION   Sequence 29 from patent US 5820866.
ACCESSION    AR047950
VERSION      AR047950.1 GI:5970293
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.

REFERENCE
AUTHORS      Kappler,J.W. and Marrack,P.
TITLE        Product and process for T cell regulation
JOURNAL      Patent: US 5820866-A 29 13-OCT-1998;
              Location/Qualifiers
FEATURES
source       1..33
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

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ACCESSION AR336409
VERSION AR336409.1 GI:33722217
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 13811 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 1 TCGGTACGGTCTAATGACC 20
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Db 35 TCGCNTTCGGCCTAACGGCC 16
RESULT 17
AR455837
LOCUS AR455837 38 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 83 from patent US 6686154.
ACCESSION AR455837
VERSION AR455837.1 GI:42690729
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: US 6686154-A 83 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 2 CGGTACGGTCTAATGACC 20
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Db 12 CGCGGACATTGTAATGACC 30
RESULT 18
AX219207/c
LOCUS AX219207 38 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 4649 from Patent WO0159103.
ACCESSION AX219207
VERSION AX219207.1 GI:15546931
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 4649 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
modified_base 31
/mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 1 TCGGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16
RESULT 19
AX219231/c
LOCUS AX219231 38 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 4673 from Patent WO0159103.
ACCESSION AX219231
VERSION AX219231.1 GI:15546955
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 4673 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
modified_base 31
/mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05; 5; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 1 TCGGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16
RESULT 20
AX351248
LOCUS AX351248 38 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 83 from Patent WO0194950.
ACCESSION AX351248
VERSION AX351248.1 GI:18616596
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell culture
JOURNAL Patent: WO 0194950-A 83 13-DEC-2001;
Zymyx, Inc. (US)
FEATURES Location/Qualifiers
source 1..38

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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="MWK24 primer"

ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTTAATGACC 20
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Db 12 CGCGGACATTGTAATGACC 30

RESULT 21
AX424618/c
LOCUS      AX424618      38 bp      RNA
DEFINITION Sequence 2954 from Patent WO0188124.
ACCESSION  AX424618
VERSION     AX424618.1 GI:21528000
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
           Randi, A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 2954 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES   source
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           /db_xref="taxon:32630"
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misc_feature 31
           /note="n stands for inosine"

ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TC CGGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 22
AX424731/c
LOCUS      AX424731      38 bp      RNA
DEFINITION Sequence 3067 from Patent WO0188124.
ACCESSION  AX424731
VERSION     AX424731.1 GI:21528113
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
           Randi, A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 3067 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES   source
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           /db_xref="taxon:32630"
           /note="Enzymatic Nucleic Acid"
misc_feature 31
           /note="n stands for inosine"

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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TC CGGTACGGTCTTAATGACC 20
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Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 23
AX581188/c
LOCUS      AX581188      38 bp      RNA
DEFINITION Sequence 3026 from Patent WO0211674.
ACCESSION  AX581188
VERSION     AX581188.1 GI:27652998
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
           and Grupe, A.
TITLE      Method and reagent for the inhibition of calcium activated chloride
           channel-1 (clca-1)
JOURNAL    Patent: WO 0211674-A 3026 14-FEB-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
           Thompson, James (US)
FEATURES   source
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           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Enzymatic Nucleic Acid"
modified_base 31
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ORIGIN
Query Match      60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TC CGGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 24
AX581359/c
LOCUS      AX581359      38 bp      RNA
DEFINITION Sequence 3197 from Patent WO0211674.
ACCESSION  AX581359
VERSION     AX581359.1 GI:27653169
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
           and Grupe, A.
TITLE      Method and reagent for the inhibition of calcium activated chloride
           channel-1 (clca-1)
JOURNAL    Patent: WO 0211674-A 3197 14-FEB-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
           Thompson, James (US)
FEATURES   source
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           /organism="synthetic construct"
           /mol_type="unassigned RNA"
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           /note="Enzymatic Nucleic Acid"

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modified_base 31 /mod_base=i
ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTTAATGACC 20
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Db 35 TCGCNTTGGCTTAACGGCC 16

RESULT 25
AX291100 A65234 42 bp DNA linear PAT 29-MAR-1999
LOCUS A65234/c
DEFINITION Sequence 5 from Patent WO9735011.
ACCESSION A65234
VERSION A65234.1 GI:4531029
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Silvestrini, M.C., Cutruzzola, F., Ciabatti, Ilaria, Zennaro, E.,
        Visco, C., Discepolo and Massimo.
TITLE RECOMBINANT PROCESS FOR THE PRODUCTION IN PSEUDOMONAS PUTIDA OF THE
        CYTOCHROME C551 OF PSEUDOMONAS AERUGINOSA
JOURNAL Patent: WO 9735011-A 5 25-SEP-1997;
        MINI RICERCA SCIENIT TECNOLOG (IT)
COMMENT Other publication IT MI960515 19970915.
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

ORIGIN
Query Match 60.0%; Score 12.6; DB 6; Length 42;
Best Local Similarity 78.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAATGACCG 21
    |||||
Db 37 GCGTACGGTTTCATCAGG 19

RESULT 26
AX295733 AX295733 20 bp DNA linear PAT 21-NOV-2001
LOCUS AX295733
DEFINITION Sequence 7495 from Patent WO0179548.
ACCESSION AX295733
VERSION AX295733.1 GI:17057422
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
        sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7495 25-OCT-2001;
        CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Hypothetical Probe Sequence"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAAT 16
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Db 2 GCGCACGGTCTTAAT 15

RESULT 27
AX291100 AX291100 24 bp DNA linear PAT 21-NOV-2001
LOCUS AX291100
DEFINITION Sequence 2862 from Patent WO0179548.
ACCESSION AX291100
VERSION AX291100.1 GI:17052783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
        sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 2862 25-OCT-2001;
        CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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    /organism="synthetic construct"
    /mol_type="unassigned DNA"
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    /note="Hypothetical Probe Sequence"

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Best Local Similarity 92.9%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAAT 16
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Db 2 GCGCACGGTCTTAAT 15

RESULT 28
AX464504 AX464504 34 bp DNA linear PAT 16-JUL-2002
LOCUS AX464504
DEFINITION Sequence 39 from Patent EP1219635.
ACCESSION AX464504
VERSION AX464504.1 GI:21899300
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Couture, F., Hamel, J., Brodeur, B.R. and Martin, D.
TITLE Chlamydia pneumoniae antigens
JOURNAL Patent: EP 1219635-A 39 03-JUL-2002;
        SHIRE BIOCHEM INC. (CA)
FEATURES
    source
    1..34
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="oligonucleotide primer"

ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 34;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGTACGGTCTTAATG 17
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Db 21 CGTACGGTCTTAGG 34

RESULT 29
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AR046887 AR046887 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1680 from patent US 5817796.
DEFINITION AR046887
ACCESSION AR046887
VERSION AR046887.1 GI:5968352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2',5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1680 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GTACGGTCTAATGA 18
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Db 2 GTACGGTCTGATGA 15
RESULT 30
I53939 I53939 38 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1680 from patent US 5646042.
DEFINITION I53939
ACCESSION I53939
VERSION I53939.1 GI:2475142
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1680 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GTACGGTCTAATGA 18
|||||
Db 2 GTACGGTCTGATGA 15
RESULT 31
AX220204 AX220204 38 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 5646 from Patent WO0159103.
DEFINITION AX220204
ACCESSION AX220204
VERSION AX220204.1 GI:15547928
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 5646 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ACGGTCTAATGACC 20
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Db 24 AAGGTCTAATGACC 37
RESULT 32
AR314417 AR314417 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 4954 from patent US 6559294.
DEFINITION AR314417
ACCESSION AR314417
VERSION AR314417.1 GI:31707843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4954 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CGCGTACGGTCTAATGA 18
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Db 2 CGCGTACGGTCTAATGA 18
RESULT 33
AR364921 AR364921 21 bp DNA linear PAT 03-SEP-2003
LOCUS Sequence 8 from patent US 5451502.
DEFINITION AR364921
ACCESSION AR364921
VERSION AR364921.1 GI:34428117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS George,A.L. Jr.
TITLE Restriction amplification assay
JOURNAL Patent: US 5451502-A 8 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TCGCGTACGGTCTAATG 17

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5 TCGCTAGGTCGAATG 21

Db

RESULT 34
AX392054
LOCUS AX392054 linear PAT 23-MAR-2002
DEFINITION Sequence 13 from Patent WO0215920.
ACCESSION AX392054
VERSION AX392054.1 GI:19700558
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ward,S.B., Bavik,C.B., Cork,M.B. and Tazi-Ahmini,R.B.
TITLE Treatment of hyperproliferative diseases
JOURNAL Patent: WO 0215920-A 13 28-FEB-2002;
THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGAC 19
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Db 2 GCTCAGGCTTATGAC 18

RESULT 35
AX755148/c
LOCUS AX755148 linear PAT 23-JUN-2003
DEFINITION Sequence 29 from Patent WO03025003.
ACCESSION AX755148
VERSION AX755148.1 GI:32167628
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 29 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 32;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTTAATG 17
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Db 17 TCGGGCGGCTCTTAATG 1

RESULT 36
AX755156/c
LOCUS AX755156 linear PAT 23-JUN-2003
DEFINITION Sequence 37 from Patent WO03025003.

AX755156 GI:32167636
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.
TITLE Vaccines
JOURNAL Patent: WO 03025003-A 37 27-MAR-2003;
GLAXO GROUP LIMITED (GB)
FEATURES
source
1..32
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="PCR primer"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 32;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTTAATG 17
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Db 17 TCGGGCGGCTCTTAATG 1

RESULT 37
AX351239
LOCUS AX351239 37 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 74 from Patent WO0194950.
ACCESSION AX351239
VERSION AX351239.1 GI:18616587
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Nock,S. and Kassner,P.D.
TITLE Screening of phage displayed peptides without clearing of the cell
JOURNAL Patent: WO 0194950-A 74 13-DEC-2001;
Zyomix, Inc. (US)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="MVK15 primer"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 37;
Best Local Similarity 73.7%; Pred. No. 1.7e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGACC 20
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Db 12 CGCGGACATTTTGATGACC 30

RESULT 38
AX581788
LOCUS AX581788 37 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 3626 from Patent WO0211674.
ACCESSION AX581788
VERSION AX581788.1 GI:27653598
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3626 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CGCGTACGGTCTAATGA 18
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Db 18 CGAGTGAGGCTCTAATGA 34
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RESULT 39
AX581793 37 bp RNA linear PAT 10-JAN-2003
LOCUS
DEFINITION Sequence 3631 from Patent WO0211674.
ACCESSION AX581793
VERSION AX581793.1 GI:27653603
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3631 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..37
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
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Query Match 58.1%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CGCGTACGGTCTAATGA 18
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Db 18 CGAGTGAGGCTCTAATGA 34
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RESULT 40
AX581826 37 bp RNA linear PAT 10-JAN-2003
LOCUS
DEFINITION Sequence 3664 from Patent WO0211674.
ACCESSION AX581826
VERSION AX581826.1 GI:27653636
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride

channel-1 (clca-1)
Patent: WO 0211674-A 3664 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
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Query Match 58.1%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CGCGTACGGTCTAATGA 18
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Db 18 CGAGTGAGGCTCTAATGA 34
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Job time : 381.157 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 112.708 Seconds
(without alignments)
978.085 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21

Sequence: 1 tcgcgtacggtctaatgacgc 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	67.6	25	9	ACI56056 Human mic
C 2	13.6	64.8	29	3	AAA16755 Human sec
C 3	13.4	63.8	25	9	ACI09445 Human mic
C 4	13.2	62.9	25	9	ACI18862 Human mic
C 5	13.2	62.9	25	9	ACI188244 Human mic
C 6	13.2	62.9	35	2	AAV61559 Adaptor N
C 7	13.2	62.9	37	6	ACN31831 WNV minus
C 8	13.2	62.9	39	2	AAV61560 Adaptor N
C 9	13.2	61.0	25	9	ACI171017 Human mic
C 10	12.8	61.0	30	10	ADD12949 HCV NS3 p
C 11	12.8	61.0	20	6	AB195516 Capture o
C 12	12.6	60.0	24	6	AB187602 Capture o
C 13	12.6	60.0	24	6	AB187603 Capture o
C 14	12.6	60.0	25	9	ACI125753 Human mic
C 15	12.6	60.0	25	9	ACK18838 Human mic
C 16	12.6	60.0	25	9	ACK18838 Human mic
C 17	12.6	60.0	25	9	ACI56057 Human mic
C 18	12.6	60.0	25	9	ACK18839 Human mic
C 19	12.6	60.0	26	4	AAV97127 Cytochrom
C 20	12.6	60.0	31	3	AAZ50914 PCR primer
C 21	12.6	60.0	33	2	AAT04264 Primer #2

22	12.6	60.0	36	8	ACA10066	Acad0066 Necrosis
23	12.6	60.0	36	8	ACD66384	Anti-HCV
24	12.6	60.0	37	6	ACN19551	WNV Zinz
25	12.6	60.0	37	6	ACN31602	WNV Zinz
26	12.6	60.0	37	6	ACN19001	WNV Zinz
27	12.6	60.0	37	8	ACA07993	Necrosis
28	12.6	60.0	38	4	ABK04673	Human NOG
29	12.6	60.0	38	4	ABK04649	Human NOG
30	12.6	60.0	38	6	ABQ72447	PCR prime
31	12.6	60.0	38	6	ABK20307	Human ERG
32	12.6	60.0	38	6	ABK20420	Human ERG
33	12.6	60.0	38	6	ABK58655	Human CLC
34	12.6	60.0	38	6	ABK58826	Human CLC
35	12.6	60.0	38	6	ACN17900	WNV Inoz
36	12.6	60.0	38	6	ACN17240	WNV Inoz
37	12.6	60.0	38	6	ACN16711	WNV Inoz
38	12.6	60.0	38	6	ACN30373	WNV minus
39	12.6	60.0	38	6	ACN29690	WNV minus
40	12.6	60.0	38	6	ACN27931	WNV minus
41	12.6	60.0	38	6	ACN29837	WNV minus
42	12.6	60.0	38	6	ACN16782	WNV Inoz
43	12.6	60.0	38	6	ACN17833	WNV Inoz
44	12.6	60.0	38	6	ACN29184	WNV minus
45	12.6	60.0	38	6	ACN29870	WNV minus
46	12.6	60.0	38	8	ACA07350	Necrosis
47	12.6	60.0	38	8	ACD52230	HBV inoz
48	12.6	60.0	38	8	ACD52781	HBV inoz
49	12.6	60.0	38	11	ADL75366	Human PTG
50	12.6	60.0	38	11	ADL75456	Human PTG
51	12.6	60.0	38	11	ADL75286	Human PTG
52	12.6	60.0	38	12	ADM61334	Hepatitis
53	12.6	60.0	38	12	ADM61630	Hepatitis
54	12.6	60.0	40	2	AAT86270	P. aerugi
55	12.4	59.0	42	6	AB195775	Capture o
56	12.4	59.0	24	6	AB188121	Capture o
57	12.4	59.0	24	6	AB188120	Capture o
58	12.4	59.0	32	12	ADH36452	Human pur
59	12.4	59.0	34	6	ABQ92506	C. pneumo
60	12.4	59.0	38	4	ABK05646	Human NOG
61	12.2	58.1	20	2	AAV95628	PCR prime
62	12.2	58.1	25	9	ACI17482	Human mic
63	12.2	58.1	25	9	ACI27184	Human mic
64	12.2	58.1	25	9	ACI26438	Human mic
65	12.2	58.1	25	9	ACI36708	Human mic
66	12.2	58.1	32	10	ACC69881	HIV-1 pla
67	12.2	58.1	32	10	ACC69889	HIV-1 pla
68	12.2	58.1	32	12	ADH56317	Retroviro
69	12.2	58.1	34	12	ADN00529	Anti-apol
70	12.2	58.1	34	12	ADM98149	Anti-apol
71	12.2	58.1	37	6	ABQ72438	PCR prime
72	12.2	58.1	37	6	ABK59293	Human CLC
73	12.2	58.1	37	6	ABK59255	Human CLC
74	12.2	58.1	37	6	ABK59260	Human CLC
75	12.2	58.1	37	6	ACN31660	WNV minus
76	12.2	58.1	40	12	ADH56313	A. thalia
77	12.2	58.1	41	3	AAZ48334	Primer sp
78	12.2	58.1	41	4	AAH45154	Human pro
79	12.2	58.1	20	10	ADK66022	Standardi
80	12.2	58.1	21	2	AAV32506	GAPDH CDN
81	12.2	58.1	23	9	ADA22715	Human GAP
82	12.2	58.1	25	9	ACK22315	Human mic
83	12.2	58.1	25	9	ACI03832	Human mic
84	12.2	58.1	25	9	ACK16701	Human mic
85	12.2	58.1	25	9	ACK28413	Human mic
86	12.2	58.1	25	9	ACI68761	Human mic
87	12.2	58.1	25	9	ACI03833	Human mic
88	12.2	58.1	25	9	ACI16661	Human mic
89	12.2	58.1	29	4	AAI70164	Human uro
90	12.2	58.1	29	5	AAH43542	Primer 12
91	12.2	58.1	29	5	AAH87256	Fusion pr
92	12.2	58.1	32	3	AAV55266	GAPDH qow
93	12.2	58.1	32	3	AAZ36904	PCR prime
94	12.2	58.1	36	6	ABX01948	HCV hamme

c 95	12	57.1	36	6	ABX02182	Abx02182 HCV hamme	c 168	11.6	55.2	25	9	ACI00796	AcI00796 Human mic
c 96	12	57.1	36	6	ABX02155	Abx02155 HCV hamme	c 169	11.6	55.2	25	9	ACI88245	AcI88245 Human mic
c 97	12	57.1	36	6	ABX02284	Abx02284 HCV hamme	c 170	11.6	55.2	26	4	AAC97085	Aac97085 Cytochrom
c 98	12	57.1	37	6	ABX59280	Abx59280 Human ClC	c 171	11.6	55.2	26	4	AAC97064	Aac97064 Cytochrom
99	12	57.1	37	6	ACN19032	Acn19032 WNV Zinz	c 172	11.6	55.2	32	12	ADOS9622	Ado59622 HCV RNA p
100	12	57.1	37	6	ACN30898	Acn30898 WNV minus	c 173	11.6	55.2	32	12	ADOS9629	Ado59629 HCV RNA p
101	12	57.1	37	6	ACN18814	Acn18814 WNV Zinz	c 174	11.6	55.2	32	12	ADOS9633	Ado59633 HCV RNA p
102	12	57.1	37	6	ACN18893	Acn18893 WNV Zinz	c 175	11.6	55.2	32	12	ADOS9625	Ado59625 HCV RNA p
103	12	57.1	37	6	ACN19198	Acn19198 WNV Zinz	c 176	11.6	55.2	32	12	ADOS9628	Ado59628 HCV RNA p
104	12	57.1	37	6	ACN30720	Acn30720 WNV minus	c 177	11.6	55.2	32	12	ADOS9635	Ado59635 HCV RNA p
105	12	57.1	37	6	ACN19979	Acn19979 WNV Zinz	c 178	11.6	55.2	32	12	ADOS9632	Ado59632 HCV RNA p
106	12	57.1	37	6	ACN31491	Acn31491 WNV minus	c 179	11.6	55.2	32	12	ADOS9624	Ado59624 HCV RNA p
107	12	57.1	37	6	ACN31195	Acn31195 WNV minus	c 180	11.6	55.2	32	12	ADOS9630	Ado59630 HCV RNA p
108	12	57.1	37	6	ACN31240	Acn31240 WNV minus	c 181	11.6	55.2	32	12	ADOS9634	Ado59634 HCV RNA p
109	12	57.1	37	8	ACA08151	AcA08151 Necrosis	c 182	11.6	55.2	32	12	ADOS9636	Ado59636 HCV RNA p
110	12	57.1	37	11	ADL52699	AdL52699 Human NOG	c 183	11.6	55.2	32	12	ADOS9623	Ado59623 HCV RNA p
111	12	57.1	37	11	ADL54425	AdL54425 Human IKK	c 184	11.6	55.2	32	12	ADOS9627	Ado59627 HCV RNA p
112	12	57.1	37	11	ADL73501	AdL73501 Human PKR	c 185	11.6	55.2	32	12	ADOS9631	Ado59631 HCV RNA p
c 113	12	57.1	37	11	ADL73524	AdL73524 Human PKR	c 186	11.6	55.2	32	12	ADOS9626	Ado59626 HCV RNA p
c 114	12	57.1	38	6	ABX58095	Abx58095 Human ClC	c 187	11.6	55.2	34	8	ACA10065	AcA10065 Necrosis
c 115	12	57.1	38	6	ACN27173	Acn27173 WNV minus	c 188	11.6	55.2	35	2	AAV61557	Aav61557 Adaptor N
c 116	12	57.1	38	6	ACN16487	Acn16487 WNV Hamme	c 189	11.6	55.2	36	12	ADI59444	AdI59444 Incozyme s
c 117	12	57.1	38	6	ACN27061	Acn27061 WNV minus	c 190	11.6	55.2	37	5	AAH41019	Aah41019 PCR prime
c 118	12	57.1	38	6	ACN27710	Acn27710 WNV minus	c 191	11.6	55.2	37	6	ABK59250	Abk59250 Human ClC
c 119	12	57.1	38	6	ACN16108	Acn16108 WNV Hamme	c 192	11.6	55.2	37	6	ABK59311	Abk59311 Human ClC
c 120	12	57.1	38	6	ACN16340	Acn16340 WNV Hamme	c 193	11.6	55.2	37	6	ACN31481	Acn31481 WNV minus
c 121	12	57.1	38	6	ACN16550	Acn16550 WNV Hamme	c 194	11.6	55.2	37	6	ACN30995	Acn30995 WNV minus
c 122	12	57.1	38	6	ACN16547	Acn16547 WNV Hamme	c 195	11.6	55.2	37	6	ACN31582	Acn31582 WNV minus
c 123	12	57.1	38	6	ACD51020	AcD51020 HBV hamme	c 196	11.6	55.2	37	6	ACN30780	Acn30780 WNV minus
c 124	12	57.1	38	11	ADL53578	AdL53578 Human IKK	c 197	11.6	55.2	37	6	ACN31436	Acn31436 WNV minus
c 125	12	57.1	38	11	ADL56069	AdL56069 Human PKR	c 198	11.6	55.2	37	6	ACN37009	Acn37009 WNV enzym
c 126	12	57.1	38	11	ADL55761	AdL55761 Human PKR	c 199	11.6	55.2	37	6	ACN31816	Acn31816 WNV minus
c 127	12	57.1	38	12	ADM60741	AdM60741 Hepatitis	c 200	11.6	55.2	37	6	ACN31773	Acn31773 WNV minus
c 128	12	57.1	45	2	AAx83391	Aax83391 Mouse pro	c 201	11.6	55.2	37	11	ADL54295	AdL54295 Human IKK
c 129	12	57.1	50	8	ABZ68287	Abz68287 Nucleotid	c 202	11.6	55.2	38	4	ABK04734	Abk04734 Human NOG
c 130	12	57.1	50	10	ADD31953	AdD31953 BBP-Bix a	c 203	11.6	55.2	38	4	ABK04713	Abk04713 Human NOG
c 131	11.8	56.2	15	3	AAZ64070	Aaz64070 Substrate	c 204	11.6	55.2	38	4	ABK04626	Abk04626 Human NOG
c 132	11.8	56.2	15	6	ABX01123	Abx01123 Hepatitis	c 205	11.6	55.2	38	4	ABK05250	Abk05250 Human NOG
c 133	11.8	56.2	17	8	ACD59069	AcD59069 HCV DNaz	c 206	11.6	55.2	38	4	ABK05292	Abk05292 Human NOG
c 134	11.8	56.2	17	12	ADI83905	AdI83905 HCV DNaz	c 207	11.6	55.2	38	4	ABK04552	Abk04552 Human NOG
c 135	11.8	56.2	25	9	ACI98341	AcI98341 Human mic	c 208	11.6	55.2	38	4	ABK04620	Abk04620 Human NOG
c 136	11.8	56.2	25	9	ACI36939	AcI36939 Human mic	c 209	11.6	55.2	38	4	ABK04722	Abk04722 Human NOG
c 137	11.8	56.2	25	9	ACI28871	AcI28871 Human mic	c 210	11.6	55.2	38	4	ABK04634	Abk04634 Human NOG
c 138	11.8	56.2	25	9	ACI09444	AcI09444 Human mic	c 211	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
c 139	11.8	56.2	25	9	ACI20469	AcI20469 Human mic	c 212	11.6	55.2	38	4	ABK04662	Abk04662 Human NOG
c 140	11.8	56.2	25	9	ACI32881	AcI32881 Human mic	c 213	11.6	55.2	38	4	ABL47651	AbL47651 Human GRI
c 141	11.8	56.2	25	9	ACI87003	AcI87003 Human mic	c 214	11.6	55.2	38	4	ABL47726	AbL47726 Human GRI
c 142	11.8	56.2	28	2	AAI38250	Aat38250 Y. pestis	c 215	11.6	55.2	38	6	ABK20206	Abk20206 Human ERG
c 143	11.8	56.2	29	2	AAAI7888	Aaai7888 Human TIE	c 216	11.6	55.2	38	6	ABK20301	Abk20301 Human ERG
c 144	11.8	56.2	34	9	ACC83715	Acc83715 Fragile X	c 217	11.6	55.2	38	6	ABK20037	Abk20037 Human ERG
c 145	11.8	56.2	38	6	ACN16238	Acn16238 WNV Hamme	c 218	11.6	55.2	38	6	ABK20350	Abk20350 Human ERG
c 146	11.8	56.2	38	8	ACD51219	AcD51219 HBV hamme	c 219	11.6	55.2	38	6	ABK20238	Abk20238 Human ERG
c 147	11.8	56.2	38	12	ADM60838	AdM60838 Hepatitis	c 220	11.6	55.2	38	6	ABK19972	Abk19972 Human ERG
c 148	11.6	55.2	20	3	AAZ55942	Aaz55942 Xenopus l	c 221	11.6	55.2	38	6	ABK20342	Abk20342 Human ERG
c 149	11.6	55.2	20	6	ABI87571	Abi87571 Capture o	c 222	11.6	55.2	38	6	ABK20287	Abk20287 Human ERG
c 150	11.6	55.2	24	6	ABI87712	Abi87712 Capture o	c 223	11.6	55.2	38	6	ABK58983	Abk58983 Human ClC
c 151	11.6	55.2	24	6	ABI89805	Abi89805 Capture o	c 224	11.6	55.2	38	6	ABK58564	Abk58564 Human ClC
c 152	11.6	55.2	24	6	ABI89804	Abi89804 Capture o	c 225	11.6	55.2	38	6	ABK58622	Abk58622 Human ClC
c 153	11.6	55.2	24	6	ABI87713	Abi87713 Capture o	c 226	11.6	55.2	38	6	ACN17225	Acn17225 WNV Inozy
c 154	11.6	55.2	25	3	AAZ47402	Aaz47402 Forward p	c 227	11.6	55.2	38	6	ACN16832	Acn16832 WNV Inozy
c 155	11.6	55.2	25	9	ACK27505	Ack27505 Human mic	c 228	11.6	55.2	38	6	ACN17021	Acn17021 WNV Inozy
c 156	11.6	55.2	25	9	ACK09489	Ack09489 Human mic	c 229	11.6	55.2	38	6	ACN17078	Acn17078 WNV Inozy
c 157	11.6	55.2	25	9	ACI77375	AcI77375 Human mic	c 230	11.6	55.2	38	6	ACN18453	Acn18453 WNV Inozy
c 158	11.6	55.2	25	9	ACI72460	AcI72460 Human mic	c 231	11.6	55.2	38	6	ACN28674	Acn28674 WNV Inozy
c 159	11.6	55.2	25	9	ACI53846	AcI53846 Human mic	c 232	11.6	55.2	38	6	ACN17229	Acn17229 WNV Inozy
c 160	11.6	55.2	25	9	ACI77677	AcI77677 Human mic	c 233	11.6	55.2	38	6	ACN17823	Acn17823 WNV Inozy
c 161	11.6	55.2	25	9	ACI88863	AcI88863 Human mic	c 234	11.6	55.2	38	6	ACN18346	Acn18346 WNV Inozy
c 162	11.6	55.2	25	9	ACI00797	AcI00797 Human mic	c 235	11.6	55.2	38	6	ACN29827	Acn29827 WNV Inozy
c 163	11.6	55.2	25	9	ACK07040	Ack07040 Human mic	c 236	11.6	55.2	38	6	ACN18161	Acn18161 WNV Inozy
c 164	11.6	55.2	25	9	ACK07040	Ack07040 Human mic	c 237	11.6	55.2	38	6	ACN18372	Acn18372 WNV Inozy
c 165	11.6	55.2	25	9	ACI46353	AcI46353 Human mic	c 238	11.6	55.2	38	6	ACN28510	Acn28510 WNV minus
c 166	11.6	55.2	25	9	ACI33578	AcI33578 Human mic	c 239	11.6	55.2	38	6	ACN28957	Acn28957 WNV minus
c 167	11.6	55.2	25	9	ACK00389	Ack00389 Human mic	c 240	11.6	55.2	38	6	ACN30573	Acn30573 WNV minus

C 241	11.6	55.2	38	6	ACN16944	Acn16944 WNV Inocy	314	11.4	54.3	20	2	AAQ45350	Aaq45350 PCR prime
C 242	11.6	55.2	38	6	ACN18309	Acn18309 WNV Inocy	C 315	11.4	54.3	22	6	ABL31902	Ab131902 Human CYP
C 243	11.6	55.2	38	6	ACN18573	Acn18573 WNV Inocy	316	11.4	54.3	23	8	ABV75861	Abv75861 Arabidops
C 244	11.6	55.2	38	6	ACN17194	Acn17194 WNV Inocy	317	11.4	54.3	23	9	ABZ81234	Abz81234 Arabidops
C 245	11.6	55.2	38	6	ACN28445	Acn28445 WNV minus	318	11.4	54.3	23	10	ADH35553	Adh35553 H+ -ATPas
C 246	11.6	55.2	38	6	ACN30165	Acn30165 WNV minus	319	11.4	54.3	23	10	ADL18214	Adl18214 H+ -ATPas
C 247	11.6	55.2	38	6	ACN18467	Acn18467 WNV Inocy	C 320	11.4	54.3	24	6	ABQ08710	Abq08710 Oligonuc1
C 248	11.6	55.2	38	6	ACN18695	Acn18695 WNV Inocy	321	11.4	54.3	24	6	ABQ02374	Abq02374 Oligonuc1
C 249	11.6	55.2	38	6	ACN28523	Acn28523 WNV minus	322	11.4	54.3	24	6	ABQ08669	Abq08669 Oligonuc1
C 250	11.6	55.2	38	6	ACN29692	Acn29692 WNV minus	C 323	11.4	54.3	24	6	AB184227	Ab184227 Capture o
C 251	11.6	55.2	38	6	ACN29037	Acn29037 WNV minus	324	11.4	54.3	24	6	AB184226	Ab184226 Capture o
C 252	11.6	55.2	38	6	ACN28657	Acn28657 WNV minus	C 325	11.4	54.3	25	9	ACI56633	Ac156633 Human mic
C 253	11.6	55.2	38	6	ACN29459	Acn29459 WNV minus	326	11.4	54.3	25	9	ACK10586	Ack10586 Human mic
C 254	11.6	55.2	38	6	ACN29488	Acn29488 WNV minus	327	11.4	54.3	25	9	ACI89575	Ac189575 Human mic
C 255	11.6	55.2	38	6	ACN30357	Acn30357 WNV minus	328	11.4	54.3	25	9	ACI89574	Ac189574 Human mic
C 256	11.6	55.2	38	6	ACN18644	Acn18644 WNV Inocy	329	11.4	54.3	25	9	ACI71603	Ac171603 Human mic
C 257	11.6	55.2	38	6	ACN29655	Acn29655 WNV Inocy	C 330	11.4	54.3	25	9	ACK04317	Ack04317 Human mic
C 258	11.6	55.2	38	6	ACN29671	Acn29671 WNV minus	331	11.4	54.3	25	9	ACI34741	Ac134741 Human mic
C 259	11.6	55.2	38	6	ACN17594	Acn17594 WNV Inocy	332	11.4	54.3	25	9	ACK04457	Ack04457 Human mic
C 260	11.6	55.2	38	6	ACN29252	Acn29252 WNV minus	C 333	11.4	54.3	25	9	ACK21465	Ack21465 Human mic
C 261	11.6	55.2	38	6	ACN17438	Acn17438 WNV Inocy	C 334	11.4	54.3	25	9	ACI69299	Ac169299 Human mic
C 262	11.6	55.2	38	6	ACN17890	Acn17890 WNV Inocy	C 335	11.4	54.3	25	9	ACH61541	Ach61541 DNA targe
C 263	11.6	55.2	38	6	ACN16983	Acn16983 WNV Inocy	C 336	11.4	54.3	25	9	ACH54299	Ach54299 DNA targe
C 264	11.6	55.2	38	8	ACA07403	ACA07403 Necrosis	337	11.4	54.3	25	9	ACH56738	Ach56738 DNA targe
C 265	11.6	55.2	38	8	ACA07508	ACA07508 Necrosis	C 338	11.4	54.3	26	6	ABT11741	Abt11741 Drosoephil
C 266	11.6	55.2	38	8	ACA07040	ACA07040 Necrosis	339	11.4	54.3	27	8	ABT17185	Abt17185 Transcrip
C 267	11.6	55.2	38	8	ACA07037	ACA07037 Necrosis	C 340	11.4	54.3	27	8	ABT17184	Abt17184 Transcrip
C 268	11.6	55.2	38	8	ABZ66597	Abz66597 Human HIV	341	11.4	54.3	27	10	ADC60797	Adc60797 Cis eleme
C 269	11.6	55.2	38	8	ACD52161	AcD52161 HBV inocy	342	11.4	54.3	27	10	ADC60796	Adc60796 Cis eleme
C 270	11.6	55.2	38	8	ACD52955	AcD52955 HBV inocy	C 343	11.4	54.3	27	10	ADF48566	Adf48566 Cis-eleme
C 271	11.6	55.2	38	8	ACD52428	AcD52428 HBV inocy	344	11.4	54.3	27	10	ADF48567	Adf48567 Cis-eleme
C 272	11.6	55.2	38	8	ACD52650	AcD52650 HBV inocy	C 345	11.4	54.3	28	3	AAA64500	Aaa64500 PCR prime
C 273	11.6	55.2	38	8	ACD52433	AcD52433 HBV inocy	346	11.4	54.3	34	2	AAAX91910	Aax91910 Porphorym
C 274	11.6	55.2	38	8	ACD52468	AcD52468 HBV inocy	C 347	11.4	54.3	36	9	ADA50300	Ada50300 Human PCR
C 275	11.6	55.2	38	8	ACD53061	AcD53061 HBV inocy	348	11.4	54.3	37	2	ACN26208	Acn26208 Synthetic
C 276	11.6	55.2	38	11	ADL53906	Adl53906 Human IKK	349	11.4	54.3	38	6	ACN26511	Acn26511 WNV minus
C 277	11.6	55.2	38	11	ADL5242	Adl5242 Human PTG	350	11.4	54.3	42	2	AAQ28514	Aaq28514 Hypercalc
C 278	11.6	55.2	38	11	ADL75357	Adl75357 Human PTG	351	11.4	54.3	43	2	AAV34727	Aav34727 Recombina
C 279	11.6	55.2	38	11	ADL52170	Adl52170 Human NOG	352	11.4	54.3	43	2	AAV24315	Aav24315 Primer pP
C 280	11.6	55.2	38	11	ADL53903	Adl53903 Human IKK	C 353	11.2	53.3	17	10	ADB44420	Adb44420 Tumour su
C 281	11.6	55.2	38	11	ADL54002	Adl54002 Human IKK	C 354	11.2	53.3	17	10	ACC51692	Acc51692 Human tum
C 282	11.6	55.2	38	11	ADL75463	Adl75463 Human PTG	C 355	11.2	53.3	18	10	ADE15211	Adel15211 Beer spoi
C 283	11.6	55.2	38	11	ADL54079	Adl54079 Human IKK	C 356	11.2	53.3	18	10	ADE15241	Adel15241 Beer spoi
C 284	11.6	55.2	38	11	ADL75285	Adl75285 Human PTG	C 357	11.2	53.3	19	4	AAH50337	Aah50337 Bacterial
C 285	11.6	55.2	38	11	ADL75413	Adl75413 Human PTG	358	11.2	53.3	20	2	AAZ05198	Aaz05198 PCR prime
C 286	11.6	55.2	38	11	ADL52329	Adl52329 Human NOG	C 359	11.2	53.3	20	10	ADG20440	Adg20440 Aegilops
C 287	11.6	55.2	38	11	ADL52336	Adl52336 Human NOG	C 360	11.2	53.3	20	12	ADJ85254	Adj85254 Nucleic a
C 288	11.6	55.2	38	11	ADL52390	Adl52390 Human NOG	C 361	11.2	53.3	20	12	ADP44289	Adp44289 Human TEK
C 289	11.6	55.2	38	11	ADL75406	Adl75406 Human PTG	C 362	11.2	53.3	20	12	ADP44211	Adp44211 Human TEK
C 290	11.6	55.2	38	11	ADL52232	Adl52232 Human NOG	C 363	11.2	53.3	22	10	ADG20446	Adg20446 Aegilops
C 291	11.6	55.2	38	11	ADL56628	Adl56628 Human PKR	C 364	11.2	53.3	24	6	ABA99700	Abag99700 M. cerevi
C 292	11.6	55.2	38	11	ADL75325	Adl75325 Human PTG	C 365	11.2	53.3	25	9	ACI59270	Ac159270 Human mic
C 293	11.6	55.2	38	11	ADL54181	Adl54181 Human IKK	C 366	11.2	53.3	25	9	ACI34915	Ac134915 Human mic
C 294	11.6	55.2	38	11	ADL75218	Adl75218 Human PTG	C 367	11.2	53.3	25	9	ACI11940	Ac111940 Human mic
C 295	11.6	55.2	38	11	ADL52262	Adl52262 Human NOG	C 368	11.2	53.3	25	9	ACI26782	Ac126782 Human mic
C 296	11.6	55.2	38	11	ADL52304	Adl52304 Human NOG	C 369	11.2	53.3	25	9	ACI44103	Ac144103 Human mic
C 297	11.6	55.2	38	11	ADL75228	Adl75228 Human PTG	C 370	11.2	53.3	25	9	ACI72293	Ac172293 Human mic
C 298	11.6	55.2	38	11	ADL75251	Adl75251 Human PTG	C 371	11.2	53.3	25	9	ACI75169	Ac175169 Human mic
C 299	11.6	55.2	38	11	ADM54971	Adm54971 NCH riboz	C 372	11.2	53.3	25	9	ACI36189	Ac136189 Human mic
C 300	11.6	55.2	38	11	ADM55046	Adm55046 NCH riboz	C 373	11.2	53.3	25	9	ACK21477	Ack21477 Human mic
C 301	11.6	55.2	38	12	ADM61550	Adm61550 Hepatitis	C 374	11.2	53.3	25	9	ACI02089	Ac102089 Human mic
C 302	11.6	55.2	38	12	ADM61757	Adm61757 Hepatitis	C 375	11.2	53.3	25	9	ACI01027	Ac101027 Human mic
C 303	11.6	55.2	38	12	ADM61430	Adm61430 Hepatitis	C 376	11.2	53.3	25	9	ACI30581	Ac130581 Human mic
C 304	11.6	55.2	38	12	ADM61435	Adm61435 Hepatitis	C 377	11.2	53.3	25	9	ACI09687	Ac109687 Human mic
C 305	11.6	55.2	38	12	ADM61316	Adm61316 Hepatitis	C 378	11.2	53.3	25	9	ACI34418	Ac134418 Human mic
C 306	11.6	55.2	38	12	ADM61470	Adm61470 Hepatitis	C 379	11.2	53.3	25	9	ACK22045	Ack22045 Human mic
C 307	11.6	55.2	38	12	ADM61702	Adm61702 Hepatitis	C 380	11.2	53.3	25	9	ACI75771	Ac175771 Human mic
C 308	11.6	55.2	39	2	AAV61558	Aav61558 Adaptor N	C 381	11.2	53.3	25	9	ACI71016	Ac171016 Human mic
C 309	11.6	55.2	39	2	AZ231574	Az231574 PCR prime	C 382	11.2	53.3	25	9	ACK28588	Ack28588 Human mic
C 310	11.6	55.2	39	12	ADG16984	Adg16984 Anti-salm	C 383	11.2	53.3	25	9	ACK28589	Ack28589 Human mic
C 311	11.6	55.2	47	4	AAQ93008	Aaq93008 Infectiou	C 384	11.2	53.3	25	9	ACH51172	Ach51172 DNA targe
C 312	11.6	54.3	15	3	AZ264069	Az264069 Substrate	C 385	11.2	53.3	25	9	ACH59775	Ach59775 DNA targe
C 313	11.4	54.3	15	6	ABX01122	Abx01122 Hepatitis	C 386	11.2	53.3	25	9	ACH60780	Ach60780 DNA targe

C 387	11.2	53.3	25	9	ACH60892	Abc60892 DNA target	460	11	52.4	24	10	ADC57939	Adc57939 Human PRO
388	11.2	53.3	25	10	ABZ84510	Abz84510 Toxicology	461	11	52.4	24	10	ADC55303	Adc55303 Human PRO
389	11.2	53.3	28	2	AAT73081	Aat73081 UI snRNA	462	11	52.4	24	10	ADC12170	Adc12170 Human PRO
C 390	11.2	53.3	28	12	ADOL1376	Adol1376 Single mu	463	11	52.4	24	10	ADC56592	Adc56592 Human PRO
C 391	11.2	53.3	28	12	ADOL1426	Adol1426 Single mu	464	11	52.4	24	10	ADC07647	Adc07647 Human PRO
C 392	11.2	53.3	29	6	ABQ82513	Abq82513 Promoter	465	11	52.4	24	10	ADC11637	Adc11637 Human PRO
C 393	11.2	53.3	30	10	ADCB83961	Adcb83961 Human pap	466	11	52.4	24	10	ADC14759	Adc14759 Novel hum
C 394	11.2	53.3	30	10	ADF43834	Adf43834 HPV 39 de	467	11	52.4	24	10	ADD08291	Add08291 Human sec
C 395	11.2	53.3	31	2	AAT35700	Aat35700 3' VK pri	468	11	52.4	24	10	ADC82116	Adc82116 Human PRO
C 396	11.2	53.3	31	2	AAx62513	Aax62513 Granule b	469	11	52.4	24	10	AD007758	Ad007758 Human PRO
C 397	11.2	53.3	34	3	AAA62282	Aaa62282 Sample ol	470	11	52.4	24	10	ADC82649	Adc82649 Human PRO
C 398	11.2	53.3	37	6	ABK59294	Abk59294 Human CLC	471	11	52.4	24	10	ADD008829	Add008829 Human sec
C 399	11.2	53.3	37	6	ACN19390	Acn19390 WNV Zinz	472	11	52.4	24	10	ADD007078	Add007078 Human PRO
C 400	11.2	53.3	37	6	ACN30875	Acn30875 WNV minus	473	11	52.4	24	10	ADC83325	Adc83325 Human PRO
C 401	11.2	53.3	37	6	ACN19673	Acn19673 WNV Zinz	474	11	52.4	24	10	AD62014	Ad62014 Plasmodiu
C 402	11.2	53.3	37	6	ACN18820	Acn18820 WNV Zinz	475	11	52.4	24	10	ADP5432	Adp5432 Human PRO
C 403	11.2	53.3	37	6	ACN30634	Acn30634 WNV minus	476	11	52.4	24	10	ADP56390	Adp56390 Human PRO
C 404	11.2	53.3	37	6	ACN31064	Acn31064 WNV minus	477	11	52.4	24	10	AD554828	Ad554828 Human PRO
C 405	11.2	53.3	37	6	ACN31914	Acn31914 WNV minus	478	11	52.4	24	10	AD526982	Ad526982 Human PRO
C 406	11.2	53.3	37	6	ACN30941	Acn30941 WNV minus	479	11	52.4	24	10	AD626449	Ad626449 Novel hum
C 407	11.2	53.3	37	6	ACN31346	Acn31346 WNV minus	480	11	52.4	24	10	ADP67386	Adp67386 Human CDN
C 408	11.2	53.3	37	8	ACA08020	Aca08020 Necrosis	481	11	52.4	24	10	ADI35640	Adi35640 Human PRO
C 409	11.2	53.3	37	8	ACA08100	Aca08100 Necrosis	482	11	52.4	24	10	ADI00133	Adi00133 Novel hum
C 410	11.2	53.3	38	6	ABQ72429	Abq72429 PCR prime	483	11	52.4	24	10	ABX78017	Abx78017 Human PRO
C 411	11.2	53.3	38	10	ADC46944	Adc46944 Primer fo	484	11	52.4	24	10	ABX80429	Abx80429 Human sec
C 412	11.2	53.3	40	2	AA787214	Aat87214 Interleuk	485	11	52.4	24	10	ACA69335	Aca69335 Human sec
C 413	11.2	53.3	40	6	AB221788	Ab221788 Human ery	486	11	52.4	24	10	ABX90406	Abx90406 Human PRO
C 414	11.2	53.3	40	6	AB221789	Ab221789 Human ery	487	11	52.4	24	10	ABX90406	Abx90406 Human PRO
C 415	11.2	53.3	45	4	AA313391	Aas13391 Alanine s	488	11	52.4	24	12	ADP35585	Adp35585 Human PRO
C 416	11.2	53.3	50	6	ABZ06239	Abz06239 Human leu	489	11	52.4	24	12	ADG11835	Adg11835 Human PRO
C 417	11	52.4	16	3	AAZ47286	Aaz47286 C-myc pro	490	11	52.4	24	12	ADH19705	Adh19705 Human PRO
C 418	11	52.4	17	2	AAZ75296	Aaz75296 Mouse fit	491	11	52.4	24	12	ADH21198	Adh21198 Human PRO
C 419	11	52.4	17	2	AAZ75297	Aaz75297 Mouse fit	492	11	52.4	24	12	ADH20238	Adh20238 Human PRO
C 420	11	52.4	20	2	AAZ96177	Aaz96177 PCR prime	493	11	52.4	24	12	ADI37421	Adi37421 M. tuberc
C 421	11	52.4	20	3	AAZ72519	Aaz72519 Human bia	494	11	52.4	25	9	ACI74364	Act74364 Human mic
C 422	11	52.4	21	12	ADM92428	Adm92428 Pancreat	495	11	52.4	25	9	ACI31851	Act31851 Human mic
C 423	11	52.4	22	6	AB159233	Ab159233 Antisense	496	11	52.4	25	9	ACI14671	Act14671 Human mic
C 424	11	52.4	22	12	ADP86451	Adp86451 Mouse GAP	497	11	52.4	25	9	ACI190851	Act190851 Human mic
C 425	11	52.4	23	4	AA07923	Aad07923 Human G-P	498	11	52.4	25	9	ACI28866	Act28866 Human mic
C 426	11	52.4	24	2	AAQ2089	Aaq2089 Human rec	499	11	52.4	25	9	ACI04993	Act04993 Human mic
C 427	11	52.4	24	2	AAZ35284	Aaz35284 PCR prime	500	11	52.4	25	9	ACI18687	Act18687 Human mic
C 428	11	52.4	24	2	AAZ58316	Aaz58316 Human PRO	501	11	52.4	25	9	ACI16965	Act16965 Human mic
C 429	11	52.4	24	5	AAAF44420	Aaf44420 Human PRO	502	11	52.4	25	9	ACK00553	Act00553 Human mic
C 430	11	52.4	24	5	AAAF44420	Aaf44420 Human PRO	503	11	52.4	25	9	ACK00553	Act00553 Human mic
C 431	11	52.4	24	6	ABK87485	Abk87485 Synthetic	504	11	52.4	25	9	ACI28682	Act28682 Human mic
C 432	11	52.4	24	6	ABK87486	Abk87486 Synthetic	505	11	52.4	25	9	ACI194261	Act194261 Human mic
C 433	11	52.4	24	6	ABQ03239	Abq03239 Oligonuc	506	11	52.4	25	9	ACK12417	Act12417 Human mic
C 434	11	52.4	24	6	ABQ79141	Abq79141 Primer #1	507	11	52.4	25	9	ACI175267	Act175267 Human mic
C 435	11	52.4	24	8	ACA64474	Aca64474 Novel hum	508	11	52.4	25	9	ACI25752	Act25752 Human mic
C 436	11	52.4	24	8	ABX80933	Abx80933 Human sec	509	11	52.4	25	9	ACI196369	Act196369 Human mic
C 437	11	52.4	24	8	ACD44442	Act44442 Human PRO	510	11	52.4	25	9	ACH64101	Act64101 DNA targe
C 438	11	52.4	24	8	ABX79613	Abx79613 Human sec	511	11	52.4	25	9	ACH64227	Act64227 Streptomy
C 439	11	52.4	24	8	ACA93634	Aca93634 Novel hum	512	11	52.4	25	12	ADL72525	Adl72525 Streptomy
C 440	11	52.4	24	8	ABX81316	Abx81316 Human sec	513	11	52.4	25	12	ADL71141	Adl71141 Streptomy
C 441	11	52.4	24	8	ACA93132	Aca93132 Novel hum	514	11	52.4	28	2	AAQ46856	Aaq46856 Interleuk
C 442	11	52.4	24	8	ABX17216	Abx17216 Human PRO	515	11	52.4	28	6	ABL91518	Ab191518 Chlamydia
C 443	11	52.4	24	9	ACA68071	Aca68071 Novel hum	516	11	52.4	31	4	AAI29879	Aai29879 Human sin
C 444	11	52.4	24	9	ACA88520	Aca88520 Human sec	517	11	52.4	32	3	AAZ99084	Aaz99084 UBQ10 gen
C 445	11	52.4	24	9	ACD82027	Act82027 Human PRO	518	11	52.4	33	3	AAZ64927	Aaz64927 Control R
C 446	11	52.4	24	9	ADA37970	Ada37970 Human PRO	519	11	52.4	33	6	ABX03349	Abx03349 Ribozyme
C 447	11	52.4	24	9	ADA21656	Ada21656 Human sec	520	11	52.4	33	12	ADP84085	Adp84085 Small nuc
C 448	11	52.4	24	9	ADA10443	Ada10443 Human PRO	521	11	52.4	34	10	ADP13553	Adp13553 GPVI gene
C 449	11	52.4	24	9	ADA17987	Ada17987 Human PRO	522	11	52.4	35	6	ABK54214	Abk54214 Pantothan
C 450	11	52.4	24	9	ADA28095	Ada28095 Human PRO	523	11	52.4	35	8	ACA10009	Aca10009 Necrosis
C 451	11	52.4	24	9	ADA94675	Ada94675 Human PRO	524	11	52.4	35	8	ACA10011	Aca10011 Necrosis
C 452	11	52.4	24	9	ADA38900	Ada38900 Human PRO	525	11	52.4	36	2	AAV11874	Aav11874 Synthetic
C 453	11	52.4	24	9	ADA93021	Ada93021 Human PRO	526	11	52.4	36	2	AAV19025	Aav19025 Plasmid p
C 454	11	52.4	24	9	ACH65588	Act65588 Human PRO	527	11	52.4	36	6	ABX01900	Abx01900 HCV hamme
C 455	11	52.4	24	9	ADA22582	Ada22582 Human sec	528	11	52.4	36	6	ABX02596	Abx02596 HCV hamme
C 456	11	52.4	24	9	ACD39578	Act39578 Human PRO	529	11	52.4	36	6	ABX02112	Abx02112 HCV hamme
C 457	11	52.4	24	9	ADA06748	Ada06748 Human sec	530	11	52.4	36	6	ABX02392	Abx02392 HCV hamme
C 458	11	52.4	24	9	ADA39441	Ada39441 Human PRO	531	11	52.4	36	6	ABX02676	Abx02676 HCV hamme
C 459	11	52.4	24	9	ADB96467	Adb96467 Human PRO	532	11	52.4	36	6		

C 533	11	52.4	36	6	ABX02836	Abx02836 HCV hamme	C 606	11	52.4	38	4	ABK05210	Abk05210 Human NOG
C 534	11	52.4	36	6	ABX02270	Abx02270 HCV hamme	C 607	11	52.4	38	4	ABK04785	Abk04785 Human NOG
C 535	11	52.4	36	6	ABX02731	Abx02731 HCV hamme	C 608	11	52.4	38	4	ABK04953	Abk04953 Human NOG
C 536	11	52.4	36	6	ABX02408	Abx02408 HCV hamme	C 609	11	52.4	38	4	ABK05212	Abk05212 Human NOG
C 537	11	52.4	36	6	ABX02198	Abx02198 HCV hamme	C 610	11	52.4	38	4	ABK03884	Abk03884 Human NOG
C 538	11	52.4	36	6	ABX02402	Abx02402 HCV hamme	C 611	11	52.4	38	4	ABK05178	Abk05178 Human NOG
C 539	11	52.4	36	6	ABX02026	Abx02026 HCV hamme	C 612	11	52.4	38	4	ABK08311	Abk08311 Human CD2
C 540	11	52.4	36	6	ABX02602	Abx02602 HCV hamme	C 613	11	52.4	38	4	ABK03825	Abk03825 Human NOG
C 541	11	52.4	36	6	ABX02319	Abx02319 HCV hamme	C 614	11	52.4	38	4	ABK04543	Abk04543 Human NOG
C 542	11	52.4	36	6	ABX01863	Abx01863 HCV hamme	C 615	11	52.4	38	4	ABK05160	Abk05160 Human NOG
C 543	11	52.4	36	6	ABX02404	Abx02404 HCV hamme	C 616	11	52.4	38	4	ABK08344	Abk08344 Human CD2
C 544	11	52.4	36	6	ABX02705	Abx02705 HCV hamme	C 617	11	52.4	38	4	ABK04527	Abk04527 Human NOG
C 545	11	52.4	36	6	ABX02219	Abx02219 HCV hamme	C 618	11	52.4	38	4	ABK04580	Abk04580 Human NOG
C 546	11	52.4	36	8	ACD56262	AcD56262 HBV enzym	C 619	11	52.4	38	4	ABK04691	Abk04691 Human NOG
C 547	11	52.4	36	8	ACD56358	AcD56358 HBV enzym	C 620	11	52.4	38	4	ABK04765	Abk04765 Human NOG
C 548	11	52.4	36	12	ADI59388	Adi59388 Inozyme s	C 621	11	52.4	38	4	ABK08356	Abk08356 Human CD2
C 549	11	52.4	36	12	ADI59408	Adi59408 Inozyme s	C 622	11	52.4	38	4	ABK04566	Abk04566 Human NOG
C 550	11	52.4	36	12	ADI59410	Adi59410 Inozyme s	C 623	11	52.4	38	4	ABK04583	Abk04583 Human NOG
C 551	11	52.4	36	12	ADI59425	Adi59425 Inozyme s	C 624	11	52.4	38	4	ABK04646	Abk04646 Human NOG
C 552	11	52.4	36	12	ADI59437	Adi59437 Inozyme s	C 625	11	52.4	38	4	ABK08260	Abk08260 Human CD2
C 553	11	52.4	36	12	ADI59396	Adi59396 Inozyme s	C 626	11	52.4	38	4	ABK08382	Abk08382 Human CD2
C 554	11	52.4	36	12	ADI59457	Adi59457 Inozyme s	C 627	11	52.4	38	4	ABK05112	Abk05112 Human NOG
C 555	11	52.4	37	3	Az64928	Aaz64928 RPI motif	C 628	11	52.4	38	4	ABK07994	Abk07994 Human CD2
C 556	11	52.4	37	6	ABX03427	Abx03427 Ribozyme	C 629	11	52.4	38	4	ABK08174	Abk08174 Human CD2
C 557	11	52.4	37	6	ABK59352	AbK59352 Human CLC	C 630	11	52.4	38	4	ABK08243	Abk08243 Human CD2
C 558	11	52.4	37	6	ABK59388	AbK59388 Human CLC	C 631	11	52.4	38	4	ABK04529	Abk04529 Human NOG
C 559	11	52.4	37	6	ABK59340	AbK59340 Human CLC	C 632	11	52.4	38	4	ABK04985	Abk04985 Human NOG
C 560	11	52.4	37	6	ACN18985	Acn18985 WNV Zinzy	C 633	11	52.4	38	4	ABK05127	Abk05127 Human NOG
C 561	11	52.4	37	6	ACN18992	Acn18992 WNV Zinzy	C 634	11	52.4	38	4	ABK08277	Abk08277 Human CD2
C 562	11	52.4	37	6	ACN31308	Acn31308 WNV minus	C 635	11	52.4	38	4	ABK08316	Abk08316 Human CD2
C 563	11	52.4	37	6	ACN19493	Acn19493 WNV Zinzy	C 636	11	52.4	38	4	ABK03855	Abk03855 Human NOG
C 564	11	52.4	37	6	ACN19321	Acn19321 WNV Zinzy	C 637	11	52.4	38	4	ABK04698	Abk04698 Human NOG
C 565	11	52.4	37	6	ACN19329	Acn19329 WNV Zinzy	C 638	11	52.4	38	4	ABK04824	Abk04824 Human NOG
C 566	11	52.4	37	6	ACN19323	Acn19323 WNV Zinzy	C 639	11	52.4	38	4	ABK05306	Abk05306 Human NOG
C 567	11	52.4	37	6	ACN19355	Acn19355 WNV Zinzy	C 640	11	52.4	38	4	ABK08435	Abk08435 Human CD2
C 568	11	52.4	37	6	ACN19418	Acn19418 WNV Zinzy	C 641	11	52.4	38	4	ABK04862	Abk04862 Human NOG
C 569	11	52.4	37	6	ACN19889	Acn19889 WNV Zinzy	C 642	11	52.4	38	4	ABK04963	Abk04963 Human NOG
C 570	11	52.4	37	6	ACN31939	Acn31939 WNV minus	C 643	11	52.4	38	4	ABK05042	Abk05042 Human NOG
C 571	11	52.4	37	6	ACN19246	Acn19246 WNV Zinzy	C 644	11	52.4	38	4	ABK08305	Abk08305 Human CD2
C 572	11	52.4	37	6	ACN19519	Acn19519 WNV Zinzy	C 645	11	52.4	38	4	ABL47584	AbL47584 Human GRI
C 573	11	52.4	37	6	ACN37010	Acn37010 WNV enzym	C 646	11	52.4	38	4	ABL47630	AbL47630 Human GRI
C 574	11	52.4	37	6	ACN31978	Acn31978 WNV minus	C 647	11	52.4	38	4	ABL47555	AbL47555 Human GRI
C 575	11	52.4	37	6	ACN31928	Acn31928 WNV minus	C 648	11	52.4	38	4	ABL47620	AbL47620 Human GRI
C 576	11	52.4	37	6	ACN31151	Acn31151 WNV minus	C 649	11	52.4	38	4	ABL47500	AbL47500 Human GRI
C 577	11	52.4	37	6	ACN31700	Acn31700 WNV minus	C 650	11	52.4	38	4	ABL47479	AbL47479 Human GRI
C 578	11	52.4	37	6	ACN30899	Acn30899 WNV minus	C 651	11	52.4	38	4	ABL47551	AbL47551 Human GRI
C 579	11	52.4	37	8	ACA10034	Aca10034 Necrosis	C 652	11	52.4	38	4	ABL47475	AbL47475 Human GRI
C 580	11	52.4	37	8	ACA08160	Aca08160 Necrosis	C 653	11	52.4	38	4	ABL47530	AbL47530 Human GRI
C 581	11	52.4	37	8	ACA08072	Aca08072 Necrosis	C 654	11	52.4	38	6	ABQ72443	AbQ72443 PCR prime
C 582	11	52.4	37	8	ACA10010	Aca10010 Necrosis	C 655	11	52.4	38	6	ABQ72448	AbQ72448 PCR prime
C 583	11	52.4	37	8	ACA07927	Aca07927 Necrosis	C 656	11	52.4	38	6	ABK19546	AbK19546 Human ERG
C 584	11	52.4	37	11	ADL75687	Adl75687 Human PTG	C 657	11	52.4	38	6	ABK20611	AbK20611 Human ERG
C 585	11	52.4	37	11	ADL52737	Adl52737 Human NOG	C 658	11	52.4	38	6	ABK20602	AbK20602 Human ERG
C 586	11	52.4	37	11	ADL54427	Adl54427 Human IKK	C 659	11	52.4	38	6	ABK20586	AbK20586 Human ERG
C 587	11	52.4	37	11	ADL75730	Adl75730 Human PTG	C 660	11	52.4	38	6	ABK20090	AbK20090 Human ERG
C 588	11	52.4	37	11	ADL54222	Adl54222 Human IKK	C 661	11	52.4	38	6	ABK20145	AbK20145 Human ERG
C 589	11	52.4	37	11	ADL73674	Adl73674 Human PKR	C 662	11	52.4	38	6	ABK20145	AbK20145 Human ERG
C 590	11	52.4	37	11	ADL75675	Adl75675 Human PTG	C 663	11	52.4	38	6	ABK20161	AbK20161 Human ERG
C 591	11	52.4	37	12	ADM64239	Adm64239 Hepatitis	C 664	11	52.4	38	6	ABK20303	AbK20303 Human ERG
C 592	11	52.4	37	12	ADM64143	Adm64143 Hepatitis	C 665	11	52.4	38	6	ABK19639	AbK19639 Human ERG
C 593	11	52.4	37	12	ADI92342	Adi92342 Anti-HCV	C 666	11	52.4	38	6	ABK20081	AbK20081 Human ERG
C 594	11	52.4	38	4	AAH96508	Aah96508 Human Chk	C 667	11	52.4	38	6	ABK20415	AbK20415 Human ERG
C 595	11	52.4	38	4	AAH96621	Aah96621 Human Chk	C 668	11	52.4	38	6	ABK20181	AbK20181 Human ERG
C 596	11	52.4	38	4	AAH96520	Aah96520 Human Chk	C 669	11	52.4	38	6	ABK20216	AbK20216 Human ERG
C 597	11	52.4	38	4	AAH96453	Aah96453 Human Chk	C 670	11	52.4	38	6	ABK20559	AbK20559 Human ERG
C 598	11	52.4	38	4	ABK04658	AbK04658 Human NOG	C 671	11	52.4	38	6	ABK19485	AbK19485 Human ERG
C 600	11	52.4	38	4	ABK04965	AbK04965 Human NOG	C 672	11	52.4	38	6	ABK20075	AbK20075 Human ERG
C 601	11	52.4	38	4	ABK05131	AbK05131 Human NOG	C 673	11	52.4	38	6	ABK20275	AbK20275 Human ERG
C 602	11	52.4	38	4	ABK05154	AbK05154 Human NOG	C 674	11	52.4	38	6	ABK20379	AbK20379 Human ERG
C 603	11	52.4	38	4	ABK05066	AbK05066 Human NOG	C 675	11	52.4	38	6	ABK20563	AbK20563 Human ERG
C 604	11	52.4	38	4	ABK05101	AbK05101 Human NOG	C 676	11	52.4	38	6	ABK20267	AbK20267 Human ERG
C 605	11	52.4	38	4	ABK04871	AbK04871 Human NOG	C 677	11	52.4	38	6	ABK20126	AbK20126 Human ERG
							C 678	11	52.4	38	6	ABK20391	AbK20391 Human ERG

C 679	11	52.4	38	6	ABK20483	Abk20483 Human ERG	C 752	11	52.4	38	6	ACN18355	Acn18355 WNV Inozy
C 680	11	52.4	38	6	ABK20593	Abk20593 Human ERG	C 753	11	52.4	38	6	ACN29005	Acn29005 WNV minus
C 681	11	52.4	38	6	ABK20087	Abk20087 Human ERG	C 754	11	52.4	38	6	ACN29142	Acn29142 WNV minus
C 682	11	52.4	38	6	ABK20244	Abk20244 Human ERG	C 755	11	52.4	38	6	ACN30123	Acn30123 WNV minus
C 683	11	52.4	38	6	ABK58122	Abk58122 Human CLC	C 756	11	52.4	38	6	ACN30260	Acn30260 WNV minus
C 684	11	52.4	38	6	ABK58769	Abk58769 Human CLC	C 757	11	52.4	38	6	ACN30315	Acn30315 WNV minus
C 685	11	52.4	38	6	ABK58447	Abk58447 Human CLC	C 758	11	52.4	38	6	ACN16816	Acn16816 WNV Inozy
C 686	11	52.4	38	6	ABK58819	Abk58819 Human CLC	C 759	11	52.4	38	6	ACN17288	Acn17288 WNV Inozy
C 687	11	52.4	38	6	ABK58411	Abk58411 Human CLC	C 760	11	52.4	38	6	ACN18040	Acn18040 WNV Inozy
C 688	11	52.4	38	6	ABK58709	Abk58709 Human CLC	C 761	11	52.4	38	6	ACN27900	Acn27900 WNV minus
C 689	11	52.4	38	6	ABK59011	Abk59011 Human CLC	C 762	11	52.4	38	6	ACN27910	Acn27910 WNV minus
C 690	11	52.4	38	6	ABK58560	Abk58560 Human CLC	C 763	11	52.4	38	6	ACN28558	Acn28558 WNV minus
C 691	11	52.4	38	6	ABK58624	Abk58624 Human CLC	C 764	11	52.4	38	6	ACN29274	Acn29274 WNV minus
C 692	11	52.4	38	6	ABK58913	Abk58913 Human CLC	C 765	11	52.4	38	6	ACN29354	Acn29354 WNV minus
C 693	11	52.4	38	6	ABK58753	Abk58753 Human CLC	C 766	11	52.4	38	6	ACN29399	Acn29399 WNV minus
C 694	11	52.4	38	6	ABK58832	Abk58832 Human CLC	C 767	11	52.4	38	6	ACN29677	Acn29677 WNV minus
C 695	11	52.4	38	6	ABK58832	Abk58832 Human CLC	C 768	11	52.4	38	6	ACN30104	Acn30104 WNV minus
C 696	11	52.4	38	6	ABK58745	Abk58745 Human CLC	C 769	11	52.4	38	6	ACN30273	Acn30273 WNV minus
C 697	11	52.4	38	6	ABK58462	Abk58462 Human CLC	C 770	11	52.4	38	6	ACN16820	Acn16820 WNV Inozy
C 698	11	52.4	38	6	ABK58485	Abk58485 Human CLC	C 771	11	52.4	38	6	ACN17460	Acn17460 WNV Inozy
C 699	11	52.4	38	6	ABK58667	Abk58667 Human CLC	C 772	11	52.4	38	6	ACN18547	Acn18547 WNV Inozy
C 700	11	52.4	38	6	ACN16957	Acn16957 WNV Inozy	C 773	11	52.4	38	6	ACN26565	Acn26565 WNV minus
C 701	11	52.4	38	6	ACN17961	Acn17961 WNV Inozy	C 774	11	52.4	38	6	ACN27006	Acn27006 WNV minus
C 702	11	52.4	38	6	ACN18702	Acn18702 WNV Inozy	C 775	11	52.4	38	6	ACN28084	Acn28084 WNV minus
C 703	11	52.4	38	6	ACN26995	Acn26995 WNV minus	C 776	11	52.4	38	6	ACN28733	Acn28733 WNV minus
C 704	11	52.4	38	6	ACN28105	Acn28105 WNV minus	C 777	11	52.4	38	6	ACN28773	Acn28773 WNV minus
C 705	11	52.4	38	6	ACN28136	Acn28136 WNV minus	C 778	11	52.4	38	6	ACN29740	Acn29740 WNV minus
C 706	11	52.4	38	6	ACN28157	Acn28157 WNV minus	C 779	11	52.4	38	6	ACN30310	Acn30310 WNV minus
C 707	11	52.4	38	6	ACN28240	Acn28240 WNV minus	C 780	11	52.4	38	6	ACN30517	Acn30517 WNV minus
C 708	11	52.4	38	6	ACN28476	Acn28476 WNV minus	C 781	11	52.4	38	6	ACN30588	Acn30588 WNV minus
C 709	11	52.4	38	6	ACN28689	Acn28689 WNV minus	C 782	11	52.4	38	6	ACN15616	Acn15616 WNV Hamme
C 710	11	52.4	38	6	ACN29388	Acn29388 WNV minus	C 783	11	52.4	38	6	ACN15956	Acn15956 WNV Hamme
C 711	11	52.4	38	6	ACN29477	Acn29477 WNV minus	C 784	11	52.4	38	6	ACN17088	Acn17088 WNV Inozy
C 712	11	52.4	38	6	ACN17601	Acn17601 WNV Inozy	C 785	11	52.4	38	6	ACN17550	Acn17550 WNV Inozy
C 713	11	52.4	38	6	ACN18460	Acn18460 WNV Inozy	C 786	11	52.4	38	6	ACN18481	Acn18481 WNV Inozy
C 714	11	52.4	38	6	ACN18571	Acn18571 WNV Inozy	C 787	11	52.4	38	6	ACN28044	Acn28044 WNV minus
C 715	11	52.4	38	6	ACN26148	Acn26148 WNV minus	C 788	11	52.4	38	6	ACN28074	Acn28074 WNV minus
C 716	11	52.4	38	6	ACN26491	Acn26491 WNV minus	C 789	11	52.4	38	6	ACN28260	Acn28260 WNV minus
C 717	11	52.4	38	6	ACN28227	Acn28227 WNV minus	C 790	11	52.4	38	6	ACN28612	Acn28612 WNV minus
C 718	11	52.4	38	6	ACN28248	Acn28248 WNV minus	C 791	11	52.4	38	6	ACN29159	Acn29159 WNV minus
C 719	11	52.4	38	6	ACN28336	Acn28336 WNV minus	C 792	11	52.4	38	6	ACN30301	Acn30301 WNV minus
C 720	11	52.4	38	6	ACN28714	Acn28714 WNV minus	C 793	11	52.4	38	6	ACN15754	Acn15754 WNV Hamme
C 721	11	52.4	38	6	ACN28832	Acn28832 WNV minus	C 794	11	52.4	38	6	ACN15808	Acn15808 WNV Hamme
C 722	11	52.4	38	6	ACN28890	Acn28890 WNV minus	C 795	11	52.4	38	6	ACN17155	Acn17155 WNV Inozy
C 723	11	52.4	38	6	ACN28896	Acn28896 WNV minus	C 796	11	52.4	38	6	ACN27460	Acn27460 WNV minus
C 724	11	52.4	38	6	ACN29186	Acn29186 WNV minus	C 797	11	52.4	38	6	ACN27977	Acn27977 WNV minus
C 725	11	52.4	38	6	ACN29258	Acn29258 WNV minus	C 798	11	52.4	38	6	ACN28190	Acn28190 WNV minus
C 726	11	52.4	38	6	ACN30266	Acn30266 WNV minus	C 799	11	52.4	38	6	ACN28200	Acn28200 WNV minus
C 727	11	52.4	38	6	ACN16287	Acn16287 WNV Hamme	C 800	11	52.4	38	6	ACN28828	Acn28828 WNV minus
C 728	11	52.4	38	6	ACN16916	Acn16916 WNV Inozy	C 801	11	52.4	38	6	ACN28862	Acn28862 WNV minus
C 729	11	52.4	38	6	ACN18442	Acn18442 WNV Inozy	C 802	11	52.4	38	6	ACN29056	Acn29056 WNV minus
C 730	11	52.4	38	6	ACN28317	Acn28317 WNV minus	C 803	11	52.4	38	6	ACN29365	Acn29365 WNV minus
C 731	11	52.4	38	6	ACN28845	Acn28845 WNV minus	C 804	11	52.4	38	6	ACN29395	Acn29395 WNV minus
C 732	11	52.4	38	6	ACN29129	Acn29129 WNV minus	C 805	11	52.4	38	6	ACN30263	Acn30263 WNV minus
C 733	11	52.4	38	6	ACN15795	Acn15795 WNV Hamme	C 806	11	52.4	38	6	ACN30263	Acn30263 WNV minus
C 734	11	52.4	38	6	ACN16946	Acn16946 WNV Inozy	C 807	11	52.4	38	6	ACN17108	Acn17108 WNV Inozy
C 735	11	52.4	38	6	ACN26710	Acn26710 WNV minus	C 808	11	52.4	38	6	ACN17324	Acn17324 WNV Inozy
C 736	11	52.4	38	6	ACN27240	Acn27240 WNV minus	C 809	11	52.4	38	6	ACN17380	Acn17380 WNV Inozy
C 737	11	52.4	38	6	ACN27890	Acn27890 WNV minus	C 810	11	52.4	38	6	ACN17711	Acn17711 WNV Inozy
C 738	11	52.4	38	6	ACN27940	Acn27940 WNV minus	C 811	11	52.4	38	6	ACN17894	Acn17894 WNV Inozy
C 739	11	52.4	38	6	ACN28391	Acn28391 WNV minus	C 812	11	52.4	38	6	ACN18041	Acn18041 WNV Inozy
C 740	11	52.4	38	6	ACN28563	Acn28563 WNV minus	C 813	11	52.4	38	6	ACN27999	Acn27999 WNV minus
C 741	11	52.4	38	6	ACN28588	Acn28588 WNV minus	C 814	11	52.4	38	6	ACN29957	Acn29957 WNV minus
C 742	11	52.4	38	6	ACN28599	Acn28599 WNV minus	C 815	11	52.4	38	6	ACN17485	Acn17485 WNV Inozy
C 743	11	52.4	38	6	ACN29103	Acn29103 WNV minus	C 816	11	52.4	38	6	ACN17578	Acn17578 WNV Inozy
C 744	11	52.4	38	6	ACN29501	Acn29501 WNV minus	C 817	11	52.4	38	6	ACN17764	Acn17764 WNV Inozy
C 745	11	52.4	38	6	ACN30440	Acn30440 WNV minus	C 818	11	52.4	38	6	ACN17937	Acn17937 WNV Inozy
C 746	11	52.4	38	6	ACN16780	Acn16780 WNV Inozy	C 819	11	52.4	38	6	ACN18052	Acn18052 WNV Inozy
C 747	11	52.4	38	6	ACN16875	Acn16875 WNV Inozy	C 820	11	52.4	38	6	ACN18201	Acn18201 WNV Inozy
C 748	11	52.4	38	6	ACN17072	Acn17072 WNV Inozy	C 821	11	52.4	38	6	ACN18216	Acn18216 WNV Inozy
C 749	11	52.4	38	6	ACN17627	Acn17627 WNV Inozy	C 822	11	52.4	38	6	ACN26930	Acn26930 WNV minus
C 750	11	52.4	38	6	ACN17717	Acn17717 WNV Inozy	C 823	11	52.4	38	6	ACN28373	Acn28373 WNV minus
C 751	11	52.4	38	6	ACN17925	Acn17925 WNV Inozy	C 824	11	52.4	38	6	ACN28406	Acn28406 WNV minus
C 751	11	52.4	38	6	ACN18329	Acn18329 WNV Inozy	C 824	11	52.4	38	6	ACN28406	Acn28406 WNV minus

C 825	11	52.4	38	6	ACN28443	ACN28443	WNV minus	C 898	11	52.4	38	8	ACA07471	ACA07471	Necrosis
C 826	11	52.4	38	6	ACN28810	ACN28810	WNV minus	C 899	11	52.4	38	8	ACA07599	ACA07599	Necrosis
C 827	11	52.4	38	6	ACN28885	ACN28885	WNV minus	C 900	11	52.4	38	8	ACA07377	ACA07377	Necrosis
C 828	11	52.4	38	6	ACN29256	ACN29256	WNV minus	C 901	11	52.4	38	8	ACA07332	ACA07332	Necrosis
C 829	11	52.4	38	6	ACN29922	ACN29922	WNV minus	C 902	11	52.4	38	8	ACA07457	ACA07457	Necrosis
C 830	11	52.4	38	6	ACN29953	ACN29953	WNV minus	C 903	11	52.4	38	8	ACA07558	ACA07558	Necrosis
C 831	11	52.4	38	6	ACN30579	ACN30579	WNV minus	C 904	11	52.4	38	8	ACA06952	ACA06952	Necrosis
C 832	11	52.4	38	6	ACN30579	ACN30579	WNV minus	C 905	11	52.4	38	8	ACA06968	ACA06968	Necrosis
C 833	11	52.4	38	6	ACN17136	ACN17136	WNV Inoxy	C 906	11	52.4	38	8	ACA07582	ACA07582	Necrosis
C 834	11	52.4	38	6	ACN17634	ACN17634	WNV Inoxy	C 907	11	52.4	38	8	ACA07274	ACA07274	Necrosis
C 835	11	52.4	38	6	ACN17918	ACN17918	WNV Inoxy	C 908	11	52.4	38	8	ACA07171	ACA07171	Necrosis
C 836	11	52.4	38	6	ACN18044	ACN18044	WNV Inoxy	C 909	11	52.4	38	8	ACA06902	ACA06902	Necrosis
C 837	11	52.4	38	6	ACN18084	ACN18084	WNV Inoxy	C 910	11	52.4	38	8	ACA07132	ACA07132	Necrosis
C 838	11	52.4	38	6	ACN28708	ACN28708	WNV minus	C 911	11	52.4	38	8	ACA07486	ACA07486	Necrosis
C 839	11	52.4	38	6	ACN28738	ACN28738	WNV minus	C 912	11	52.4	38	8	ACA07208	ACA07208	Necrosis
C 840	11	52.4	38	6	ACN28907	ACN28907	WNV minus	C 913	11	52.4	38	8	ACA07211	ACA07211	Necrosis
C 841	11	52.4	38	6	ACN29169	ACN29169	WNV minus	C 914	11	52.4	38	8	ACA07386	ACA07386	Necrosis
C 842	11	52.4	38	6	ACN29180	ACN29180	WNV minus	C 915	11	52.4	38	8	ACA07091	ACA07091	Necrosis
C 843	11	52.4	38	6	ACN29563	ACN29563	WNV minus	C 916	11	52.4	38	8	ACA07247	ACA07247	Necrosis
C 844	11	52.4	38	6	ACN30084	ACN30084	WNV minus	C 917	11	52.4	38	8	ACA07263	ACA07263	Necrosis
C 845	11	52.4	38	6	ACN16310	ACN16310	WNV Hamme	C 918	11	52.4	38	8	ACA07568	ACA07568	Necrosis
C 846	11	52.4	38	6	ACN17199	ACN17199	WNV Inoxy	C 919	11	52.4	38	8	ACD52556	ACD52556	HBV inoxy
C 847	11	52.4	38	6	ACN17556	ACN17556	WNV Inoxy	C 920	11	52.4	38	8	ACD52259	ACD52259	HBV inoxy
C 848	11	52.4	38	6	ACN17661	ACN17661	WNV Inoxy	C 921	11	52.4	38	8	ACD52146	ACD52146	HBV inoxy
C 849	11	52.4	38	6	ACN18473	ACN18473	WNV Inoxy	C 922	11	52.4	38	8	ACD52647	ACD52647	HBV inoxy
C 850	11	52.4	38	6	ACN29017	ACN29017	WNV minus	C 923	11	52.4	38	8	ACD51846	ACD51846	HBV inoxy
C 851	11	52.4	38	6	ACN29109	ACN29109	WNV minus	C 924	11	52.4	38	8	ACD51853	ACD51853	HBV inoxy
C 852	11	52.4	38	6	ACN29662	ACN29662	WNV minus	C 925	11	52.4	38	8	ACD52059	ACD52059	HBV inoxy
C 853	11	52.4	38	6	ACN29849	ACN29849	WNV minus	C 926	11	52.4	38	8	ACD52884	ACD52884	HBV inoxy
C 854	11	52.4	38	6	ACN30114	ACN30114	WNV minus	C 927	11	52.4	38	8	ACD53068	ACD53068	HBV inoxy
C 855	11	52.4	38	6	ACN30291	ACN30291	WNV minus	C 928	11	52.4	38	8	ACD51000	ACD51000	HBV hamme
C 856	11	52.4	38	6	ACN15696	ACN15696	WNV Hamme	C 929	11	52.4	38	8	ACD52977	ACD52977	HBV inoxy
C 857	11	52.4	38	6	ACN16680	ACN16680	WNV Hamme	C 930	11	52.4	38	8	ACD50914	ACD50914	HBV hamme
C 858	11	52.4	38	6	ACN17566	ACN17566	WNV Inoxy	C 931	11	52.4	38	8	ACD51754	ACD51754	HBV inoxy
C 859	11	52.4	38	6	ACN17785	ACN17785	WNV Inoxy	C 932	11	52.4	38	8	ACD52661	ACD52661	HBV inoxy
C 860	11	52.4	38	6	ACN18063	ACN18063	WNV Inoxy	C 933	11	52.4	38	8	ACD50997	ACD50997	HBV hamme
C 861	11	52.4	38	6	ACN18465	ACN18465	WNV Inoxy	C 934	11	52.4	38	8	ACD51642	ACD51642	HBV hamme
C 862	11	52.4	38	6	ACN28121	ACN28121	WNV minus	C 935	11	52.4	38	8	ACD52243	ACD52243	HBV inoxy
C 863	11	52.4	38	6	ACN28284	ACN28284	WNV minus	C 936	11	52.4	38	8	ACD52637	ACD52637	HBV inoxy
C 864	11	52.4	38	6	ACN28574	ACN28574	WNV minus	C 937	11	52.4	38	8	ACD52664	ACD52664	HBV inoxy
C 865	11	52.4	38	6	ACN29324	ACN29324	WNV minus	C 938	11	52.4	38	8	ACD52673	ACD52673	HBV inoxy
C 866	11	52.4	38	6	ACN29616	ACN29616	WNV minus	C 939	11	52.4	38	8	ACD52981	ACD52981	HBV inoxy
C 867	11	52.4	38	6	ACN29697	ACN29697	WNV minus	C 940	11	52.4	38	8	ACD51940	ACD51940	HBV inoxy
C 868	11	52.4	38	6	ACN29765	ACN29765	WNV minus	C 941	11	52.4	38	8	ACD53074	ACD53074	HBV inoxy
C 869	11	52.4	38	6	ACN30340	ACN30340	WNV Hamme	C 942	11	52.4	38	8	ACD52268	ACD52268	HBV inoxy
C 870	11	52.4	38	6	ACN15599	ACN15599	WNV Hamme	C 943	11	52.4	38	8	ACD52343	ACD52343	HBV inoxy
C 871	11	52.4	38	6	ACN17500	ACN17500	WNV Inoxy	C 944	11	52.4	38	8	ACD52959	ACD52959	HBV inoxy
C 872	11	52.4	38	6	ACN17782	ACN17782	WNV Inoxy	C 945	11	52.4	38	8	ACD52460	ACD52460	HBV inoxy
C 873	11	52.4	38	6	ACN28162	ACN28162	WNV minus	C 946	11	52.4	38	8	ACD52646	ACD52646	HBV inoxy
C 874	11	52.4	38	6	ACN28211	ACN28211	WNV minus	C 947	11	52.4	38	8	ACD53152	ACD53152	HBV inoxy
C 875	11	52.4	38	6	ACN28291	ACN28291	WNV minus	C 948	11	52.4	38	8	ACD52548	ACD52548	HBV inoxy
C 876	11	52.4	38	6	ACN29165	ACN29165	WNV minus	C 949	11	52.4	38	8	ACD52775	ACD52775	HBV inoxy
C 877	11	52.4	38	6	ACN30093	ACN30093	WNV minus	C 950	11	52.4	38	8	ACD51858	ACD51858	HBV inoxy
C 878	11	52.4	38	6	ACN30562	ACN30562	WNV minus	C 951	11	52.4	38	8	ACD53141	ACD53141	HBV inoxy
C 879	11	52.4	38	6	ACN15580	ACN15580	WNV Hamme	C 952	11	52.4	38	11	ADL52282	ADL52282	Human NOG
C 880	11	52.4	38	6	ACN17256	ACN17256	WNV Inoxy	C 953	11	52.4	38	11	ADL53719	ADL53719	Human IKK
C 881	11	52.4	38	6	ACN17935	ACN17935	WNV Inoxy	C 954	11	52.4	38	11	ADL53750	ADL53750	Human IKK
C 882	11	52.4	38	6	ACN18449	ACN18449	WNV Inoxy	C 955	11	52.4	38	11	ADL53761	ADL53761	Human IKK
C 883	11	52.4	38	6	ACN18450	ACN18450	WNV Inoxy	C 956	11	52.4	38	11	ADL53913	ADL53913	Human IKK
C 884	11	52.4	38	6	ACN18506	ACN18506	WNV Inoxy	C 957	11	52.4	38	11	ADL54077	ADL54077	Human IKK
C 885	11	52.4	38	6	ACN28560	ACN28560	WNV minus	C 958	11	52.4	38	11	ADL75070	ADL75070	Human PTG
C 886	11	52.4	38	6	ACN28668	ACN28668	WNV minus	C 959	11	52.4	38	11	ADL52399	ADL52399	Human NOG
C 887	11	52.4	38	6	ACN28716	ACN28716	WNV minus	C 960	11	52.4	38	11	ADL74977	ADL74977	Human PTG
C 888	11	52.4	38	6	ACN29218	ACN29218	WNV minus	C 961	11	52.4	38	11	ADL75375	ADL75375	Human PTG
C 889	11	52.4	38	6	ACN29811	ACN29811	WNV minus	C 962	11	52.4	38	11	ADL52036	ADL52036	Human NOG
C 890	11	52.4	38	8	ACA07220	ACA07220	Necrosis	C 963	11	52.4	38	11	ADL52435	ADL52435	Human NOG
C 891	11	52.4	38	8	ACA07476	ACA07476	Necrosis	C 964	11	52.4	38	11	ADL53838	ADL53838	Human IKK
C 892	11	52.4	38	8	ACA07410	ACA07410	Necrosis	C 965	11	52.4	38	11	ADL75222	ADL75222	Human PTG
C 893	11	52.4	38	8	ACA07570	ACA07570	Necrosis	C 966	11	52.4	38	11	ADL52135	ADL52135	Human NOG
C 894	11	52.4	38	8	ACA07379	ACA07379	Necrosis	C 967	11	52.4	38	11	ADL52228	ADL52228	Human NOG
C 895	11	52.4	38	8	ACA06956	ACA06956	Necrosis	C 968	11	52.4	38	11	ADL52407	ADL52407	Human NOG
C 896	11	52.4	38	8	ACA07113	ACA07113	Necrosis	C 969	11	52.4	38	11	ADL53997	ADL53997	Human IKK
C 897	11	52.4	38	8	ACA07319	ACA07319	Necrosis	C 970	11	52.4	38	11	ADL54011	ADL54011	Human IKK

c 971 11 52.4 38 11 ADL54087
 c 972 11 52.4 38 11 ADL53909
 c 973 11 52.4 38 11 ADL53943
 c 974 11 52.4 38 11 ADL54018
 c 975 11 52.4 38 11 ADL54083
 c 976 11 52.4 38 11 ADL54136
 c 977 11 52.4 38 11 ADL56310
 c 978 11 52.4 38 11 ADL52242
 c 979 11 52.4 38 11 ADL52269
 c 980 11 52.4 38 11 ADL53552
 c 981 11 52.4 38 11 ADL54014
 c 982 11 52.4 38 11 ADL53383
 c 983 11 52.4 38 11 ADL52346
 c 984 11 52.4 38 11 ADL56617
 c 985 11 52.4 38 11 ADL75194
 c 986 11 52.4 38 11 ADL75403
 c 987 11 52.4 38 11 ADL52249
 c 988 11 52.4 38 11 ADL53782
 c 989 11 52.4 38 11 ADL54164
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 c 992 11 52.4 38 11 ADL56599
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 c 994 11 52.4 38 11 ADL75390
 c 995 11 52.4 38 11 ADL52144
 c 996 11 52.4 38 11 ADL53775
 c 997 11 52.4 38 11 ADL75487
 c 998 11 52.4 38 11 ADL54016
 c 999 11 52.4 38 11 ADL56557
 c1000 11 52.4 38 11 ADL56601

ALIGNMENTS

RESULT 1
 ACI56056/c
 ID ACI56056 standard; DNA; 25 BP.
 XX
 AC ACI56056;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 56047.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW Genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 XX 15-MAR-2002; 2002US-00098263.
 XX
 XX 16-MAR-2001; 2001US-0276759P.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 XX
 XX Mittmann MP;
 XX
 XX WPI; 2003-567953/53.
 XX
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 XX Southern, Northern or dot-blot hybridization to identify or detect the
 XX sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 56047; 9pp; English.
 XX
 XX The invention discloses a microarray comprising a plurality of nucleic
 XX acid probes including one of 2,018,500 fully defined sequences, or its

CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 67.6%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. NO. 5.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCGCGTACGGTCTAATGAC 19

Db 24 TCGAACACGGTCTAATGAC 6

RESULT 2

AAA16755/c

ID AAA16755 standard; DNA; 29 BP.

AC AAA16755;

DT 16-JUN-2000 (first entry)

DE Human secreted protein clone LL89_3 probe SEQ ID NO:218.

KW Human; secreted protein; immunostimulant; immunosuppressant; virucide;
 KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
 KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
 KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
 KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
 KW connective tissue disease; multiple sclerosis; erythematosis;
 KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KW insulin dependent diabetes mellitus; graft-versus-host-disease;
 KW autoimmune inflammatory eye disease; allergy; hybridisation; probe; ss.

XX Homo sapiens.

XX WO200009552-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 99WO-US018298.

XX 14-AUG-1998; 98US-0096622P.

XX 17-AUG-1998; 98US-0096815P.

XX 04-SEP-1998; 98US-009229P.

XX 23-OCT-1998; 98US-0105368P.

XX 08-JAN-1999; 99US-0115234P.

XX 12-FEB-1999; 99US-011931P.

XX 18-FEB-1999; 99US-0120575P.

XX 30-APR-1999; 99US-0132020P.

XX 11-AUG-1999; 99US-0148424P.

XX (GEMY) GENETICS INST INC.

XX Mittmann MP;
XX WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 88853; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0

Oy 1 TC CGGTACGGTCTTAATGA 18
||| ||| ||| ||| ||| ||| ||| |||
Db 25 TC CGGTACGGTCTTAATGA 8

RESULT 5
ACI88244/C
ID ACI88244 standard; DNA; 25 BP.
XX
XX ACI88244;
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 88235.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
FN US2003104410-A1.
XX
PD 05-JUN-2003.
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (APFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 88235; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0

Qy 1 TC CGGTACGGTCTAATGA 18
||| ||| ||| ||| ||| ||| |||
Db 24 TC CGGTACGGTCTATTGA 7

RESULT 6
AAV61559/c
ID AAV61559 standard; DNA; 35 BP.
XX AAV61559;
AC AAV61559;
DT 08-DEC-1998 (first entry)
DE Adaptor NNNN-CIGSR (+ strand).
KW Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;
KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;
KW internal standard; calibration curve; ss.
XX Synthetic.
OS Mus sp.
XX EP870842-A2.
PN 14-OCT-1998.
PD 07-APR-1998; 98EP-00302726.
XX 07-APR-1997; 97JP-00088495.
PR (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
PA Kato K;
XX

DR WPI; 1998-523164/45.
 XX Determination of gene expression levels - using combinations of different
 PT cDNA samples tagged with different PCR adaptors.
 XX
 PS Example 2; Page 10; 22pp; English.
 XX
 CC The present sequence represents an adaptor which was used in the method
 CC of the invention to determine the amount ratio between a cDNA coding for
 CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney
 CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-
 CC PCR). This method allows gene expression to be quantitatively determined,
 CC and because internal standards are not required to prepare a calibration
 CC curve, it is a quicker and less laborious process
 XX
 SQ Sequence 35 BP; 8 A; 9 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 2; Length 35;
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CGCGTACGGTCTTAATGAC 19
 ||||| ||||| ||||| |||||
 DB 27 CGCGTACGGTCTTAACGAC 10
 RESULT 7
 ACN31831
 ID ACN31831 standard; RNA; 37 BP.
 AC ACN31831;
 XX
 XX 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Zinzyne SEQ ID NO 31847.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 OS West Nile Virus.
 XX
 FN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 24; SEQ ID NO 31847; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 37 BP; 13 A; 7 C; 12 G; 0 T; 5 U; 0 Other;
 Query Match 62.9%; Score 13.2; DB 6; Length 37;
 Best Local Similarity 61.1%; Pred. No. 1.9e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CGCGTACGGTCTTAATGAC 19
 ||||| ||||| ||||| |||||
 DB 18 CGAGUGAGGUCUAUGAC 35
 RESULT 8
 AAV61560
 ID AAV61560 standard; DNA; 39 BP.
 XX
 AC AAV61560;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Adaptor NNNN-CIGSR (- strand).
 XX
 KW Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;
 KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;
 KW internal standard; calibration curve; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 FN EP870842-A2.
 XX
 PD 14-OCT-1998.
 XX
 PF 07-APR-1998; 98EP-00302726.
 XX
 PR 07-APR-1997; 97JP-00088495.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Kato K;
 XX
 DR WPI; 1998-523164/45.
 XX
 PT Determination of gene expression levels - using combinations of different
 PT cDNA samples tagged with different PCR adaptors.
 XX
 PS Example 2; Page 10; 22pp; English.
 XX
 CC The present sequence represents an adaptor which was used in the method
 CC of the invention to determine the amount ratio between a cDNA coding for
 CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney
 CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-
 CC PCR). This method allows gene expression to be quantitatively determined,
 CC and because internal standards are not required to prepare a calibration
 CC curve, it is a quicker and less laborious process
 XX
 SQ Sequence 39 BP; 9 A; 9 C; 9 G; 8 T; 0 U; 4 Other;
 Query Match 62.9%; Score 13.2; DB 2; Length 39;
 Best Local Similarity 83.3%; Pred. No. 2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CGCGTACGGTCTTAATGAC 19
 ||||| ||||| ||||| |||||
 DB 13 CGCGTACGGTCTTAACGAC 30

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RESULT 9
ACI71602
ID ACI71602 standard; DNA; 25 BP.
XX AC
XX ACI71602;
XX AC
XX ACI71602;
XX DT 14-OCT-2003 (first entry)
XX DE
XX DE Human microarray DNA oligonucleotide SEQ ID NO 71593.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX OS
XX PN US2003104410-A1.
XX PN
XX PD 05-JUN-2003.
XX PD
XX PF 15-MAR-2002; 2002US-00098263.
XX PF
XX PR 16-MAR-2001; 2001US-0276759P.
XX PR
XX PA (AFFY-) AFFYMETRIX INC.
XX PA
XX PI Mittmann MP;
XX PI
XX PI
XX DR WPI; 2003-567953/53.
XX DR
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 71593; 9pp; English.
XX PS
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX CC
XX SQ Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
XX SQ
Query Match 61.9%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCTACGGTCTATGACCG 21
   |||||
DB 1 TCTCGTACGGACTACCCACCG 21
   |||||

RESULT 10
ID ACI71017 standard; DNA; 25 BP.
XX AC
XX ACI71017;
XX AC
XX ACI71017;
XX DT 14-OCT-2003 (first entry)
XX DE
XX DE Human microarray DNA oligonucleotide SEQ ID NO 71008.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX OS
XX PN US2003104410-A1.
XX PN
XX PD 05-JUN-2003.
XX PD
XX PF 15-MAR-2002; 2002US-00098263.
XX PF
XX PR 16-MAR-2001; 2001US-0276759P.
XX PR
XX PA (AFFY-) AFFYMETRIX INC.
XX PA
XX PI Mittmann MP;
XX PI
XX PI
XX DR WPI; 2003-567953/53.
XX DR
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 71008; 9pp; English.
XX PS
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX CC
XX SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;
XX SQ
Query Match 61.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGTACGGTCTATGAC 19
   |||||
DB 20 CGTACGGTCACTGAC 5
   |||||

RESULT 11
ID ADD12949 standard; DNA; 30 BP.

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